

=> fil reg; d que l10; fil capl; d que l12
FILE 'REGISTRY' ENTERED AT 10:30:59 ON 06 MAY 2004
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STRUCTURE FILE UPDATES: 4 MAY 2004 HIGHEST RN 679784-15-7
DICTIONARY FILE UPDATES: 4 MAY 2004 HIGHEST RN 679784-15-7

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 6, 2004

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Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

L1 33212 SEA FILE=REGISTRY ABB=ON D.C.D/SQSP
L10 1086 SEA FILE=REGISTRY ABB=ON L1 AND SQL<72

*= any amino acid
had to limit to <72 rather than
<101 because there were too
many answers*

FILE 'CAPLUS' ENTERED AT 10:31:00 ON 06 MAY 2004
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FILE COVERS 1907 - 6 May 2004 VOL 140 ISS 19
FILE LAST UPDATED: 5 May 2004 (20040505/ED)

This file contains CAS Registry Numbers for easy and accurate
substance identification.

'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE

L1 33212 SEA FILE=REGISTRY ABB=ON D.C.D/SQSP
L4 26638 SEA FILE=CAPLUS ABB=ON (SAPOSIN B OR ?ANGIOGEN? OR KAPOSI?)/BI
L5 474421 SEA FILE=CAPLUS ABB=ON CANCER?/OBI OR TUMOR?/OBI OR NEOPLAS?/O
BI
L10 1086 SEA FILE=REGISTRY ABB=ON L1 AND SQL<72
L11 459 SEA FILE=CAPLUS ABB=ON L10
L12 27 SEA FILE=CAPLUS ABB=ON L11(L) (L4 OR L5)

=> d ibib ed abs hitrn 112 1-27

L12 ANSWER 1 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN
 ACCESSION NUMBER: 2004:308357 CAPLUS
 TITLE: Differentially expressed nucleic acids and their
 encoded proteins and their uses for the diagnosis and
 treatment of tumor
 INVENTOR(S): Wu, Thomas D.; Zhang, Zemin; Zhou, Yan
 PATENT ASSIGNEE(S): Genentech, Inc., USA
 SOURCE: PCT Int. Appl., 7273 pp..
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 2
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004030615	A2	20040415	WO 2003-US28547	20030929
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
WO 2004030615	A2	20040415	WO 2003-XA28547	20030929
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.: US 2002-414971P P 20021002
 WO 2003-US28547 A 20030929

ED Entered STN: 15 Apr 2004

AB The present invention provides a large no. of specific cDNA sequences which are upregulated in certain tumor tissues as compared to their normal tissue counterparts and therefore useful for the diagnosis and treatment of tumor in mammals. An expressed sequence tag (EST) DNA database was searched and interesting EST sequences identified by GEPIS (gene expression profiling in silico), a bioinformatics tool that characterizes genes of interest for new cancer therapeutic targets. Using this type of screening bioinformatics, various tumor-assocd. antigenic target (TAT) proteins (and their encoding nucleic acid mols). were identified as being significantly overexpressed in particular type of cancer or certain cancers as compared to other cancers and/or normal non-cancerous tissues. [This abstr. record is one of two records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.]

IT INDEXING IN PROGRESS

L12 ANSWER 2 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN
 ACCESSION NUMBER: 2004:252189 CAPLUS
 DOCUMENT NUMBER: 140:286142
 TITLE: Hybrid polypeptides comprising Ii-key motif and MHC class I or II-presented epitope of antigen, allergen or tumor antigen as vaccines against infection, allergy and cancer
 INVENTOR(S): Humphreys, Robert E.; Xu, Minzhen
 PATENT ASSIGNEE(S): Antigen Express, Inc., USA
 SOURCE: U.S. Pat. Appl. Publ., 90 pp.
 CODEN: USXXCO
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 3
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004058881	A1	20040325	US 2002-253286	20020924
WO 2004030616	A2	20040415	WO 2003-US28574	20030912

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
 RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2002-245871 A 20020917
 US 2002-253286 A 20020924

ED Entered STN: 26 Mar 2004

AB Disclosed is a nucleic acid mol. comprising a first expressible sequence encoding a protein of interest or polypeptide of interest which contains an MHC Class II-presented epitope. In addn., the nucleic acid mol. comprises a second expressible nucleic acid sequence encoding an antigen presentation-enhancing hybrid polypeptide. The antigen presentation enhancing hybrid polypeptide includes the following elements: i) an N-terminal element consisting essentially of 4-16 residues of the mammalian Ii-Key peptide: LRMKLPKPPKPVSKMR and non-N-terminal deletion modifications thereof that retain antigen presentation enhancing activity; ii) a C-terminal element comprising an MHC Class II-presented epitope in the form of a polypeptide or peptidomimetic structure which binds to the antigenic peptide binding site of an MHC class II mol., the MHC Class II-presented epitope being contained in the protein of interest of step a); and iii) an intervening peptidyl structure linking the N-terminal and C-terminal elements of the hybrid, the peptidyl structure having a length of about 20 amino acids or less. Exemplified proteins are allergen: Ara h 1-3, Fel d 1, Phi p 1, Phl p 5a, Bla g 5, and bee venom phospholipase A2; tumor antigen: CEA, CA-125, PSA, gp100, Pmel17, TRP-2, melanoma tyrosinase, MART-1, and Her-2 neu; pathogenic antigen: anthrax toxin lethal factor, anthrax protective antigen, Variola virus B5R protein, and Ebola virus membrane-assocd. protein VP24; and autoantigen: myelin basic protein, proteolipid protein, and myelin-oligodendrocyte glycoprotein precursor.

IT 197171-78-1D, chimeric derivs. 361366-26-9D, chimeric derivs. 676118-99-3
 RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (hybrid polypeptides comprising Ii-key motif and MHC class I or II-presented epitope of antigen, allergen or tumor antigen as vaccines against infection, allergy and cancer)
use Registry # to match citation to sequence (printed at end of search)

L12 ANSWER 3 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN
 ACCESSION NUMBER: 2004:183096 CAPLUS
 DOCUMENT NUMBER: 140:234396
 TITLE: Antibodies and other binding agents specific to
 thrombospondin fragments for diagnosis of cancer and
 other diseases
 INVENTOR(S): Williams, Kevin J.
 PATENT ASSIGNEE(S): USA
 SOURCE: PCT Int. Appl., 76 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004018995	A2	20040304	WO 2003-US26023	20030820
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2004053392	A1	20040318	US 2003-419462	20030421
PRIORITY APPLN. INFO.:			US 2002-405494P	P 20020823
			US 2003-419462	A 20030421
ED Entered STN: 05 Mar 2004				
AB The invention relates to thrombospondin fragments found in plasma, their use or use of portions thereof in diagnostic methods, as method calibrators, method indicators, and as immunogens, and as analytes for methods with substantial clin. utility; and their detection in plasma or other bodily fluids for purpose of diagnostic methods, esp. for cancer. The thrombospondin fragments include fibronectin-binding domain, procollagen homol. region, type 1 and 2 repeats, amino-terminal domain, and heparin-binding domain. The antibodies are useful for diagnosis of cancer, metastasis, renal failure, atopic dermatitis, acute vasculitis, asthma, diabetes mellitus, rheumatoid arthritis, myocardial infarction, inflammatory disease, blood clotting conditions, etc.				
IT 667973-94-6 667973-98-0				
RL: PRP (Properties) (unclaimed protein sequence; antibodies and other binding agents specific to thrombospondin fragments for diagnosis of cancer and other diseases)				

L12 ANSWER 4 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN
 ACCESSION NUMBER: 2004:3460 CAPLUS
 DOCUMENT NUMBER: 140:71000
 TITLE: Serum albumin binding peptides for tumor targeting
 INVENTOR(S): Dennis, Mark S.
 PATENT ASSIGNEE(S): USA
 SOURCE: U.S. Pat. Appl. Publ., 44 pp.
 CODEN: USXXCO
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004001827	A1	20040101	US 2002-186229	20020628

PRIORITY APPLN. INFO.: US 2002-186229 20020628

OTHER SOURCE(S): MARPAT 140:71000

ED Entered STN: 04 Jan 2004

AB Peptide ligands having affinity for serum albumin are useful for tumor targeting. Conjugate mols. comprising a serum albumin binding peptide fused to a biol. active mol. demonstrate modified pharmacokinetic properties as compared with the biol. active mol. alone, including tissue (e.g., tumor) uptake, infiltration, and diffusion. Nude mice bearing HER2-pos. tumors were administered equiv. doses of the 4D5 (IgG), 4D5-H (Fab fusion protein with albumin binding peptide SA06), and the Fab fragment. The normalized plasma concn. of the fusion protein was sustained over time as compared with that of the Fab. Tumors were stained within two hours with the 4D5-H treated animals, with diffuse staining through the tumor present at 24 h post administration.

IT 641621-76-3 641621-81-0 641623-02-1
641623-04-3 641623-05-4 641623-06-5
641623-07-6

RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(serum albumin binding peptide; serum albumin binding peptides for tumor targeting)

L12 ANSWER 5 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2003:1007100 CAPLUS

DOCUMENT NUMBER: 140:58427

TITLE: Membrane-anchored .beta.2 microglobulin covalently linked to MHC class I peptide epitopes for treating cancer and infection

INVENTOR(S): Gross, Gideon; Margalit, Alon

PATENT ASSIGNEE(S): Gavish-Galilee Bio Applications Ltd., Israel

SOURCE: PCT Int. Appl., 86 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003106616	A2	20031224	WO 2003-IL501	20030612

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2002-388273P P 20020612

ED Entered STN: 26 Dec 2003

AB The invention provides a polynucleotide comprising a sequence encoding a polypeptide comprising a .beta.2-microglobulin mol. linked through its carboxyl terminal to a polypeptide stretch that allows the anchorage of the .beta.2-microglobulin mol. to the cell membrane, and through its amino terminal to at least one antigenic peptide comprising a MHC class I

epitope, wherein said antigenic peptide is not related to an autoimmune disease and is preferably derived from a tumor-assocd. antigen or from a pathogenic antigen. Antigen presenting cells, and DNA and cellular vaccines for treatment of cancer and infectious diseases, are also provided.

IT 197171-78-1

RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(membrane-anchored .beta.2 microglobulin covalently linked to MHC class I peptide epitopes for treating **cancer** and infection)

L12 ANSWER 6 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2003:951169 CAPLUS
DOCUMENT NUMBER: 140:3787
TITLE: Mutant fibronectin and tumor metastasis
INVENTOR(S): Wang, Rong-Fu
PATENT ASSIGNEE(S): Baylor College of Medicine, USA
SOURCE: PCT Int. Appl., 137 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003100027	A2	20031204	WO 2003-US16736	20030528
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.:

WO 2003-US16736 20030528

ED Entered STN: 07 Dec 2003

AB The present invention relates to a mutated fibronectin as a class II-restricted tumor antigen recognized by tumor-reactive CD4+ T cells. In a specific embodiment, the mutation in fibronectin is responsible for the loss of FN matrix formation, leading to the enhanced migration of tumor cells. This provides an exemplary important immune target for effective cancer immunotherapy.

IT 197171-78-1

RL: PRP (Properties)
(unclaimed sequence; mutant fibronectin and **tumor** metastasis)

L12 ANSWER 7 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2003:855522 CAPLUS
DOCUMENT NUMBER: 139:346788
TITLE: Human colon and colon cancer-associated proteins, their nucleotide sequences, antibodies, and diagnostic and therapeutic uses
INVENTOR(S): Rosen, Craig A.; Birse, Charles E.
PATENT ASSIGNEE(S): Human Genome Sciences, Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 211 pp., Cont.-in-part of Appl. No. PCT/US00/22157.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003203361	A1	20031030	US 2001-997003	20011130
WO 2001012781	A1	20010222	WO 2000-US22157	20000811

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-148680P P 19990813
WO 2000-US22157 A2 20000811

ED Entered STN: 31 Oct 2003

AB This invention relates to newly identified colon or colon cancer related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "colon or colon cancer antigens", and the use of such colon antigens for detecting disorders of the gastrointestinal system, particularly the presence of colon cancer and colon cancer metastases. This invention relates to colon or colon cancer antigens as well as vectors, host cells, antibodies directed to colon or colon cancer antigens and the recombinant methods and synthetic methods for producing the same. Also provided are diagnostic methods for detecting, treating, preventing and/or prognosing disorders related to the colon, including colon cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of colon or colon cancer antigens of the invention. The present invention further relates to inhibiting the prodn. and function of the polypeptides of the present invention.

IT 618465-04-6, Protein (human clone HCLB047)

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; human colon and colon **cancer**-assocd. proteins, their nucleotide sequences, antibodies, and diagnostic and therapeutic uses)

IT 326813-00-7

RL: PRP (Properties)

(unclaimed sequence; human colon and colon **cancer**-assocd. proteins, their nucleotide sequences, antibodies, and diagnostic and therapeutic uses)

L12 ANSWER 8 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2003:377029 CAPLUS

DOCUMENT NUMBER: 138:400512

TITLE: Nucleic acid and corresponding protein designated 161P2F10B useful in treatment and detection of cancer

INVENTOR(S): Jakobovits, Aya; Raitano, Arthur B.; Faris, Mary; Hubert, Rene S.; Ge, Wangmao; Morrison, Karen Jane Meyrick; Morrison, Robert Kendall; Challita-Eid, Pia M.

PATENT ASSIGNEE(S): Agensys, Inc., USA

SOURCE: PCT Int. Appl., 269 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003040340	A2	20030515	WO 2002-US36002	20021107
WO 2003040340	C2	20030807		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2003191073	A1	20031009	US 2001-5480	20011107
US 2003165505	A1	20030904	US 2002-62109	20020131
WO 2003085081	A2	20031016	WO 2002-US10132	20020401
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
WO 2003085121	A2	20031016	WO 2002-US10220	20020401
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2003206905	A1	20031106	US 2002-291241	20021107
PRIORITY APPLN. INFO.:				
			US 2001-5480	A 20011107
			US 2002-62109	A 20020131

ED Entered STN: 16 May 2003

AB A novel gene 0161P2F10B (also designated 161P2F10B) and its encoded protein, and variants thereof, are described wherein 161P2F10B exhibits tissue-specific expression in normal adult tissue, and is aberrantly over-expressed in several cancers. Consequently, 161P2F10B provides a diagnostic, prognostic, prophylactic and/or therapeutic target for cancer. The 161P2F10B gene is 100% identical to a previously cloned and sequenced gene, namely ectonucleotide pyrophosphatase/phosphodiesterase 3, also known as phosphodiesterase-I.beta., gp130RB13-6, E-NNP3 (ENPP3), PDNP3, and DC203c. The 161P2F10B gene of fragment thereof, or its encoded protein, or variants thereof, or a fragment thereof, can be used to elicit a humoral or cellular immune response; antibodies or T cells reactive with 161P2F10B can be used in active or passive immunization.

IT 525539-87-1 525540-40-3 525540-43-6
 525540-47-0 525541-62-2 525541-65-5 52554
 1-66-6 525541-68-8 525543-47-9
 525544-74-5 525546-66-1 525546-75-2
 525547-98-2 525549-64-8 525550-83-8
 525551-78-4 525554-65-8 525555-14-0
 525555-15-1 525555-16-2 525555-17-3
 525555-18-4 525555-19-5 525555-20-8
 525555-36-6 525555-43-5 525555-89-9
 525555-90-2 525555-93-5 525556-16-5

525556-17-6 525557-34-0

RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(epitope peptide; nucleic acid and corresponding protein designated 161P2F10B useful in treatment and detection of **cancer**)

IT 528836-21-7 528836-22-8 528836-23-9

528836-24-0 528836-25-1

RL: PRP (Properties)

(unclaimed sequence; nucleic acid and corresponding protein designated 161P2F10B useful in treatment and detection of **cancer**)

L12 ANSWER 9 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2003:1208 CAPLUS

DOCUMENT NUMBER: 138:66666

TITLE: Inhibitors of angiogenesis and tumor growth

INVENTOR(S): Gill, Parkash S.

PATENT ASSIGNEE(S): University of Southern California, USA

SOURCE: U.S., 48 pp., Cont.-in-part of U.S. Provisional Ser. No. 92,647.

CODEN: USXXAM

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6500431	B1	20021231	US 1999-352548	19990712
PRIORITY APPLN. INFO.:			US 1998-92647P	P 19980713

ED Entered STN: 02 Jan 2003

AB This invention provides for polypeptides that have surprising anti-angiogenic activity. These peptides are derived from Saposin B, a previously known protein involved in the hydrolysis of sphingolipids. In addn., methods of treating mammals with these anti-angiogenic polypeptides are provided, as well as the pharmaceutical compns. to be used. Furthermore, the polypeptides of this invention can be used in fusion proteins, wherein the fusion proteins also comprise cell targeting or cytotoxic moieties. Also provided is the receptor to which these polypeptides bind.

IT 480474-30-4 480474-31-5 480474-32-6

480474-33-7 480474-34-8 480474-35-9

480474-36-0 480474-37-1 480474-38-2

480474-39-3 480474-40-6 480474-41-7

480474-42-8 480474-43-9 481111-14-2

RL: PRP (Properties)

(unclaimed protein sequence; inhibitors of **angiogenesis** and **tumor** growth)

IT 255365-72-1 255365-80-1 255365-83-4

255365-84-5 255365-85-6 255365-86-7

255365-87-8 255365-92-5 255365-94-7

255365-95-8 255365-96-9 255365-97-0

255365-98-1 255365-99-2 480433-06-5

RL: PRP (Properties)

(unclaimed sequence; inhibitors of **angiogenesis** and **tumor** growth)

REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 10 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:906465 CAPLUS

DOCUMENT NUMBER: 138:12774

TITLE: BTF3: an inhibitor of apoptosis in *Cenorhabditis elegans*, its uses in modulating programmed cell death

and cancer therapy
 INVENTOR(S): Rothman, Joel H.; Bloss, Tim; Witze, Eric
 PATENT ASSIGNEE(S): The Regents of the University of California, USA
 SOURCE: PCT Int. Appl., 84 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002095001	A2	20021128	WO 2002-US16230	20020521
WO 2002095001	A3	20040129		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
 RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2003004124	A1	20030102	US 2002-153344	20020521
			US 2001-292559P	P 20010521

PRIORITY APPLN. INFO.:

ED Entered STN: 29 Nov 2002

AB This invention pertains to the discovery that *Cenorhabditis elegans* BTF3 plays a crit., neg.- regulatory role in programmed cell death (PCD) in *C. elegans* and other species. Overexpression of BTF3 leads to decreased programmed cell death, while inactivation of BTF3 leads to increased programmed cell death. Methods of modulating (upregulating or downregulating) programmed cell death by increasing or decreasing expression and/or activity of BTF3 are provided. These methods are useful in the treatment of various pathologies including, but not limited to cancer and neurodegenerative diseases.

IT 477519-67-8

RL: PRP (Properties)

(unclaimed sequence; bTF3, an inhibitor of apoptosis in *Cenorhabditis elegans*, its uses in modulating programmed cell death and cancer therapy)

L12 ANSWER 11 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:658227 CAPLUS

DOCUMENT NUMBER: 137:196748

TITLE: Protein and cDNA sequences of novel human breast-specific genes and proteins and their use for cancer diagnosis, drug screening, and vaccines

INVENTOR(S): Salceda, Susana; Macina, Roberto A.; Hu, Ping; Recipon, Herve; Karra, Kalpana; Cafferkey, Robert; Sun, Yongming; Liu, Chenghua

PATENT ASSIGNEE(S): Diadexus, Inc., USA

SOURCE: PCT Int. Appl., 254 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002066605	A2	20020829	WO 2002-US4284	20020214
WO 2002066605	A3	20021107		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,

CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,
TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,
BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2003044815 A1 20030306 US 2002-78090 20020214

PRIORITY APPLN. INFO.:

US 2001-268999P P 20010215

ED Entered STN: 30 Aug 2002

AB The present invention provides sequences of 115 newly identified nucleic acids and 95 proteins present in normal and neoplastic breast cells, including fragments, variants and derivs. of the nucleic acids and polypeptides. The present invention also relates to antibodies to the polypeptides of the invention, as well as agonists and antagonists of the polypeptides of the invention. The invention also relates to compns. comprising the nucleic acids, polypeptides, antibodies, variants, derivs., agonists and antagonists of the invention and methods for the use of these compns. These uses include identifying, diagnosing, monitoring, staging, imaging and treating breast cancer and non-cancerous disease states in breast tissue, identifying breast tissue, monitoring and identifying and/or designing agonists and antagonists of polypeptides of the invention. The uses also include gene therapy, prodn. of transgenic animals and cells, and prodn. of engineered breast tissue for treatment and research.

IT 452381-07-6P

RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified);
DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL
(Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; protein and cDNA sequences of novel human
breast-specific genes and proteins and their use for **cancer**
diagnosis, drug screening, and vaccines)

L12 ANSWER 12 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:444531 CAPLUS

DOCUMENT NUMBER: 137:17034

TITLE: cDNA encoding mouse, guinea pig or human eotaxin and
its use in treatment of inflammation and tumorigenesis

INVENTOR(S): Luster, Andrew D.; Leder, Philip; Rothenberg, Marc;
Garcia, Eduardo

PATENT ASSIGNEE(S): President and Fellows of Harvard College, USA; The
General Hospital Corporation

SOURCE: U.S., 42 pp., Cont. of U.S. Ser. No. 522,713,
abandoned.

CODEN: USXXAM

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6403782	B1	20020611	US 1999-366887	19990804
PRIORITY APPLN. INFO.:			US 1995-449P	P 19950622
			US 1995-522713	B1 19950901

ED Entered STN: 13 Jun 2002

AB Disclosed is substantially pure eotaxin DNA sequence and eotaxin polypeptide, and methods of using such DNA and polypeptide to direct chemotaxis of eosinophils. Methods are provided for the treatment diseases and disorders such as inflammation and tumorigenesis. Sequences of mouse, guinea pig and human eotaxin are provided.

IT 434530-02-6

RL: PRP (Properties)

(unclaimed protein sequence; cDNA encoding mouse, guinea pig or human eotaxin and its use in treatment of inflammation and tumorigenesis)

REFERENCE COUNT: 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 13 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:353300 CAPLUS

DOCUMENT NUMBER: 136:368444

TITLE: Polynucleotides expressing fusion protein of human .beta.2 microglobulin and cancer or non-cancer epitopes for cancer therapy

INVENTOR(S): Tafuro, Sabrina; Meier, Ute-Christiane; McMichael, Andrew James; Bell, John Irving; Layton, Guy; Hunter, Michael

PATENT ASSIGNEE(S): Isis Innovation Limited, UK

SOURCE: PCT Int. Appl., 46 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002036146	A2	20020510	WO 2001-GB4844	20011101
WO 2002036146	A3	20021017		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

AU 2002012472 A5 20020515 AU 2002-12472 20011101

EP 1330259 A2 20030730 EP 2001-980679 20011101

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

PRIORITY APPLN. INFO.: GB 2000-26812 A 20001102
WO 2001-GB4844 W 20011101

ED Entered STN: 12 May 2002

AB The present invention relates to polynucleotides for use in cancer therapy. In particular, the invention provides a polynucleotide capable of expressing an epitope-.beta.2m fusion protein; for use in the generation of cytotoxic T lymphocyte (CTL) responses against a tumor; and a polynucleotide capable of expressing an epitope-.beta.2m fusion protein; for use in a method of restoring antigen presentation in the tumor of a host. The epitope is derived from latent membrane protein, EBNA-3C antigen, BZLF1 or BMLF1 of Epstein-Barr virus; lower matrix protein pp65 of cytomegalovirus; nucleoprotein or matrix protein of influenza; and tumor antigens of human.

IT 197171-78-1

RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(polynucleotides expressing fusion protein of human .beta.2 microglobulin and **cancer** or non-**cancer** epitopes for **cancer** therapy)

L12 ANSWER 14 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:352368 CAPLUS
 DOCUMENT NUMBER: 137:183364
 TITLE: The XAGE family of cancer/testis-associated genes: alignment and expression profile in normal tissues, melanoma lesions and Ewing's sarcoma
 AUTHOR(S): Zendman, Albert J. W.; Van Kraats, Annemieke A.; Weidle, Ulrich H.; Ruiter, Dirk J.; Van Muijen, Goos N. P.
 CORPORATE SOURCE: Department of Pathology, University Medical Center St. Radboud, Nijmegen, 6500 HB, Neth.
 SOURCE: International Journal of Cancer (2002), 99(3), 361-369
 CODEN: IJCNAW; ISSN: 0020-7136
 PUBLISHER: Wiley-Liss, Inc.
 DOCUMENT TYPE: Journal
 LANGUAGE: English

ED Entered STN: 12 May 2002

AB The existence of XAGE genes was first reported after database homol. searches for PAGE-like sequences identified 3 XAGE EST clusters. One of these clusters, XAGE-1, has in later studies been identified as a cancer/testis-assocd. gene. Here, we report the expression profiles of all 3 reported XAGE genes, as well as several splice variants of XAGE-1, in normal human tissues, Ewing's sarcoma and melanocytic tumors. We also provide the genetic structure of the corresponding genes. Moreover, by searching the databases for XAGE homologues, we identified 3 addnl. GAGE-like genes. RT-PCR studies showed frequent expression in melanoma metastases and Ewing's sarcoma for 2 XAGE-1-derived transcripts. XAGE-2 was expressed at lower frequency in these tissues, while XAGE-3 was seen only in normal placenta. Due to a frameshift, the largest XAGE-1 putative protein is far less homologous to GAGE-like proteins than the other XAGEs. Interestingly, all GAGE-like genes contain a large secondary open reading frame, coding for putative proteins homologues to the XAGE-1 primary protein. The XAGE family of cancer/testis-assocd. genes is located on chromosome Xp11.21-Xp11.22. The data outline a superfamily of GAGE-like cancer/testis antigens, consisting of at least 19 genes.

IT 449815-87-6, Protein (human gene XAGE-4 fragment)
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; XAGE family of cancer/testis-assocd. genes, alignment and expression profile in normal tissues, melanoma lesions and Ewing's sarcoma)

REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 15 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:256317 CAPLUS
 DOCUMENT NUMBER: 136:277467
 TITLE: Neuroblastoma tumor suppressor genes associated with a translocation between human chromosomes 1 and 17
 INVENTOR(S): Van Roy, Frans; Speleman, Frank
 PATENT ASSIGNEE(S): Vlaams Interuniversitair Instituut voor Biotechnologie, Belg.
 SOURCE: PCT Int. Appl., 352 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002026815	A2	20020404	WO 2001-EP11199	20010927
WO 2002026815	A3	20030619		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,

CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL,
PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,
US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

AU 2002023568 A5 20020408 AU 2002-23568 20010927
EP 1339841 A2 20030903 EP 2001-985712 20010927

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

PRIORITY APPLN. INFO.:

EP 2000-870219 A 20000927
WO 2001-EP11199 W 20010927

ED Entered STN: 05 Apr 2002

AB The present invention relates to a new tumor suppressor gene family (NBG) assocd. with a translocation between chromosomes 1 and 17. More specifically the present invention relates to a tumor suppressor involved in suppression of neuroblastoma. Said tumor suppressor is involved in the generation of micronuclei and in the removal of acentric chromosomal fragments that might contain amplified DNA. The gene was identified by cloning the breakpoint region and genome walking PCR. Alternative splicing is used to generate a large no. of variant gene products. The protein is found predominantly in the cytoplasm and expression of the gene at high levels induces the formation of micronuclei.

IT 406618-33-5 406618-34-6 406618-35-7
406618-36-8

RL: PRP (Properties)

(unclaimed sequence; neuroblastoma tumor suppressor genes
assocd. with a translocation between human chromosomes 1 and 17)

L12 ANSWER 16 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:185155 CAPLUS

DOCUMENT NUMBER: 136:246382

TITLE: Novel human cancer-testis antigen and gene for cancer diagnosis/therapy and screening of immunostimulant and immunosuppressant

INVENTOR(S): Takimoto, Masato; Kuzumaki, Noboru; Sato, Noriyuki;
Sahara, Hiroeki

PATENT ASSIGNEE(S): Japan Science and Technology Corporation, Japan

SOURCE: PCT Int. Appl., 151 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: Japanese

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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WO 2002020560	A1	20020314	WO 2001-JP7784	20010907
W: CA, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR				
JP 2002085071	A2	20020326	JP 2000-274218	20000908
EP 1316560	A1	20030604	EP 2001-963516	20010907
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR				

US 2004029197 A1 20040212 US 2003-363791 20030307

PRIORITY APPLN. INFO.:

JP 2000-274218 A 20000908
WO 2001-JP7784 W 20010907

ED Entered STN: 15 Mar 2002

AB Disclosed is a cancer-testis antigen applicable to the diagnosis and immunotherapy for cancer, namely, a cancer-testis antigen which is not

expressed in normal tissues except testis but expressed in various cancers over a broad range and thus induces an immune reaction in a host; a cancer-testis gene encoding the same, etc. By using a yeast two-hybrid system, proteins and peptides that bind specifically to GCF (GC element binding factor), which has been reported as a transcriptional regulatory factor, are screened. Then a gene of this protein specifically binding to GCF is cloned. It is confirmed that protein D40, which is the gene product thereof, is a cancer-testis antigen not substantially expressed in human normal tissues except testis but is expressed in human primary cancers originating in various tissues and cells. Further, it is found out that D40 has a high affinity for HLAs and has a sequence consisting of 9 or 10 amino acid residues binding to a plural no. of HLAs. D40 protein, D40-derived HLA class I-binding peptides, fusion proteins, and antibodies are useful for cancer diagnosis and therapy, as well as screening of immunostimulant and immunosuppressant.

IT 404387-68-4

RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (human D40 protein or **cancer**-testis antigen and gene for **cancer** diagnosis/therapy and screening of immunostimulant and immunosuppressant)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 17 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2001:687367 CAPLUS

DOCUMENT NUMBER: 135:251951

TITLE: Cancer diagnosis and therapy based on mutations in TGF-.beta. receptors

INVENTOR(S): Markowitz, Sanford D.; Brattain, Michael G.; Willson, James K. V.

PATENT ASSIGNEE(S): Case Western Reserve University, USA; Medical College of Ohio

SOURCE: U.S., 30 pp., Cont.-in-part of U.S. 5,866,323.

CODEN: USXXAM

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6291237	B1	20010918	US 1999-239864	19990129
US 5866323	A	19990202	US 1995-445520	19950522
US 2002064786	A1	20020530	US 2001-878905	20010613
US 6630326	B2	20031007		
US 2004038284	A1	20040226	US 2003-646640	20030821
PRIORITY APPLN. INFO.:			US 1995-417867	B2 19950407
			US 1995-445520	A2 19950522
			US 1999-239864	A3 19990129
			US 2001-878905	A3 20010613

ED Entered STN: 20 Sep 2001

AB This invention is based on the discovery that the type II TGF.beta. receptor (RII) is a cancer suppressor gene which is genetically inactivated (mutated) in approx. 25 of colon cancers, including nearly all colon cancers of the class identified as mutator/microsatellite instability/RER. It is another object of this invention to provide a nucleotide sequence encoding a mutant form of human RII, to provide mutant RII protein and to provide antibodies specifically immunoreactive with mutant RII. Methods are provided for detecting inactivation of RII for use in cancer diagnosis or prognosis.

IT 183815-68-1

RL: PRP (Properties)

(unclaimed protein sequence; **cancer** diagnosis and therapy
based on mutations in TGF-.beta. receptors)

REFERENCE COUNT: 97 THERE ARE 97 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 18 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2001:265449 CAPLUS

DOCUMENT NUMBER: 134:290398

TITLE: Improved ricin-like toxins for treatment of cancer

INVENTOR(S): Braun, Curtis; Purac, Admir; Borgford, Thor

PATENT ASSIGNEE(S): Twinstrand Therapeutics Inc., Can.

SOURCE: PCT Int. Appl., 146 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001025267	A2	20010412	WO 2000-CA1162	20001004
WO 2001025267	A3	20020328		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,
YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ,
CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-157807P P 19991004
US 2000-197409P P 20000414

ED Entered STN: 13 Apr 2001

AB The present invention provides a protein having an A chain of a ricin-like toxin, a B chain of a ricin-like toxin and a novel heterologous linker amino acid sequence, linking the A and B chains. The linker sequence contains a cleavage recognition site for a specific protease such as those found in inflammatory cells and cancer cells. The invention also relates to a nucleic acid mol. encoding the protein and to expression vectors incorporating the nucleic acid mol. Also provided is a method of inhibiting or destroying cells having a specific protease, such as cancer cells or inflammatory cells utilizing the nucleic acid mols. and proteins of the invention and pharmaceutical compns. for treating human inflammation and cancer.

IT 334660-11-6 334660-13-8 334660-22-9

RL: PRP (Properties)

(amino acid sequence; improved ricin-like toxins for treatment of
cancer)

L12 ANSWER 19 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2001:247459 CAPLUS

DOCUMENT NUMBER: 134:294083

TITLE: Characterization and diagnostic and therapeutic uses
of cancer-associated membrane type serine protease 1
(MT-SP1)

INVENTOR(S): Craik, Charles S.; Takeuchi, Toshihiko; Shuman, Marc

PATENT ASSIGNEE(S): The Regents of the University of California, USA

SOURCE: PCT Int. Appl., 102 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001023524	A2	20010405	WO 2000-US27250	20001002
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 2000079913	A5	20010430	AU 2000-79913	20001002
PRIORITY APPLN. INFO.:			US 1999-410362	A 19990930
			WO 2000-US27250	W 20001002

ED Entered STN: 06 Apr 2001

AB This invention provides cDNA and encoded amino acid sequences of a novel membrane-type serine protease (designated MT-SP1) elevated expression of which is assocd. with cancer. In one embodiment, this invention provides a method obtaining a prognosis or of detecting or staging a cancer in an organism. The method involves providing a biol. sample from the organism and detecting the level of a membrane-type serine protease 1 (MT-SP1) in the sample, where an elevated level of the membrane-type serine protease, as compared to the level of the protease in a biol. sample from a normal healthy organism indicates the presence or stage of the cancer.

IT **334490-78-7**
 RL: PRP (Properties)
 (unclaimed sequence; characterization and diagnostic and therapeutic uses of **cancer**-assocd. membrane type serine protease 1 (MT-SP1))

L12 ANSWER 20 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2001:137346 CAPLUS

DOCUMENT NUMBER: 134:191834

TITLE: Genes expressed in normal human colon and in colon cancer and their associated proteins

INVENTOR(S): Birse, Charles E.; Rosen, Craig A.

PATENT ASSIGNEE(S): Human Genome Sciences, Inc., USA

SOURCE: PCT Int. Appl., 330 pp.
 CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001012781	A1	20010222	WO 2000-US22157	20000811
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1208191	A1	20020529	EP 2000-959224	20000811
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				
JP 2003507033	T2	20030225	JP 2001-517666	20000811

US 2003203361 A1 20031030 US 2001-997003 20011130
 PRIORITY APPLN. INFO.: US 1999-148680P P 19990813
 WO 2000-US22157 W 20000811

ED Entered STN: 25 Feb 2001

AB This invention relates to newly identified colon or colon cancer related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "colon cancer antigens", and the use of such colon antigens for detecting disorders of the gastrointestinal system, particularly the presence of colon cancer and colon cancer metastases. This invention relates to colon cancer antigens as well as vectors, host cells, antibodies directed to colon cancer antigens and the recombinant methods and synthetic methods for producing the same. Also provided are diagnostic methods for detecting, treating, preventing and/or in prognosis of disorders related to the colon, including colon cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of colon cancer antigens of the invention. The present invention further relates to inhibiting the prodn. and function of the polypeptides of the present invention. Possible assignment of functions to gene products using sequence homol. is discussed.

IT 326893-82-7

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)

(amino acid sequence; genes expressed in normal human colon and in colon **cancer** and their assocd. proteins)

IT 326813-00-7

RL: PRP (Properties)

(unclaimed sequence; genes expressed in normal human colon and in colon **cancer** and their assocd. proteins)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 21 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2000:645893 CAPLUS

DOCUMENT NUMBER: 133:234748

TITLE: Matriptase, a serine protease and its applications in detection of breast or other cancers

INVENTOR(S): Dickson, Robert B.; Lin, Chen-Yong; Johnson, Michael; Wang, Shaomeng; Enyedy, Istvan

PATENT ASSIGNEE(S): Georgetown University, USA

SOURCE: PCT Int. Appl., 116 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000053232	A1	20000914	WO 2000-US6111	20000310
W: CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 1161266	A1	20011212	EP 2000-914875	20000310
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002539093	T2	20021119	JP 2000-603721	20000310
PRIORITY APPLN. INFO.:				
US 1999-124006P P 19990312				
WO 2000-US6111 W 20000310				

ED Entered STN: 15 Sep 2000

AB The invention is directed to a method of detecting a malignancy or a pre-malignant lesion in breast or other tissue, or a pathol. condition, by

detecting the presence of single-chain or two-chain forms of matriptase in the tissue. The invention is further directed to a method of treating malignancies, which have the phenotype of matriptase prodn. by administering a tumor formation inhibiting effective amt. of a conc. of Bowman-Birk inhibitor (BBIC), or other matriptase inhibitor. The invention also is directed to nucleic acids encoding a matriptase protein or fragments thereof, and their use for structure elucidation and modeling to identify other inhibitors of matriptase, as well as to methods of identifying matriptase modulating agents, including activators and inhibitors.

IT 293307-71-8

RL: PRP (Properties)

(unclaimed protein sequence; matriptase, a serine protease and its applications in detection of breast or other **cancers**)

REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 22 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2000:53678 CAPLUS

DOCUMENT NUMBER: 132:102830

TITLE: Saposin B polypeptides as novel inhibitors of angiogenesis and tumor growth

INVENTOR(S): Gill, Parkash S.

PATENT ASSIGNEE(S): USA

SOURCE: PCT Int. Appl., 78 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000002902	A1	20000120	WO 1999-US15772	19990712
W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
CA 2337438	AA	20000120	CA 1999-2337438	19990712
AU 9950979	A1	20000201	AU 1999-50979	19990712
EP 1097165	A1	20010509	EP 1999-935517	19990712
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
JP 2002530273	T2	20020917	JP 2000-559131	19990712
PRIORITY APPLN. INFO.:			US 1998-92647P P	19980713
			WO 1999-US15772 W	19990712

ED Entered STN: 23 Jan 2000

AB This invention provides for polypeptides derived from Saposin B, a previously known protein involved in the hydrolysis of sphingolipids, that have surprising anti-angiogenic activity. In addn., methods of treating mammals with these anti-angiogenic polypeptides are provided, as well as the pharmaceutical compns. used. Furthermore, the polypeptides of this invention can be used in fusion proteins, wherein the fusion proteins also comprise cell targeting or cytotoxic moieties. Also provided is the receptor to which these polypeptides bind. For example, a dose-dependent inhibition of tumor growth was obsd. in nude mice injected with 2x10⁶ KS-SLK or KS-Y-1 cells and treated after one week of tumor development by s.c. Saposin B (1, 10, and 20 .mu.g/kg for a total protein concn. of 100

.mu.g/kg body wt.). Saposin B had no effect on the growth of these cells. In further expts., KS tumors were allowed to grow for 5 days before treatment with Saposin B (1 and 5 mg/kg daily at a distal site from the tumor). Inhibition of tumor growth was obsd. in Saposin B-treated mice with wts. of excised tumors being approx. 23% that of the controls. Saposin B-treated tumors showed an increase in apoptosis and decrease in blood vessel d.

IT 255365-72-1 255365-78-7 255365-80-1
255365-83-4 255365-84-5 255365-85-6
255365-86-7 255365-87-8 255365-92-5
255365-94-7 255365-95-8 255365-96-9
255365-97-0 255365-98-1 255365-99-2

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(polypeptides of **Saposin B** as inhibitors of **angiogenesis** and **tumor** growth)

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 23 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1999:511060 CAPLUS

DOCUMENT NUMBER: 131:155368

TITLE: Targeting immunoreagents useful in therapeutic and diagnostic compositions and methods

INVENTOR(S): Snow, Robert A.; Delecki, Daniel J.; Shah, Chandra; Black, Christopher; Wolfe, Henry

PATENT ASSIGNEE(S): Nycomed Imaging As, Norway; Matthews, Derek Peter

SOURCE: PCT Int. Appl., 79 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9939748	A1	19990812	WO 1999-GB396	19990208
W:	AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
AU 9925301	A1	19990823	AU 1999-25301	19990208
PRIORITY APPLN. INFO.:			US 1998-20233	19980206
			WO 1999-GB396	19990208

OTHER SOURCE(S): MARPAT 131:155368

ED Entered STN: 18 Aug 1999

AB A targeting immunoreagent comprising a metal ion, a residue of a complexing agent and an immunoreactive group linked to said complexing agent having structure (I), wherein each R and R1 is independently selected from hydrogen, alkyl, alkoxy, hydroxyalkyl, alkoxyalkyl, hydroxyalkyloxy, alkoxyalkyloxy, alkylthio, alkylthioalkyl, alkylthioalkyloxy, hydroxyalkylthio, hydroxyalkylthioalkyl, hydroxyalkylthioalkyloxy, N,N--dialkylamino, N-(hydroxyalkyl)-N-alkylamino, N,N--bis(hydroxyalkyl)amino, N,N-dialkylaminoalkyl, N--(hydroxyalkyl)-N-alkylaminoalkyl, N-N-bis(hydroxyalkyloaminoalkyl), alkylformamido, formamidoalkyl, aryl, alkylaryl, alkoxyaryl, hydroxyalkylaryl, alkoxyalkylaryl, hydroxyalkyloxyaryl, alkoxyalkyloxyaryl, alkylthioaryl, hydroxyalkylthioaryl,

hydroxyalkylthioalkylaryl, hydroxyalkylthioalkyloxyaryl, aralkyl, aralkyloxy, alkoxyaralkyl, alkoxyaralkyloxy, aryloxy, alkylarylaxyl, alkoxyaryloxy, and heterocyclyl; each Q is independently selected from hydrogen, alkyl, hydroxyl, carboxyl, carboxyalkyl, hydroxyalkyl, alkylthioalkyl, sulfhydryl, thioalkyl, alkoxy, alkylthio, alkylamino, aminoalkyl, aminoalkylaminoalkyl, hydroxy-alkylaminoalkyl, hydroxylaminoalkyl, hydroxamido, formamidoalkyl, alkylformamido, aryl, including substituted aryl, aryloxy, heterocyclyl, carbonyliminodiacetic acid, methyle eiminodiacetic acid, methylenethioethylene-iminodiacetic acid, carboxyalkylthioalkyl, a residue of ethylenediaminetetraacetic acid (EDTA), a residue of diethylenetriaminepentaacetic acid. The immunoreagent comprises a ST receptor binding (targeting) moiety derived from e.g. Escherichia coli heat-labile enterotoxin. Since ST receptors occur naturally only in the intestine lumen and are found elsewhere in the body only as a result of metastasis of colon cancer, therefore, the disclosed immunoreagents are useful for diagnostic imaging and radiol. treatment of tumors.

IT 237055-26-4DP, radioisotope conjugates

RL: SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(ST receptor-targeting immunoreagents comprising radioisotope and chelator and enterotoxin for tumor diagnosis and therapy)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 24 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1999:84056 CAPLUS

DOCUMENT NUMBER: 130:163170

TITLE: Cancer diagnosis, prognosis and therapy based on mutation of receptors for transforming growth factor .beta.

INVENTOR(S): Markowitz, Sanford D.; Brattain, Michael G.; Willson, James K. V.

PATENT ASSIGNEE(S): Case Western Reserve University, USA; Medical College of Ohio

SOURCE: U.S., 27 pp., Cont.-in-part of U.S. Ser. No. 417,867, abandoned.

CODEN: USXXAM

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5866323	A	19990202	US 1995-445520	19950522
CA 2217697	AA	19961010	CA 1996-2217697	19960405
WO 9631605	A1	19961010	WO 1996-US4727	19960405
W:	AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI			
RW:	KE, LE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN			
AU 9655361	A1	19961023	AU 1996-55361	19960405
EP 820510	A1	19980128	EP 1996-912590	19960405
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, FI			
JP 11505322	T2	19990518	JP 1996-530516	19960405
US 6291237	B1	20010918	US 1999-239864	19990129
US 2002064786	A1	20020530	US 2001-878905	20010613
US 6630326	B2	20031007		
US 2004038284	A1	20040226	US 2003-646640	20030821

PRIORITY APPLN. INFO.:

US 1995-417867 B2 19950407
 US 1995-445520 A 19950522
 WO 1996-US4727 W 19960405
 US 1999-239864 A3 19990129
 US 2001-878905 A3 20010613

ED Entered STN: 09 Feb 1999

AB This invention is based on the discovery that the type II TGF-.beta. receptor (RII) is a cancer suppressor gene that is inactivated by mutation in approx. 25% of colon cancers, including nearly all colon cancers of the class identified as mutator/microsatellite instability/RER. Methods are provided for detecting inactivation of RII for use in cancer diagnosis or prognosis. The receptor is not detected in RER+ cell lines or in tumor xenografts. Characterization of the receptors from some of these lines is described and the mutations giving rise to the inactivation of the receptor are identified. The gene is inactivated in a no. of cancers of the digestive tract and estrogen-responsive breast cancers.

IT 183815-68-1

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)

(fragment of mutant transforming growth factor.beta. receptor II;
cancer diagnosis prognosis and therapy based on mutation of
 receptors for transforming growth factor .beta. and homologous growth
 controlling factors)

REFERENCE COUNT: 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS
 RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 25 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1996:728965 CAPLUS

DOCUMENT NUMBER: 126:4193

TITLE: Colon cancer diagnosis and therapy based on mutations
 in the gene for the transforming growth factor .beta.
 receptor II

INVENTOR(S): Markowitz, Sanford D.; Brattain, Michael G.; Willson,
 James K. V.

PATENT ASSIGNEE(S): Case Western Reserve University, USA; Medical College
 of Ohio

SOURCE: PCT Int. Appl., 69 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9631605	A1	19961010	WO 1996-US4727	19960405
W:				
AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE,				
ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT,				
LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE,				
SG, SI				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR,				
IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN				
US 5866323	A	19990202	US 1995-445520	19950522
AU 9655361	A1	19961023	AU 1996-55361	19960405
EP 820510	A1	19980128	EP 1996-912590	19960405
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,				
IE, SI, FI				
JP 11505322	T2	19990518	JP 1996-530516	19960405
PRIORITY APPLN. INFO.:			US 1995-417867	A 19950407
			US 1995-445520	A2 19950522
			WO 1996-US4727	W 19960405

ED Entered STN: 12 Dec 1996

AB This invention is based on the discovery that the type II TGF.β. receptor (RII) is a cancer suppressor gene that is genetically inactivated in approx. 25 % of colon cancers, including nearly all colon cancers of the class identified as mutator/microsatellite instability/RER. Methods are provided for detecting inactivation of RII for use in cancer diagnosis or prognosis. Treatment of the cancer by vaccinating the patient with the mutant form of the receptor is also discussed. The receptor was not detected in RER+ cell lines or in tumor xenografts. Characterization of the receptors from some of these lines is described and the mutations giving rise to the inactivation of the receptor are identified. The gene is inactivated in a no. of cancers of the digestive tract and estrogen-responsive breast cancers.

IT 183815-68-1

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)

(fragment of mutant transforming growth factor .β. receptor II; colon **cancer** diagnosis and therapy based on mutations in gene for transforming growth factor .β. receptor II)

L12 ANSWER 26 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1996:379895 CAPLUS

DOCUMENT NUMBER: 125:107052

TITLE: Selection of antigen-binding peptides (abtides) from peptide libraries in a two-stage process

INVENTOR(S): Alvarez, Vernon L.

PATENT ASSIGNEE(S): Cytogen Corporation, USA

SOURCE: PCT Int. Appl., 103 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9609411	A1	19960328	WO 1995-US11934	19950920
W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, UZ, VN				
RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 5885577	A	19990323	US 1995-488161	19950607
AU 9537193	A1	19960409	AU 1995-37193	19950920
EP 789783	A1	19970820	EP 1995-935014	19950920
EP 789783	B1	20020508		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 10506463	T2	19980623	JP 1995-511046	19950920
AT 217344	E	20020515	AT 1995-935014	19950920
PRIORITY APPLN. INFO.:			US 1994-310192	A 19940921
			US 1995-488161	A 19950607
			WO 1995-US11934	W 19950920

ED Entered STN: 02 Jul 1996

AB Abtides are peptides identified by a two-step process of screening random peptide libraries. In the first step, the target ligand is an antibody or receptor (or deriv. thereof). The peptides identified in the first screening step are used as target ligands in the second screening step. The peptides identified as binding the antigens in the second screening step are abtides. Abtides possess binding specificities that are similar to the binding specificities of the antibodies or receptors that are used in the first screening step. Abtides may be used in place of antibodies in many assays or therapeutic applications. Abtides binding to

polymorphic epithelial mucin (PEM) are provided. Also provided are methods of obtaining abtides as well as diagnostic and therapeutic compds. contg. abtides.

IT 178095-95-9P

RL: PRP (Properties); PUR (Purification or recovery); PREP (Preparation) (breast **cancer**-specific antigen-binding peptide; selection of antigen-binding peptides (abtides) from peptide libraries in two-stage process)

L12 ANSWER 27 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1995:541444 CAPLUS

DOCUMENT NUMBER: 122:285668

TITLE: Synthetic peptides for use in tumor detection

INVENTOR(S): Stuttle, Alan W. J.

PATENT ASSIGNEE(S): Antisoma Limited, UK

SOURCE: U.S., 7 pp. Cont.-in-part of U.S. Ser. No. 659,343, abandoned.

CODEN: USXXAM

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5395609	A	19950307	US 1993-57045	19930503
JP 10259195	A2	19980929	JP 1997-277888	19900618
US 5843402	A	19981201	US 1997-816922	19970312
US 6217846	B1	20010417	US 1998-10290	19980121
PRIORITY APPLN. INFO.:			GB 1989-14020	A 19890619
			US 1991-659343	B2 19910321
			US 1989-8914020	A 19890619
			JP 1990-509749	A3 19900618
			WO 1990-GB9333	W 19900618
			US 1992-963127	B1 19921019
			US 1997-816922	A1 19970312

ED Entered STN: 11 May 1995

AB Radioactively labeled peptides comprising oligopeptides of 3-10 peptide units and contg. the sequence RGD and particularly the oligopeptides RGDSY and RGDFY, are disclosed as in vivo thrombus, tumor or CAM markers for the in vivo diagnosis and detection of thrombi, tumors or CAM in mammals.

IT 162929-41-1D, iodine-123 labeled

RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses) (radiolabeled peptides for imaging of thrombi, **tumors**, or cell adhesion mols.)

=
=> sel hit rn l12 1-
E1 THROUGH E101 ASSIGNED

L13 FILE 'REGISTRY' ENTERED AT 10:32:08 ON 06 MAY 2004
101 S E1-E101

=> s l13 and l10
L14 101 L13 AND L10

=> d cn kwic nte l14 1

L14 ANSWER 1 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN INDEX NAME NOT YET ASSIGNED
OTHER NAMES:

*hit Registry #'s
Selected out of references,
crossed into Registry file, &
combined w/ seq search
answer set to get
sequence records*

CN 418: PN: US20040058881 TABLE: 14.7 claimed sequence
 RN 676118-99-3 REGISTRY *use Registry # to match sequence to citation*
 SQL 32 *SQL = sequence length*
 SEQ 1 LRMKXDAEKS DICTDEYQNI LLSNAPLGPQ FP
 =====

HITS AT: 11-15

RELATED SEQUENCES AVAILABLE WITH SEQLINK
 NTE modified

type	location	description
terminal mod.	Leu-1	N-acetyl
terminal mod.	Pro-32	C-terminal amide
uncommon	Oaa-5	-

=> d cn kwic nte l14 2-101; fil hom

L14 ANSWER 2 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
 CN L-Aspartic acid, L-.alpha.-aspartyl-L-asparaginyl-L-cysteinyl-L-arginyl-L-leucyl-L-valyl-L-prolyl-L-asparaginyl-L-prolyl-L-.alpha.-aspartyl-L-glutaminyl-L-lysyl-L-.alpha.-aspartyl-L-seryl-L-.alpha.-aspartylglycyl-L-.alpha.-aspartylglycyl-L-arginylglycyl-L-.alpha.-aspartyl-L-alanyl-L-cysteinyl-L-lysyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-phenylalanyl-L-.alpha.-aspartyl-L-histidyl-L-.alpha.-aspartyl-L-seryl-L-valyl-L-prolyl-L-.alpha.-aspartyl-L-isoleucyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 53: PN: WO2004018995 SEQID: 52 unclaimed protein
 RN 667973-98-0 REGISTRY
 SQL 36

SEQ 1 DNCRLVPNPD QKDSGDGGRG DACKDDFDHD SVPDID
 =====

HITS AT: 21-25

L14 ANSWER 3 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
 CN L-Arginine, L-.alpha.-aspartyl-L-asparaginyl-L-cysteinyl-L-prolyl-L-asparaginyl-L-leucyl-L-prolyl-L-asparaginyl-L-serylglycyl-L-glutaminyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-tyrosyl-L-.alpha.-aspartyl-L-lysyl-L-.alpha.-aspartylglycyl-L-isoleucylglycyl-L-.alpha.-aspartyl-L-alanyl-L-cysteinyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-asparaginyl-L-.alpha.-aspartyl-L-lysyl-L-isoleucyl-L-prolyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 47: PN: WO2004018995 SEQID: 46 unclaimed protein
 RN 667973-94-6 REGISTRY
 SQL 36

SEQ 1 DNCPNLPNSG QEDYDKDGIG DACDDDDND KIPDDR
 =====

HITS AT: 21-25

L14 ANSWER 4 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
 CN L-Alanine, L-.alpha.-aspartyl-L-threonyl-L-cysteinyl-L-seryl-L-.alpha.-aspartyl-L-leucyl-L-valylglycyl-L-leucylglycyl-L-leucyl-L-.alpha.-glutamyl-L-cysteinyl-L-tryptophyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 163: PN: US20040001827 SEQID: 173 claimed sequence
 RN 641623-07-6 REGISTRY

SQL 15

SEQ 1 DTCS DLVGLG LECWA

=====

HITS AT: 1-5

L14 ANSWER 5 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Alanine, L-.alpha.-aspartyl-L-seryl-L-cysteinyglycyl-L-.alpha.-aspartyl-L-leucyl-L-leucyl-L-arginyl-L-leucylglycyl-L-leucyl-L-.alpha.-glutamyl-L-cysteiny-L-tryptophyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 162: PN: US20040001827 SEQID: 172 claimed sequence

RN 641623-06-5 REGISTRY

SQL 15

SEQ 1 DSCGDLRLG LECWA

=====

HITS AT: 1-5

L14 ANSWER 6 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Alanine, L-.alpha.-aspartyl-L-threonyl-L-cysteiny-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-leucyl-L-valyl-L-arginyl-L-leucylglycyl-L-leucyl-L-.alpha.-glutamyl-L-cysteiny-L-tryptophyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 161: PN: US20040001827 SEQID: 171 claimed sequence

RN 641623-05-4 REGISTRY

SQL 15

SEQ 1 DTCE DLVRLG LECWA

=====

HITS AT: 1-5

L14 ANSWER 7 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Alanine, L-.alpha.-aspartyl-L-threonyl-L-cysteiny-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-leucyl-L-valyl-L-glutaminy-L-leucylglycyl-L-leucyl-L-.alpha.-glutamyl-L-cysteiny-L-tryptophyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 160: PN: US20040001827 SEQID: 170 claimed sequence

RN 641623-04-3 REGISTRY

SQL 15

SEQ 1 DTCDDLVLQLG LECWA

=====

HITS AT: 1-5

L14 ANSWER 8 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Alanine, L-.alpha.-aspartyl-L-threonyl-L-cysteiny-L-alanyl-L-.alpha.-aspartyl-L-leucyl-L-valyl-L-arginyl-L-leucylglycyl-L-leucyl-L-.alpha.-glutamyl-L-cysteiny-L-tryptophyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 158: PN: US20040001827 SEQID: 168 claimed sequence

RN 641623-02-1 REGISTRY

SQL 15

SEQ 1 DTCADLVRLG LECWA

=====

HITS AT: 1-5

L14 ANSWER 9 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Methionine, L-methionyl-L-.alpha.-glutamyl-L-leucyl-L-tryptophyl-L-cysteiny-L-.alpha.-aspartyl-L-seryl-L-threonyl-L-leucyl-L-methionyl-L-alanyl-L-tyrosyl-L-.alpha.-aspartyl-L-leucyl-L-cysteinyglycyl-L-.alpha.-aspartyl-L-phenylalanyl-L-asparaginy-L- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 44: PN: US20040001827 SEQID: 48 claimed sequence
RN 641621-81-0 REGISTRY
SQL 20

SEQ 1 MELWCDSTLM AYDLGDFNM
=====

HITS AT: 13-17

L14 ANSWER 10 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN Glycine, L-.alpha.-aspartyl-L-threonyl-L-cysteinyl-L-valyl-L-.alpha.-
aspartyl-L-leucyl-L-valyl-L-arginyl-L-leucylglycyl-L-leucyl-L-.alpha.-
glutamyl-L-cysteinyl-L-tryptophyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 29: PN: US20040001827 TABLE: 1 claimed sequence
RN 641621-76-3 REGISTRY
SQL 15

SEQ 1 DTCVDLVRIG LECWG
=====

HITS AT: 1-5

L14 ANSWER 11 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN Protein (human clone HCLB047) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 51: PN: US20030203361 SEQID: 45 claimed protein
RN 618465-04-6 REGISTRY
SQL 56

SEQ 1 HEENQKDPLA VDKIMKDLQ CRDGKVGFS FFSLIAGLTI ACNDYFVVHM
== ==

HITS AT: 19-23

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L14 ANSWER 12 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Glutamic acid, L-leucyl-L-.alpha.-glutamyl-L-alanyl-L-seryl-L-leucyl-L-
cysteinyl-L-seryl-L-cysteinyl-L-seryl-L-.alpha.-aspartyl-L-.alpha.-
aspartyl-L-cysteinyl-L-leucyl-L-glutamyl-L-arginyl-L-lysyl-L-.alpha.-
aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-tyrosyl-L-
lysyl-L-seryl-L-valyl-L-cysteinyl-L-glutamylglycyl- (9CI) (CA INDEX
NAME)

OTHER NAMES:

CN 576: PN: WO03040340 SEQID: 84 unclaimed sequence
RN 528836-25-1 REGISTRY
SQL 29

SEQ 1 LEASLCSCSD DCLQRKDCCA DYKSVCQGE
=====

HITS AT: 17-21

L14 ANSWER 13 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Serine, L-cysteinyl-L-seryl-L-cysteinyl-L-seryl-L-.alpha.-aspartyl-L-
.alpha.-aspartyl-L-cysteinyl-L-leucyl-L-glutamyl-L-arginyl-L-lysyl-L-
.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-
tyrosyl-L-lysyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 575: PN: WO03040340 SEQID: 83 unclaimed sequence
RN 528836-24-0 REGISTRY
SQL 19

SEQ 1 CSCSDDCLQR KDCCADYKS
=====

HITS AT: 12-16

L14 ANSWER 14 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Lysine, L-seryl-L-cysteinyl-L-seryl-L-.alpha.-aspartyl-L-.alpha.-
aspartyl-L-cysteinyl-L-leucyl-L-glutaminyl-L-arginyl-L-lysyl-L-.alpha.-
aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-tyrosyl-
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 574: PN: WO03040340 SEQID: 82 unclaimed sequence

RN 528836-23-9 REGISTRY

SQL 17

SEQ 1 SCSDDCLQRK DCCADYK

=====

HITS AT: 11-15

L14 ANSWER 15 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Cysteine, L-cysteinyl-L-seryl-L-cysteinyl-L-seryl-L-.alpha.-aspartyl-L-
.alpha.-aspartyl-L-cysteinyl-L-leucyl-L-glutaminyl-L-lysyl-L-lysyl-L-
.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-
tyrosyl-L-lysyl-L-seryl-L-valyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 573: PN: WO03040340 SEQID: 80 unclaimed sequence

RN 528836-22-8 REGISTRY

SQL 21

SEQ 1 CSCSDDCLQK KDCCADYKSV C

=====

HITS AT: 12-16

L14 ANSWER 16 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Cysteine, L-cysteinyl-L-arginyl-L-cysteinyl-L-.alpha.-aspartyl-L-valyl-L-
alanyl-L-cysteinyl-L-lysyl-L-.alpha.-aspartyl-L-arginylglycyl-L-.alpha.-
aspartyl-L-cysteinyl-L-cysteinyl-L-tryptophyl-L-.alpha.-aspartyl-L-
phenylalanyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-threonyl- (9CI) (CA
INDEX NAME)

OTHER NAMES:

CN 572: PN: WO03040340 SEQID: 79 unclaimed sequence

RN 528836-21-7 REGISTRY

SQL 21

SEQ 1 CRCDVACKDR GDCCWDFEDT C

=====

HITS AT: 12-16

L14 ANSWER 17 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Aspartic acid, L-seryl-L-cysteinyl-L-seryl-L-.alpha.-aspartyl-L-.alpha.-
aspartyl-L-cysteinyl-L-leucyl-L-glutaminyl-L-lysyl-L-lysyl-L-.alpha.-
aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl- (9CI) (CA INDEX NAME)

RN 525557-34-0 REGISTRY

SQL 15

SEQ 1 SCSDDCLQKK DCCAD

=====

HITS AT: 11-15

L14 ANSWER 18 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Glutamic acid, L-arginyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-
cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-tyrosyl-L-lysyl-L-seryl-L-valyl-L-
cysteinyl-L-glutaminylglycyl- (9CI) (CA INDEX NAME)

RN 525556-17-6 REGISTRY

SQL 15

SEQ 1 RKDCCADYKS VCQGE

=====

HITS AT: 3-7

L14 ANSWER 19 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Valine, L-.alpha.-aspartyl-L-cysteinyl-L-leucyl-L-glutaminyl-L-arginyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-tyrosyl-L-lysyl-L-seryl- (9CI) (CA INDEX NAME)

RN 525556-16-5 REGISTRY

SQL 15

SEQ 1 DCLQRKDCCA DYKSV

=====

HITS AT: 7-11

L14 ANSWER 20 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Glutamic acid, L-lysyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-tyrosyl-L-lysyl-L-seryl-L-valyl-L-cysteinyl-L-glutaminylglycyl- (9CI) (CA INDEX NAME)

RN 525555-93-5 REGISTRY

SQL 15

SEQ 1 KKDCCADYKS VCQGE

=====

HITS AT: 3-7

L14 ANSWER 21 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Serine, L-arginylglycyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-tryptophyl-L-.alpha.-aspartyl-L-phenylalanyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-threonyl-L-cysteinyl-L-valyl-L-.alpha.-glutamyl- (9CI) (CA INDEX NAME)

RN 525555-90-2 REGISTRY

SQL 15

SEQ 1 RGDCCWDFED TCVES

=====

HITS AT: 3-7

L14 ANSWER 22 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Aspartic acid, L-arginyl-L-cysteinyl-L-.alpha.-aspartyl-L-valyl-L-alanyl-L-cysteinyl-L-lysyl-L-.alpha.-aspartyl-L-arginylglycyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-tryptophyl- (9CI) (CA INDEX NAME)

RN 525555-89-9 REGISTRY

SQL 15

SEQ 1 RCDVACKDRG DCCWD

=====

HITS AT: 11-15

L14 ANSWER 23 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Threonine, L-alanyl-L-cysteinyl-L-lysyl-L-.alpha.-aspartyl-L-arginylglycyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-tryptophyl-L-.alpha.-aspartyl-L-phenylalanyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)

RN 525555-43-5 REGISTRY

SQL 15

SEQ 1 ACKDRGDCCW DFEDT

=====

HITS AT: 7-11

L14 ANSWER 24 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Valine, L-.alpha.-aspartyl-L-cysteinyl-L-leucyl-L-glutaminyl-L-lysyl-L-

lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-
aspartyl-L-tyrosyl-L-lysyl-L-seryl- (9CI) (CA INDEX NAME)
RN 525555-36-6 REGISTRY
SQL 15

SEQ 1 DCLQKKDCCA DYKSV
=====

HITS AT: 7-11

L14 ANSWER 25 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Tyrosine, L-cysteinyl-L-seryl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-
cysteinyl-L-leucyl-L-glutaminyl-L-arginyl-L-lysyl-L-.alpha.-aspartyl-L-
cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)
RN 525555-20-8 REGISTRY
SQL 15

SEQ 1 CSDDCLQRKD CCADY
= =====

HITS AT: 10-14

L14 ANSWER 26 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Serine, L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-leucyl-L-
glutaminyl-L-arginyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-
alanyl-L-.alpha.-aspartyl-L-tyrosyl-L-lysyl- (9CI) (CA INDEX NAME)
RN 525555-19-5 REGISTRY
SQL 15

SEQ 1 DDCLQRKDCC ADYKS
=== ==

HITS AT: 8-12

L14 ANSWER 27 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Lysine, L-seryl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-
leucyl-L-glutaminyl-L-arginyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-
cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-tyrosyl- (9CI) (CA INDEX NAME)
RN 525555-18-4 REGISTRY
SQL 15

SEQ 1 SDDCLQRKDC CADYK
== ===

HITS AT: 9-13

L14 ANSWER 28 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN Glycine, L-glutaminyl-L-arginyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-
cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-tyrosyl-L-lysyl-L-seryl-L-valyl-L-
cysteinyl-L-glutaminyl- (9CI) (CA INDEX NAME)
RN 525555-17-3 REGISTRY
SQL 15

SEQ 1 QRKDCCADYK SVCQG
=====

HITS AT: 4-8

L14 ANSWER 29 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Glutamine, L-leucyl-L-glutaminyl-L-arginyl-L-lysyl-L-.alpha.-aspartyl-L-
cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-tyrosyl-L-lysyl-L-
seryl-L-valyl-L-cysteinyl- (9CI) (CA INDEX NAME)
RN 525555-16-2 REGISTRY
SQL 15

SEQ 1 LQRKDCCADY KSVCO
=====

HITS AT: 5-9

L14 ANSWER 30 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Cysteine, L-cysteinyl-L-leucyl-L-glutaminyl-L-arginyl-L-lysyl-L-.alpha.-
aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-tyrosyl-L-
lysyl-L-seryl-L-valyl- (9CI) (CA INDEX NAME)
RN 525555-15-1 REGISTRY
SQL 15

SEQ 1 CLQRKDCCAD YKSVC
=====

HITS AT: 6-10

L14 ANSWER 31 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Aspartic acid, L-seryl-L-cysteinyl-L-seryl-L-.alpha.-aspartyl-L-.alpha.-
aspartyl-L-cysteinyl-L-leucyl-L-glutaminyl-L-arginyl-L-lysyl-L-.alpha.-
aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl- (9CI) (CA INDEX NAME)
RN 525555-14-0 REGISTRY
SQL 15

SEQ 1 SCSDDCLQRK DCCAD
=====

HITS AT: 11-15

L14 ANSWER 32 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Arginine, L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-tryptophyl-L-
.alpha.-aspartyl-L-phenylalanyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-
threonyl-L-cysteinyl-L-valyl-L-.alpha.-glutamyl-L-seryl-L-threonyl- (9CI)
(CA INDEX NAME)
RN 525554-65-8 REGISTRY
SQL 15

SEQ 1 DCCWDFEDTC VESTR
=====

HITS AT: 1-5

L14 ANSWER 33 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Phenylalanine, L-lysyl-L-.alpha.-aspartyl-L-arginylglycyl-L-.alpha.-
aspartyl-L-cysteinyl-L-cysteinyl-L-tryptophyl-L-.alpha.-aspartyl- (9CI)
(CA INDEX NAME)
RN 525551-78-4 REGISTRY
SQL 10

SEQ 1 KDRGDCCWDF
=====

HITS AT: 5-9

L14 ANSWER 34 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Aspartic acid, L-cysteinyl-L-leucyl-L-glutaminyl-L-lysyl-L-lysyl-L-
.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl- (9CI) (CA INDEX NAME)
RN 525550-83-8 REGISTRY
SQL 10

SEQ 1 CLQKKDCCAD
=====

HITS AT: 6-10

L14 ANSWER 35 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Valine, L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-
aspartyl-L-tyrosyl-L-lysyl-L-seryl- (9CI) (CA INDEX NAME)
RN 525549-64-8 REGISTRY
SQL 9

SEQ 1 DCCADYKSV

=====

HITS AT: 1-5

L14 ANSWER 36 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Phenylalanine, L-.alpha.-aspartyl-L-arginylglycyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-tryptophyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)
RN 525547-98-2 REGISTRY
SQL 9

SEQ 1 DRGDCCWDF

=====

HITS AT: 4-8

L14 ANSWER 37 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Tyrosine, L-leucyl-L-glutaminyl-L-lysyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)
RN 525546-75-2 REGISTRY
SQL 10

SEQ 1 LQKKDCCADY

=====

HITS AT: 5-9

L14 ANSWER 38 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Tyrosine, L-glutaminyl-L-lysyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)
RN 525546-66-1 REGISTRY
SQL 9

SEQ 1 QKKDCCADY

=====

HITS AT: 4-8

L14 ANSWER 39 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Lysine, L-glutaminyl-L-lysyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-tyrosyl- (9CI) (CA INDEX NAME)
RN 525544-74-5 REGISTRY
SQL 10

SEQ 1 QKKDCCADYK

=====

HITS AT: 4-8

L14 ANSWER 40 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Valine, L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-tyrosyl-L-lysyl-L-seryl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 361: PN: WO03040340 TABLE: 11 claimed protein
RN 525543-47-9 REGISTRY
SQL 10

SEQ 1 KDCCADYKSV

=====

HITS AT: 2-6

L14 ANSWER 41 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Aspartic acid, L-cysteinyl-L-leucyl-L-glutaminyl-L-arginyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 110: PN: WO03040340 TABLE: 9 claimed protein
RN 525541-68-8 REGISTRY
SQL 10

SEQ 1 CLQRKDCCAD

=====

HITS AT: 6-10

L14 ANSWER 42 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Lysine, L-glutaminyl-L-arginyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-tyrosyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 108: PN: WO03040340 TABLE: 9 claimed protein

RN 525541-66-6 REGISTRY

SQL 10

SEQ 1 QRKDCCADYK

=====

HITS AT: 4-8

L14 ANSWER 43 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Tyrosine, L-leucyl-L-glutaminyl-L-arginyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 107: PN: WO03040340 TABLE: 9 claimed protein

RN 525541-65-5 REGISTRY

SQL 10

SEQ 1 LQRKDCCADY

=====

HITS AT: 5-9

L14 ANSWER 44 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Serine, L-arginyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-tyrosyl-L-lysyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 104: PN: WO03040340 TABLE: 9 claimed protein

RN 525541-62-2 REGISTRY

SQL 10

SEQ 1 RKDCCADYKS

=====

HITS AT: 3-7

L14 ANSWER 45 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Aspartic acid, L-leucyl-L-glutaminyl-L-arginyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 109: PN: WO03040340 TABLE: 8 claimed protein

RN 525540-47-0 REGISTRY

SQL 9

SEQ 1 LQRKDCCAD

=====

HITS AT: 5-9

L14 ANSWER 46 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Tyrosine, L-glutaminyl-L-arginyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 105: PN: WO03040340 TABLE: 8 claimed protein

RN 525540-43-6 REGISTRY

SQL 9

SEQ 1 QRKDCCADY

=====

HITS AT: 4-8

L14 ANSWER 47 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
 CN L-Lysine, L-arginyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-tyrosyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 102: PN: W003040340 TABLE: 8 claimed protein

RN 525540-40-3 REGISTRY

SQL 9

SEQ 1 RKDCCADYK

=====

HITS AT: 3-7

L14 ANSWER 48 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
 CN L-Lysine, L-lysyl-L-lysyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-.alpha.-aspartyl-L-tyrosyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 49: PN: W003040340 TABLE: 8 claimed protein

RN 525539-87-1 REGISTRY

SQL 9

SEQ 1 KKDCCADYK

=====

HITS AT: 3-7

L14 ANSWER 49 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
 CN 45: PN: US6500431 SEQID: 45 unclaimed protein (9CI) (CA INDEX NAME)

RN 481111-14-2 REGISTRY

SQL 70

SEQ 1 XXXXXXDVQCQ DXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX

=====

HITS AT: 7-11

RELATED SEQUENCES AVAILABLE WITH SEQLINK

NTE

type	location	description
uncommon	Aaa-1	-
uncommon	Aaa-2	-
uncommon	Aaa-3	-
uncommon	Aaa-4	-
uncommon	Aaa-5	-
uncommon	Aaa-6	-
uncommon	Aaa-12	-
uncommon	Aaa-13	-
uncommon	Aaa-14	-
uncommon	Aaa-15	-
uncommon	Aaa-16	-
uncommon	Aaa-17	-
uncommon	Aaa-18	-
uncommon	Aaa-19	-
uncommon	Aaa-20	-
uncommon	Aaa-21	-
uncommon	Aaa-22	-
uncommon	Aaa-23	-
uncommon	Aaa-24	-
uncommon	Aaa-25	-
uncommon	Aaa-26	-
uncommon	Aaa-27	-
uncommon	Aaa-28	-

uncommon	Aaa-29	-	-
uncommon	Aaa-30	-	-
uncommon	Aaa-31	-	-
uncommon	Aaa-32	-	-
uncommon	Aaa-33	-	-
uncommon	Aaa-34	-	-
uncommon	Aaa-35	-	-
uncommon	Aaa-36	-	-
uncommon	Aaa-37	-	-
uncommon	Aaa-38	-	-
uncommon	Aaa-39	-	-
uncommon	Aaa-40	-	-
uncommon	Aaa-41	-	-
uncommon	Aaa-42	-	-
uncommon	Aaa-43	-	-
uncommon	Aaa-44	-	-
uncommon	Aaa-45	-	-
uncommon	Aaa-46	-	-
uncommon	Aaa-47	-	-
uncommon	Aaa-48	-	-
uncommon	Aaa-49	-	-
uncommon	Aaa-50	-	-
uncommon	Aaa-51	-	-
uncommon	Aaa-52	-	-
uncommon	Aaa-53	-	-
uncommon	Aaa-54	-	-
uncommon	Aaa-55	-	-
uncommon	Aaa-56	-	-
uncommon	Aaa-57	-	-
uncommon	Aaa-58	-	-
uncommon	Aaa-59	-	-
uncommon	Aaa-60	-	-
uncommon	Aaa-61	-	-
uncommon	Aaa-62	-	-
uncommon	Aaa-63	-	-
uncommon	Aaa-64	-	-
uncommon	Aaa-65	-	-
uncommon	Aaa-66	-	-
uncommon	Aaa-67	-	-
uncommon	Aaa-68	-	-
uncommon	Aaa-69	-	-
uncommon	Aaa-70	-	-

L14 ANSWER 50 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN Peptide, (Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Asp-Val-Cys-Gln-Asp-Xaa-Xaa-Xaa-Xaa-Val)
(9CI) (CA INDEX NAME)
OTHER NAMES:
CN 59: PN: US6500431 SEQID: 59 unclaimed protein
RN 480474-43-9 REGISTRY
SQL 16

SEQ 1 XXXXXDVCQ DXXXXV

==== =

HITS AT: 7-11
NTE

type	location	description
uncommon	Aaa-1	-
uncommon	Aaa-2	-
uncommon	Aaa-3	-
uncommon	Aaa-4	-

uncommon	Aaa-5	-	-
uncommon	Aaa-6	-	-
uncommon	Aaa-12	-	-
uncommon	Aaa-13	-	-
uncommon	Aaa-14	-	-
uncommon	Aaa-15	-	-

L14 ANSWER 51 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
 CN Peptide, (Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Asp-Val-Cys-Gln-Asp-Xaa-Xaa-Xaa-Met-Xaa)
 (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 58: PN: US6500431 SEQID: 58 unclaimed protein
 RN 480474-42-8 REGISTRY
 SQL 16

SEQ 1 XXXXXXDVCQ DXXXMX

==== =

HITS AT: 7-11

NTE

type	location			description
uncommon	Aaa-1	-	-	
uncommon	Aaa-2	-	-	
uncommon	Aaa-3	-	-	
uncommon	Aaa-4	-	-	
uncommon	Aaa-5	-	-	
uncommon	Aaa-6	-	-	
uncommon	Aaa-12	-	-	
uncommon	Aaa-13	-	-	
uncommon	Aaa-14	-	-	
uncommon	Aaa-16	-	-	

L14 ANSWER 52 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
 CN Peptide, (Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Asp-Val-Cys-Gln-Asp-Xaa-Xaa-Gln-Xaa-Xaa)
 (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 57: PN: US6500431 SEQID: 57 unclaimed protein
 RN 480474-41-7 REGISTRY
 SQL 16

SEQ 1 XXXXXXDVCQ DXXQXX

==== =

HITS AT: 7-11

NTE

type	location			description
uncommon	Aaa-1	-	-	
uncommon	Aaa-2	-	-	
uncommon	Aaa-3	-	-	
uncommon	Aaa-4	-	-	
uncommon	Aaa-5	-	-	
uncommon	Aaa-6	-	-	
uncommon	Aaa-12	-	-	
uncommon	Aaa-13	-	-	
uncommon	Aaa-15	-	-	
uncommon	Aaa-16	-	-	

L14 ANSWER 53 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN Peptide, (Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Asp-Val-Cys-Gln-Asp-Xaa-Ile-Xaa-Xaa-Xaa)
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 56: PN: US6500431 SEQID: 56 unclaimed protein

RN 480474-40-6 REGISTRY

SQL 16

SEQ 1 XXXXXXDVCQ DXIXXX

==== =

HITS AT: 7-11

NTE

type	location	description
uncommon	Aaa-1	-
uncommon	Aaa-2	-
uncommon	Aaa-3	-
uncommon	Aaa-4	-
uncommon	Aaa-5	-
uncommon	Aaa-6	-
uncommon	Aaa-12	-
uncommon	Aaa-14	-
uncommon	Aaa-15	-
uncommon	Aaa-16	-

L14 ANSWER 54 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN Peptide, (Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Asp-Val-Cys-Gln-Asp-Cys-Xaa-Xaa-Xaa-Xaa)
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 55: PN: US6500431 SEQID: 55 unclaimed protein

RN 480474-39-3 REGISTRY

SQL 16

SEQ 1 XXXXXXDVCQ DCXXXX

==== =

HITS AT: 7-11

NTE

type	location	description
uncommon	Aaa-1	-
uncommon	Aaa-2	-
uncommon	Aaa-3	-
uncommon	Aaa-4	-
uncommon	Aaa-5	-
uncommon	Aaa-6	-
uncommon	Aaa-13	-
uncommon	Aaa-14	-
uncommon	Aaa-15	-
uncommon	Aaa-16	-

L14 ANSWER 55 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN 53: PN: US6500431 SEQID: 53 unclaimed protein (9CI) (CA INDEX NAME)

RN 480474-38-2 REGISTRY

SQL 70

SEQ 1 XXXXNXDVCQ DXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX

==== =

HITS AT: 7-11

NTE

type	----- location -----	description
uncommon	Aaa-1	-
uncommon	Aaa-2	-
uncommon	Aaa-3	-
uncommon	Aaa-4	-
uncommon	Aaa-6	-
uncommon	Aaa-12	-
uncommon	Aaa-13	-
uncommon	Aaa-14	-
uncommon	Aaa-15	-
uncommon	Aaa-16	-
uncommon	Aaa-17	-
uncommon	Aaa-18	-
uncommon	Aaa-19	-
uncommon	Aaa-20	-
uncommon	Aaa-21	-
uncommon	Aaa-22	-
uncommon	Aaa-23	-
uncommon	Aaa-24	-
uncommon	Aaa-25	-
uncommon	Aaa-26	-
uncommon	Aaa-27	-
uncommon	Aaa-28	-
uncommon	Aaa-29	-
uncommon	Aaa-30	-
uncommon	Aaa-31	-
uncommon	Aaa-32	-
uncommon	Aaa-33	-
uncommon	Aaa-34	-
uncommon	Aaa-35	-
uncommon	Aaa-36	-
uncommon	Aaa-37	-
uncommon	Aaa-38	-
uncommon	Aaa-39	-
uncommon	Aaa-40	-
uncommon	Aaa-41	-
uncommon	Aaa-42	-
uncommon	Aaa-43	-
uncommon	Aaa-44	-
uncommon	Aaa-45	-
uncommon	Aaa-46	-
uncommon	Aaa-47	-
uncommon	Aaa-48	-
uncommon	Aaa-49	-
uncommon	Aaa-50	-
uncommon	Aaa-51	-
uncommon	Aaa-52	-
uncommon	Aaa-53	-
uncommon	Aaa-54	-
uncommon	Aaa-55	-
uncommon	Aaa-56	-
uncommon	Aaa-57	-
uncommon	Aaa-58	-
uncommon	Aaa-59	-
uncommon	Aaa-60	-
uncommon	Aaa-61	-
uncommon	Aaa-62	-
uncommon	Aaa-63	-
uncommon	Aaa-64	-
uncommon	Aaa-65	-
uncommon	Aaa-66	-
uncommon	Aaa-67	-

uncommon	Aaa-68	-	-
uncommon	Aaa-69	-	-
uncommon	Aaa-70	-	-

L14 ANSWER 56 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
 CN 52: PN: US6500431 SEQID: 52 unclaimed protein (9CI) (CA INDEX NAME)
 RN 480474-37-1 REGISTRY
 SQL 70

SEQ 1 XXXDXXDVCQ DXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX
 =====

HITS AT: 7-11

NTE

type	location			description
uncommon	Aaa-1	-	-	
uncommon	Aaa-2	-	-	
uncommon	Aaa-3	-	-	
uncommon	Aaa-5	-	-	
uncommon	Aaa-6	-	-	
uncommon	Aaa-12	-	-	
uncommon	Aaa-13	-	-	
uncommon	Aaa-14	-	-	
uncommon	Aaa-15	-	-	
uncommon	Aaa-16	-	-	
uncommon	Aaa-17	-	-	
uncommon	Aaa-18	-	-	
uncommon	Aaa-19	-	-	
uncommon	Aaa-20	-	-	
uncommon	Aaa-21	-	-	
uncommon	Aaa-22	-	-	
uncommon	Aaa-23	-	-	
uncommon	Aaa-24	-	-	
uncommon	Aaa-25	-	-	
uncommon	Aaa-26	-	-	
uncommon	Aaa-27	-	-	
uncommon	Aaa-28	-	-	
uncommon	Aaa-29	-	-	
uncommon	Aaa-30	-	-	
uncommon	Aaa-31	-	-	
uncommon	Aaa-32	-	-	
uncommon	Aaa-33	-	-	
uncommon	Aaa-34	-	-	
uncommon	Aaa-35	-	-	
uncommon	Aaa-36	-	-	
uncommon	Aaa-37	-	-	
uncommon	Aaa-38	-	-	
uncommon	Aaa-39	-	-	
uncommon	Aaa-40	-	-	
uncommon	Aaa-41	-	-	
uncommon	Aaa-42	-	-	
uncommon	Aaa-43	-	-	
uncommon	Aaa-44	-	-	
uncommon	Aaa-45	-	-	
uncommon	Aaa-46	-	-	
uncommon	Aaa-47	-	-	
uncommon	Aaa-48	-	-	
uncommon	Aaa-49	-	-	
uncommon	Aaa-50	-	-	
uncommon	Aaa-51	-	-	
uncommon	Aaa-52	-	-	

uncommon	Aaa-53	-	-
uncommon	Aaa-54	-	-
uncommon	Aaa-55	-	-
uncommon	Aaa-56	-	-
uncommon	Aaa-57	-	-
uncommon	Aaa-58	-	-
uncommon	Aaa-59	-	-
uncommon	Aaa-60	-	-
uncommon	Aaa-61	-	-
uncommon	Aaa-62	-	-
uncommon	Aaa-63	-	-
uncommon	Aaa-64	-	-
uncommon	Aaa-65	-	-
uncommon	Aaa-66	-	-
uncommon	Aaa-67	-	-
uncommon	Aaa-68	-	-
uncommon	Aaa-69	-	-
uncommon	Aaa-70	-	-

L14 ANSWER 57 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
 CN 51: PN: US6500431 SEQID: 51 unclaimed protein (9CI) (CA INDEX NAME)
 RN 480474-36-0 REGISTRY
 SQL 70

SEQ 1 XXXXXXDVCQ DXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX

=====

HITS AT: 7-11

NTE

type	location			description
uncommon	Aaa-1	-	-	
uncommon	Aaa-2	-	-	
uncommon	Aaa-4	-	-	
uncommon	Aaa-5	-	-	
uncommon	Aaa-6	-	-	
uncommon	Aaa-12	-	-	
uncommon	Aaa-13	-	-	
uncommon	Aaa-14	-	-	
uncommon	Aaa-15	-	-	
uncommon	Aaa-16	-	-	
uncommon	Aaa-17	-	-	
uncommon	Aaa-18	-	-	
uncommon	Aaa-19	-	-	
uncommon	Aaa-20	-	-	
uncommon	Aaa-21	-	-	
uncommon	Aaa-22	-	-	
uncommon	Aaa-23	-	-	
uncommon	Aaa-24	-	-	
uncommon	Aaa-25	-	-	
uncommon	Aaa-26	-	-	
uncommon	Aaa-27	-	-	
uncommon	Aaa-28	-	-	
uncommon	Aaa-29	-	-	
uncommon	Aaa-30	-	-	
uncommon	Aaa-31	-	-	
uncommon	Aaa-32	-	-	
uncommon	Aaa-33	-	-	
uncommon	Aaa-34	-	-	
uncommon	Aaa-35	-	-	
uncommon	Aaa-36	-	-	
uncommon	Aaa-37	-	-	

uncommon	Aaa-38	-	-
uncommon	Aaa-39	-	-
uncommon	Aaa-40	-	-
uncommon	Aaa-41	-	-
uncommon	Aaa-42	-	-
uncommon	Aaa-43	-	-
uncommon	Aaa-44	-	-
uncommon	Aaa-45	-	-
uncommon	Aaa-46	-	-
uncommon	Aaa-47	-	-
uncommon	Aaa-48	-	-
uncommon	Aaa-49	-	-
uncommon	Aaa-50	-	-
uncommon	Aaa-51	-	-
uncommon	Aaa-52	-	-
uncommon	Aaa-53	-	-
uncommon	Aaa-54	-	-
uncommon	Aaa-55	-	-
uncommon	Aaa-56	-	-
uncommon	Aaa-57	-	-
uncommon	Aaa-58	-	-
uncommon	Aaa-59	-	-
uncommon	Aaa-60	-	-
uncommon	Aaa-61	-	-
uncommon	Aaa-62	-	-
uncommon	Aaa-63	-	-
uncommon	Aaa-64	-	-
uncommon	Aaa-65	-	-
uncommon	Aaa-66	-	-
uncommon	Aaa-67	-	-
uncommon	Aaa-68	-	-
uncommon	Aaa-69	-	-
uncommon	Aaa-70	-	-

L14 ANSWER 58 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
 CN 50: PN: US6500431 SEQID: 50 unclaimed protein (9CI) (CA INDEX NAME)
 RN 480474-35-9 REGISTRY
 SQL 70

SEQ 1 XPXXXXDVCQ DXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX
 =====

HITS AT: 7-11
 NTE

type	location			description
uncommon	Aaa-1	-	-	
uncommon	Aaa-3	-	-	
uncommon	Aaa-4	-	-	
uncommon	Aaa-5	-	-	
uncommon	Aaa-6	-	-	
uncommon	Aaa-12	-	-	
uncommon	Aaa-13	-	-	
uncommon	Aaa-14	-	-	
uncommon	Aaa-15	-	-	
uncommon	Aaa-16	-	-	
uncommon	Aaa-17	-	-	
uncommon	Aaa-18	-	-	
uncommon	Aaa-19	-	-	
uncommon	Aaa-20	-	-	
uncommon	Aaa-21	-	-	
uncommon	Aaa-22	-	-	

uncommon	Aaa-23	-	-
uncommon	Aaa-24	-	-
uncommon	Aaa-25	-	-
uncommon	Aaa-26	-	-
uncommon	Aaa-27	-	-
uncommon	Aaa-28	-	-
uncommon	Aaa-29	-	-
uncommon	Aaa-30	-	-
uncommon	Aaa-31	-	-
uncommon	Aaa-32	-	-
uncommon	Aaa-33	-	-
uncommon	Aaa-34	-	-
uncommon	Aaa-35	-	-
uncommon	Aaa-36	-	-
uncommon	Aaa-37	-	-
uncommon	Aaa-38	-	-
uncommon	Aaa-39	-	-
uncommon	Aaa-40	-	-
uncommon	Aaa-41	-	-
uncommon	Aaa-42	-	-
uncommon	Aaa-43	-	-
uncommon	Aaa-44	-	-
uncommon	Aaa-45	-	-
uncommon	Aaa-46	-	-
uncommon	Aaa-47	-	-
uncommon	Aaa-48	-	-
uncommon	Aaa-49	-	-
uncommon	Aaa-50	-	-
uncommon	Aaa-51	-	-
uncommon	Aaa-52	-	-
uncommon	Aaa-53	-	-
uncommon	Aaa-54	-	-
uncommon	Aaa-55	-	-
uncommon	Aaa-56	-	-
uncommon	Aaa-57	-	-
uncommon	Aaa-58	-	-
uncommon	Aaa-59	-	-
uncommon	Aaa-60	-	-
uncommon	Aaa-61	-	-
uncommon	Aaa-62	-	-
uncommon	Aaa-63	-	-
uncommon	Aaa-64	-	-
uncommon	Aaa-65	-	-
uncommon	Aaa-66	-	-
uncommon	Aaa-67	-	-
uncommon	Aaa-68	-	-
uncommon	Aaa-69	-	-
uncommon	Aaa-70	-	-

L14 ANSWER 59 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN 49: PN: US6500431 SEQID: 49 unclaimed protein (9CI) (CA INDEX NAME)
RN 480474-34-8 REGISTRY
SQL 70

SEQ 1 QXXXXXDVCQ DXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX
=====

HITS AT: 7-11
NTE

type	location	description
uncommon	Aaa-2	-

uncommon	Aaa-3	-	-
uncommon	Aaa-4	-	-
uncommon	Aaa-5	-	-
uncommon	Aaa-6	-	-
uncommon	Aaa-12	-	-
uncommon	Aaa-13	-	-
uncommon	Aaa-14	-	-
uncommon	Aaa-15	-	-
uncommon	Aaa-16	-	-
uncommon	Aaa-17	-	-
uncommon	Aaa-18	-	-
uncommon	Aaa-19	-	-
uncommon	Aaa-20	-	-
uncommon	Aaa-21	-	-
uncommon	Aaa-22	-	-
uncommon	Aaa-23	-	-
uncommon	Aaa-24	-	-
uncommon	Aaa-25	-	-
uncommon	Aaa-26	-	-
uncommon	Aaa-27	-	-
uncommon	Aaa-28	-	-
uncommon	Aaa-29	-	-
uncommon	Aaa-30	-	-
uncommon	Aaa-31	-	-
uncommon	Aaa-32	-	-
uncommon	Aaa-33	-	-
uncommon	Aaa-34	-	-
uncommon	Aaa-35	-	-
uncommon	Aaa-36	-	-
uncommon	Aaa-37	-	-
uncommon	Aaa-38	-	-
uncommon	Aaa-39	-	-
uncommon	Aaa-40	-	-
uncommon	Aaa-41	-	-
uncommon	Aaa-42	-	-
uncommon	Aaa-43	-	-
uncommon	Aaa-44	-	-
uncommon	Aaa-45	-	-
uncommon	Aaa-46	-	-
uncommon	Aaa-47	-	-
uncommon	Aaa-48	-	-
uncommon	Aaa-49	-	-
uncommon	Aaa-50	-	-
uncommon	Aaa-51	-	-
uncommon	Aaa-52	-	-
uncommon	Aaa-53	-	-
uncommon	Aaa-54	-	-
uncommon	Aaa-55	-	-
uncommon	Aaa-56	-	-
uncommon	Aaa-57	-	-
uncommon	Aaa-58	-	-
uncommon	Aaa-59	-	-
uncommon	Aaa-60	-	-
uncommon	Aaa-61	-	-
uncommon	Aaa-62	-	-
uncommon	Aaa-63	-	-
uncommon	Aaa-64	-	-
uncommon	Aaa-65	-	-
uncommon	Aaa-66	-	-
uncommon	Aaa-67	-	-
uncommon	Aaa-68	-	-
uncommon	Aaa-69	-	-
uncommon	Aaa-70	-	-

L14 ANSWER 60 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN Peptide, (Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Asp-Val-Cys-Gln-Asp-Cys-Ile-Gln-Met-Val)
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 48: PN: US6500431 SEQID: 48 unclaimed protein
RN 480474-33-7 REGISTRY
SQL 16

SEQ 1 XXXXXXDVCQ DCIQMV

=====

HITS AT: 7-11

NTE

type location description

uncommon Aaa-1 - -
uncommon Aaa-2 - -
uncommon Aaa-3 - -
uncommon Aaa-4 - -
uncommon Aaa-5 - -
uncommon Aaa-6 - -

L14 ANSWER 61 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN Peptide, (Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Asp-Val-Cys-Gln-Asp-Xaa-Xaa-Xaa-Xaa)
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 47: PN: US6500431 SEQID: 47 unclaimed protein
RN 480474-32-6 REGISTRY
SQL 16

SEQ 1 XXXXXXDVCQ DXXXXXX

=====

HITS AT: 7-11

NTE

type location description

uncommon Aaa-1 - -
uncommon Aaa-2 - -
uncommon Aaa-3 - -
uncommon Aaa-4 - -
uncommon Aaa-5 - -
uncommon Aaa-6 - -
uncommon Aaa-12 - -
uncommon Aaa-13 - -
uncommon Aaa-14 - -
uncommon Aaa-15 - -
uncommon Aaa-16 - -

L14 ANSWER 62 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN 46: PN: US6500431 SEQID: 46 unclaimed protein (9CI) (CA INDEX NAME)
RN 480474-31-5 REGISTRY
SQL 70

SEQ 1 QPKDNXDVCQ DXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX

=====

HITS AT: 7-11

NTE

type	----- location -----	description
uncommon	Aaa-6	-
uncommon	Aaa-12	-
uncommon	Aaa-13	-
uncommon	Aaa-14	-
uncommon	Aaa-15	-
uncommon	Aaa-16	-
uncommon	Aaa-17	-
uncommon	Aaa-18	-
uncommon	Aaa-19	-
uncommon	Aaa-20	-
uncommon	Aaa-21	-
uncommon	Aaa-22	-
uncommon	Aaa-23	-
uncommon	Aaa-24	-
uncommon	Aaa-25	-
uncommon	Aaa-26	-
uncommon	Aaa-27	-
uncommon	Aaa-28	-
uncommon	Aaa-29	-
uncommon	Aaa-30	-
uncommon	Aaa-31	-
uncommon	Aaa-32	-
uncommon	Aaa-33	-
uncommon	Aaa-34	-
uncommon	Aaa-35	-
uncommon	Aaa-36	-
uncommon	Aaa-37	-
uncommon	Aaa-38	-
uncommon	Aaa-39	-
uncommon	Aaa-40	-
uncommon	Aaa-41	-
uncommon	Aaa-42	-
uncommon	Aaa-43	-
uncommon	Aaa-44	-
uncommon	Aaa-45	-
uncommon	Aaa-46	-
uncommon	Aaa-47	-
uncommon	Aaa-48	-
uncommon	Aaa-49	-
uncommon	Aaa-50	-
uncommon	Aaa-51	-
uncommon	Aaa-52	-
uncommon	Aaa-53	-
uncommon	Aaa-54	-
uncommon	Aaa-55	-
uncommon	Aaa-56	-
uncommon	Aaa-57	-
uncommon	Aaa-58	-
uncommon	Aaa-59	-
uncommon	Aaa-60	-
uncommon	Aaa-61	-
uncommon	Aaa-62	-
uncommon	Aaa-63	-
uncommon	Aaa-64	-
uncommon	Aaa-65	-
uncommon	Aaa-66	-
uncommon	Aaa-67	-
uncommon	Aaa-68	-
uncommon	Aaa-69	-
uncommon	Aaa-70	-

L14 ANSWER 63 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
 CN 44: PN: US6500431 SEQID: 44 unclaimed protein (9CI) (CA INDEX NAME)
 RN 480474-30-4 REGISTRY
 SQL 70

SEQ 1 XXXXXDVCQ DXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX
 =====

HITS AT: 7-11

RELATED SEQUENCES AVAILABLE WITH SEQLINK
 NTE

type	location			description
uncommon	Aaa-1	-	-	
uncommon	Aaa-2	-	-	
uncommon	Aaa-3	-	-	
uncommon	Aaa-4	-	-	
uncommon	Aaa-5	-	-	
uncommon	Aaa-6	-	-	
uncommon	Aaa-12	-	-	
uncommon	Aaa-13	-	-	
uncommon	Aaa-14	-	-	
uncommon	Aaa-15	-	-	
uncommon	Aaa-16	-	-	
uncommon	Aaa-17	-	-	
uncommon	Aaa-18	-	-	
uncommon	Aaa-19	-	-	
uncommon	Aaa-20	-	-	
uncommon	Aaa-21	-	-	
uncommon	Aaa-22	-	-	
uncommon	Aaa-23	-	-	
uncommon	Aaa-24	-	-	
uncommon	Aaa-25	-	-	
uncommon	Aaa-26	-	-	
uncommon	Aaa-27	-	-	
uncommon	Aaa-28	-	-	
uncommon	Aaa-29	-	-	
uncommon	Aaa-30	-	-	
uncommon	Aaa-31	-	-	
uncommon	Aaa-32	-	-	
uncommon	Aaa-33	-	-	
uncommon	Aaa-34	-	-	
uncommon	Aaa-35	-	-	
uncommon	Aaa-36	-	-	
uncommon	Aaa-37	-	-	
uncommon	Aaa-38	-	-	
uncommon	Aaa-39	-	-	
uncommon	Aaa-40	-	-	
uncommon	Aaa-41	-	-	
uncommon	Aaa-42	-	-	
uncommon	Aaa-43	-	-	
uncommon	Aaa-44	-	-	
uncommon	Aaa-45	-	-	
uncommon	Aaa-46	-	-	
uncommon	Aaa-47	-	-	
uncommon	Aaa-48	-	-	
uncommon	Aaa-49	-	-	
uncommon	Aaa-50	-	-	
uncommon	Aaa-51	-	-	
uncommon	Aaa-52	-	-	
uncommon	Aaa-53	-	-	

uncommon	Aaa-54	-	-
uncommon	Aaa-55	-	-
uncommon	Aaa-56	-	-
uncommon	Aaa-57	-	-
uncommon	Aaa-58	-	-
uncommon	Aaa-59	-	-
uncommon	Aaa-60	-	-
uncommon	Aaa-61	-	-
uncommon	Aaa-62	-	-
uncommon	Aaa-63	-	-
uncommon	Aaa-64	-	-
uncommon	Aaa-65	-	-
uncommon	Aaa-66	-	-
uncommon	Aaa-67	-	-
uncommon	Aaa-68	-	-
uncommon	Aaa-69	-	-
uncommon	Aaa-70	-	-

L14 ANSWER 64 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Valine, glycyl-L-.alpha.-aspartyl-L-valyl-L-cysteinyl-L-glutaminy-L-
.alpha.-aspartyl-L-cysteinyl-L-isoleucyl-L-glutaminy-L-methionyl- (9CI)
(CA INDEX NAME)

OTHER NAMES:

CN 19: PN: US6500431 SEQID: 19 unclaimed sequence
RN 480433-06-5 REGISTRY
SQL 11

SEQ 1 GDVCQDCIQM V

=====

HITS AT: 2-6

L14 ANSWER 65 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Leucine, L-alanyl-L-threonyl-L-seryl-L-arginyl-L-seryl-L-arginyl-L-
alanylglycyl-L-leucyl-L-leucyl-L-valyl-L-.alpha.-aspartyl-L-methionyl-L-
cysteinyl-L-glutaminy-L-.alpha.-aspartyl-L-histidyl-L-prolyl-L-
arginylglycyl-L-phenylalanyl-L-glutaminy-L-cysteinyl-L-leucyl-L-lysyl-L-
.alpha.-glutamyl-L-seryl-L-cysteinyl-L-lysyl-L-asparaginy-L-.alpha.-
glutamyl-L-valylglycyl-L-glutaminy-L-.alpha.-glutamyl-L-histidyl-L-leucyl-
L-valyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 26: PN: WO02095001 FIGURE: 2B unclaimed sequence
RN 477519-67-8 REGISTRY
SQL 40

SEQ 1 ATSRSRAGLL VDMCQDHPRG FQCLKESCKN EVGQEHLVDL

=====

HITS AT: 12-16

L14 ANSWER 66 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN Protein (human breast-specific fragment 70-amino acid) (9CI) (CA INDEX
NAME)

OTHER NAMES:

CN 161: PN: WO02066605 SEQID: 161 claimed protein
RN 452381-07-6 REGISTRY
SQL 70

SEQ 1 MVMCQPEGNV YAVLRSPLFL ENQQNRADHL AYHFCVLLVP GIGLWFDHCC

=====

51 DHCSADCDLQ NTESKLQSPW

=

HITS AT: 47-51

L14 ANSWER 67 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN Protein (human gene XAGE-4 fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:

CN GenBank CAC83092
CN GenBank CAC83092 (Translated from: GenBank AJ318895)
CN Tumor antigen homolog (human gene XAGE-4 fragment)
RN 449815-87-6 REGISTRY
SQL 69

SEQ 1 PPPELIGPML EPSDEEPQQE EPPTESRDPT PVPDLETDLQ ELSQSKTGDE

51 CRDGPDDKGK IQPNQSNLK

==

===

HITS AT: 49-53

L14 ANSWER 68 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Proline, L-phenylalanyl-L-lysyl-L-threonyl-L-lysyl-L-leucyl-L-alanyl-L-lysyl-L-.alpha.-aspartyl-L-isoleucyl-L-cysteiny-L-alanyl-L-.alpha.-aspartyl-L-prolyl-L-lysyl-L-lysyl-L-lysyl-L-tryptophyl-L-valyl-L-glutaminy-L-.alpha.-aspartyl-L-seryl-L-methionyl-L-lysyl-L-tyrosyl-L-leucyl-L-.alpha.-aspartyl-L-glutaminy-L-lysyl-L-seryl-L-prolyl-L-threonyl-L-prolyl-L-lysyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 25: PN: US6403782 SEQID: 22 unclaimed protein
RN 434530-02-6 REGISTRY
SQL 34

SEQ 1 FKTKLAKDIC ADPKKKWVQD SMKYLDQKSP TPKP

=== ==

HITS AT: 8-12

L14 ANSWER 69 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN 92: PN: WO0226815 SEQID: 92 unclaimed sequence (9CI) (CA INDEX NAME)
RN 406618-36-8 REGISTRY
SQL 70

SEQ 51 VVVDKSSHD ECQDALNILP

= =====

HITS AT: 60-64

L14 ANSWER 70 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN 91: PN: WO0226815 SEQID: 91 unclaimed sequence (9CI) (CA INDEX NAME)
RN 406618-35-7 REGISTRY
SQL 70

SEQ 51 LVVDRESSHD ECQDALNILP

= =====

HITS AT: 60-64

L14 ANSWER 71 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN 90: PN: WO0226815 SEQID: 90 unclaimed sequence (9CI) (CA INDEX NAME)
RN 406618-34-6 REGISTRY
SQL 70

SEQ 51 LVVDRESSHD ECQDALNILP

= =====

HITS AT: 60-64

L14 ANSWER 72 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN 89: PN: WO0226815 SEQID: 89 unclaimed sequence (9CI) (CA INDEX NAME)
RN 406618-33-5 REGISTRY
SQL 70

SEQ 51 LVVDRESSHD ECQDAVNILP

= =====

HITS AT: 60-64

L14 ANSWER 73 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Isoleucine, L-.alpha.-aspartyl-L-tyrosyl-L-cysteinyl-L-histidyl-L-.alpha.-aspartyl-L-lysyl-L-methionyl-L-isoleucyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 24: PN: WO0220560 SEQID: 27 claimed sequence

RN 404387-68-4 REGISTRY

SQL 9

SEQ 1 DYCHDKMII

=====

HITS AT: 1-5

L14 ANSWER 74 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Tyrosine, L-.alpha.-aspartyl-L-alanyl-L-.alpha.-glutamyl-L-lysyl-L-seryl-L-.alpha.-aspartyl-L-isoleucyl-L-cysteinyl-L-threonyl-L-.alpha.-aspartyl-L-.alpha.-glutamyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 376: PN: US20040058881 PAGE: 46 claimed sequence

RN 361366-26-9 REGISTRY

SQL 12

SEQ 1 DAEKSDICTD EY

=====

HITS AT: 6-10

L14 ANSWER 75 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Glutamic acid, L-cysteinyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-seryl-L-serylglycylglycyl-L-seryl-L-prolyl-L-glutaminylglycyl-L-isoleucyl-L-alanylglycyl-L-glutaminyl-L-.alpha.-aspartyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-alanyl-L-.alpha.-aspartyl-L-valyl-L-cysteinyl-L-methionyl-L-.alpha.-aspartyl-L-prolyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 49: PN: WO0125267 FIGURE: 12C claimed sequence

RN 334660-22-9 REGISTRY

SQL 29

SEQ 1 CAPPSSGGS PQGIAGQDEE DADVCMDE

=====

HITS AT: 23-27

L14 ANSWER 76 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Glutamic acid, L-cysteinyl-L-seryl-L-prolyl-L-glutaminylglycyl-L-isoleucyl-L-alanylglycyl-L-glutaminyl-L-arginyl-L-asparaginyl-L-phenylalanyl-L-asparaginyl-L-alanyl-L-.alpha.-aspartyl-L-valyl-L-cysteinyl-L-methionyl-L-.alpha.-aspartyl-L-prolyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 40: PN: WO0125267 FIGURE: 3C claimed sequence

RN 334660-13-8 REGISTRY

SQL 21

SEQ 1 CSPQGIAGQR NFNADVCMDEP E

=====

HITS AT: 15-19

L14 ANSWER 77 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Glutamic acid, L-cysteinyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-seryl-L-seryl-L-glutaminyl-L-phenylalanylglycyl-L-prolyl-L-leucylglycyl-L-methionyl-L-tryptophylglycyl-L-glutaminyl-L-arginyl-L-asparaginyl-L-phenylalanyl-L-asparaginyl-L-alanyl-L-.alpha.-aspartyl-L-valyl-L-cysteinyl-

L-methionyl-L-.alpha.-aspartyl-L-prolyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 38: PN: WO0125267 FIGURE: 1C claimed sequence
RN 334660-11-6 REGISTRY
SQL 29

SEQ 1 CAPPSSQFG PLGMWGQRNF NADVCMDE
=====

HITS AT: 23-27

L14 ANSWER 78 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN 21: PN: WO0123524 FIGURE: 4B unclaimed sequence (9CI) (CA INDEX NAME)
RN 334490-78-7 REGISTRY
SQL 42

SEQ 1 CPAQTFRC SN GKCLSKSQ NGKDDCGDGS DEASCPKVVN VT
=====

HITS AT: 24-28

L14 ANSWER 79 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN Colon cancer-associated protein (human clone HCLB047 56-amino acid) (9CI)
(CA INDEX NAME)

OTHER NAMES:

CN 45: PN: WO0112781 SEQID: 45 claimed protein
RN 326893-82-7 REGISTRY
SQL 56

SEQ 1 HEENQKDPLA VDKIMKDLQ CRDGKVGFS FFSLIAGLTI ACNDYFVVHM
== ==

HITS AT: 19-23

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L14 ANSWER 80 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Isoleucine, L-isoleucyl-L-methionyl-L-lysyl-L-.alpha.-aspartyl-L-leucyl-
L-.alpha.-aspartyl-L-glutamyl-L-cysteinyl-L-arginyl-L-.alpha.-
aspartylglycyl-L-lysyl-L-valylglycyl-L-phenylalanyl-L-glutamyl-L-seryl-L-
phenylalanyl-L-phenylalanyl-L-seryl-L-leucyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 51: PN: WO0112781 SEQID: 50 unclaimed sequence
CN 57: PN: US20030203361 SEQID: 50 unclaimed sequence
RN 326813-00-7 REGISTRY
SQL 22

SEQ 1 IMKDLQCRD GKVGFSFFS LI
=====

HITS AT: 6-10

L14 ANSWER 81 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN 22: PN: WO0053232 FIG: 11 unclaimed protein (9CI) (CA INDEX NAME)
RN 293307-71-8 REGISTRY
SQL 36

SEQ 1 SCPAQTFRC SN GKCLSKSQ CNGKDDCGDG SDEASC
=====

HITS AT: 25-29

L14 ANSWER 82 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Aspartic acid, L-.alpha.-aspartyl-L-valyl-L-cysteinyl-L-.alpha.-aspartyl-
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 28: PN: WO0002902 TABLE: 2 claimed sequence
CN 40: PN: US6500431 SEQID: 40 unclaimed sequence

RN 255365-99-2 REGISTRY
SQL 5

SEQ 1 DVCDD

=====

HITS AT: 1-5

L14 ANSWER 83 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Aspartic acid, L-.alpha.-aspartyl-L-valyl-L-cysteinyL-L-.alpha.-glutamyl-
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 27: PN: WO0002902 TABLE: 2 claimed sequence
CN 39: PN: US6500431 SEQID: 39 unclaimed sequence
RN 255365-98-1 REGISTRY
SQL 5

SEQ 1 DVCED

=====

HITS AT: 1-5

L14 ANSWER 84 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Aspartic acid, L-.alpha.-aspartyl-L-valyl-L-cysteinyL-L-seryl- (9CI)
(CA INDEX NAME)

OTHER NAMES:

CN 26: PN: WO0002902 TABLE: 2 claimed sequence
CN 38: PN: US6500431 SEQID: 38 unclaimed sequence
RN 255365-97-0 REGISTRY
SQL 5

SEQ 1 DVCSD

=====

HITS AT: 1-5

L14 ANSWER 85 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Aspartic acid, L-.alpha.-aspartyl-L-leucyl-L-cysteinyL-L-glutaminyL-
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 25: PN: WO0002902 TABLE: 2 claimed sequence
CN 37: PN: US6500431 SEQID: 37 unclaimed sequence
RN 255365-96-9 REGISTRY
SQL 5

SEQ 1 DLCQD

=====

HITS AT: 1-5

L14 ANSWER 86 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Aspartic acid, L-.alpha.-aspartyl-L-isoleucyl-L-cysteinyL-L-glutaminyL-
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 24: PN: WO0002902 TABLE: 2 claimed sequence
CN 36: PN: US6500431 SEQID: 36 unclaimed sequence
RN 255365-95-8 REGISTRY
SQL 5

SEQ 1 DICQD

=====

HITS AT: 1-5

L14 ANSWER 87 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Aspartic acid, L-.alpha.-aspartyl-L-alanyl-L-cysteinyL-L-glutaminyL-
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 23: PN: WO0002902 TABLE: 2 claimed sequence
CN 35: PN: US6500431 SEQID: 35 unclaimed sequence
RN 255365-94-7 REGISTRY
SQL 5

SEQ 1 DACQD

HITS AT: 1-5

L14 ANSWER 88 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Valine, glycyl-L-.alpha.-aspartyl-L-valyl-L-cysteinyl-L-glutaminy-L-.alpha.-aspartyl-L-seryl-L-isoleucyl-L-glutaminy-L-methionyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 21: PN: WO0002902 TABLE: 2 claimed sequence
CN 33: PN: US6500431 SEQID: 33 unclaimed sequence
RN 255365-92-5 REGISTRY
SQL 11

SEQ 1 GDVCQDSIQM V

HITS AT: 2-6

L14 ANSWER 89 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Aspartic acid, L-.alpha.-aspartyl-L-valyl-L-cysteinyl-L-glutaminy-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 16: PN: WO0002902 TABLE: 2 claimed sequence
CN 28: PN: US6500431 SEQID: 28 unclaimed sequence
RN 255365-87-8 REGISTRY
SQL 5

SEQ 1 DVCQD

HITS AT: 1-5

L14 ANSWER 90 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Cysteine, L-.alpha.-aspartyl-L-valyl-L-cysteinyl-L-glutaminy-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 15: PN: WO0002902 TABLE: 2 claimed sequence
CN 27: PN: US6500431 SEQID: 27 unclaimed sequence
RN 255365-86-7 REGISTRY
SQL 6

SEQ 1 DVCQDC

HITS AT: 1-5

L14 ANSWER 91 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN
CN L-Isoleucine, L-.alpha.-aspartyl-L-valyl-L-cysteinyl-L-glutaminy-L-.alpha.-aspartyl-L-cysteinyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 14: PN: WO0002902 TABLE: 2 claimed sequence
CN 26: PN: US6500431 SEQID: 26 unclaimed sequence
RN 255365-85-6 REGISTRY
SQL 7

SEQ 1 DVCQDCI

HITS AT: 1-5

L14 ANSWER 92 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Glutamine, L-.alpha.-aspartyl-L-valyl-L-cysteinyl-L-glutaminyl-L-.alpha.-
aspartyl-L-cysteinyl-L-isoleucyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 13: PN: WO0002902 TABLE: 2 claimed sequence
CN 25: PN: US6500431 SEQID: 25 unclaimed sequence
RN 255365-84-5 REGISTRY
SQL 8

SEQ 1 DVCQDCIQ

=====

HITS AT: 1-5

L14 ANSWER 93 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Methionine, L-.alpha.-aspartyl-L-valyl-L-cysteinyl-L-glutaminyl-L-
.alpha.-aspartyl-L-cysteinyl-L-isoleucyl-L-glutaminyl- (9CI) (CA INDEX
NAME)

OTHER NAMES:

CN 12: PN: WO0002902 TABLE: 2 claimed sequence
CN 24: PN: US6500431 SEQID: 24 unclaimed sequence
RN 255365-83-4 REGISTRY
SQL 9

SEQ 1 DVCQDCIQM

=====

HITS AT: 1-5

L14 ANSWER 94 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Valine, L-.alpha.-aspartyl-L-valyl-L-cysteinyl-L-glutaminyl-L-.alpha.-
aspartyl-L-cysteinyl-L-isoleucyl-L-glutaminyl-L-methionyl- (9CI) (CA
INDEX NAME)

OTHER NAMES:

CN 21: PN: US6500431 SEQID: 21 unclaimed sequence
CN 9: PN: WO0002902 TABLE: 2 claimed sequence
RN 255365-80-1 REGISTRY
SQL 10

SEQ 1 DVCQDCIQMV

=====

HITS AT: 1-5

L14 ANSWER 95 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Valine, L-cysteinyl-L-.alpha.-aspartyl-L-valyl-L-cysteinyl-L-glutaminyl-
L-.alpha.-aspartyl-L-cysteinyl-L-isoleucyl-L-glutaminyl-L-methionyl- (9CI)
(CA INDEX NAME)

OTHER NAMES:

CN 7: PN: WO0002902 TABLE: 2 claimed sequence
RN 255365-78-7 REGISTRY
SQL 11

SEQ 1 CDVCQDCIQM V

=====

HITS AT: 2-6

L14 ANSWER 96 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Valine, L-glutaminyl-L-prolyl-L-lysyl-L-.alpha.-aspartyl-L-
asparaginyglycyl-L-.alpha.-aspartyl-L-valyl-L-cysteinyl-L-glutaminyl-L-
.alpha.-aspartyl-L-cysteinyl-L-isoleucyl-L-glutaminyl- (9CI) (CA INDEX
NAME)

OTHER NAMES:

CN 13: PN: US6500431 SEQID: 13 unclaimed sequence
CN 1: PN: WO0002902 TABLE: 2 claimed sequence
RN 255365-72-1 REGISTRY
SQL 15

SEQ 1 QPKDNGDVCQ DCIQV

=====

HITS AT: 7-11

L14 ANSWER 97 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Tyrosine, L-seryl-L-seryl-L-.alpha.-aspartyl-L-tryptophyl-L-.alpha.-
aspartyl-L-tyrosyl-L-cysteinyl-L-cysteinyl-L-.alpha.-aspartyl-L-leucyl-L-
cysteinyl-L-cysteinyl-L-asparaginyl-L-prolyl-L-alanyl-L-cysteinyl-L-
alanylglycyl-L-cysteinyl- (9CI) (CA INDEX NAME)

RN 237055-26-4 REGISTRY

SQL 20

SEQ 1 SSDWDYCCDL CCNPACAGCY

=====

HITS AT: 5-9

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L14 ANSWER 98 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Tyrosine, L-lysyl-L-cysteinyl-L-.alpha.-aspartyl-L-isoleucyl-L-cysteinyl-
L-threonyl-L-.alpha.-aspartyl-L-.alpha.-glutamyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 24: PN: WO0236146 SEQID: 24 claimed sequence

CN 411: PN: US20040058881 TABLE: 14.5 claimed sequence

CN 62: PN: WO03106616 SEQID: 46 claimed sequence

CN 67: PN: WO03100027 SEQID: 67 unclaimed sequence

CN 72: PN: WO03098219 TABLE: 3f claimed sequence

RN 197171-78-1 REGISTRY

SQL 9

SEQ 1 KCDICTDEY

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HITS AT: 3-7

L14 ANSWER 99 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Leucine, L-lysyl-L-prolylglycyl-L-.alpha.-glutamyl-L-threonyl-L-
phenylalanyl-L-phenylalanyl-L-methionyl-L-cysteinyl-L-seryl-L-cysteinyl-L-
seryl-L-seryl-L-.alpha.-aspartyl-L-.alpha.-glutamyl-L-cysteinyl-L-
asparaginyl-L-.alpha.-aspartyl-L-asparaginyl-L-isoleucyl-L-isoleucyl-L-
phenylalanyl-L-seryl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-tyrosyl-L-
asparaginyl-L-threonyl-L-seryl-L-asparaginyl-L-prolyl-L-.alpha.-aspartyl-L-
leucyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 3: PN: US6291237 SEQID: 4 unclaimed protein

RN 183815-68-1 REGISTRY

SQL 34

SEQ 1 KPGETFFMCS CSSDECNDNI IFSEEYNTSN PDLL

=====

HITS AT: 14-18

L14 ANSWER 100 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Histidine, L-.alpha.-aspartyl-L-prolyl-L-cysteinyl-L-.alpha.-glutamyl-L-
.alpha.-aspartylglycyl-L-tyrosyl-L-tryptophyl-L-leucyl-L-seryl-L-seryl-L-
valylglycyl-L-arginyl-L-alanylglycyl-L-alanyl-L-seryl-L-isoleucyl-L-
arginylglycyl-L-cysteinylglycyl-L-alanyl-L-isoleucyl-L-arginyl-L-arginyl-L-
seryl-L-seryl-L-arginyl-L-threonyl-L-leucyl-L-threonyl-L-alanyl-L-.alpha.-
glutamyl-L-tyrosyl-L-seryl-L-threonyl-L-arginyl-L-alanyl-L-seryl-L-
asparaginyl- (9CI) (CA INDEX NAME)

RN 178095-95-9 REGISTRY

SQL 43

SEQ . 1 DPCEDGYWLS SVGRAGASIR GCGAIRRSSR TLTAEYSTR SNH

=====

HITS AT: 1-5

L14 ANSWER 101 OF 101 REGISTRY COPYRIGHT 2004 ACS on STN

CN L-Tyrosine, N-[N-[N-[N2-[N-[N-[N-(N-L-arginylglycyl)-L-.alpha.-aspartyl]-L-seryl]-L-cysteinyl]-L-arginyl]-L-.alpha.-aspartyl]-L-seryl]- (9CI) (CA INDEX NAME)

RN 162929-41-1 REGISTRY

SQL 9

SEQ 1 RGDSCRDSY

=====

HITS AT: 3-7

FILE 'HOME' ENTERED AT 10:33:48 ON 06 MAY 2004

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2004, 10:44:26 ; Search time 23 Seconds
(without alignments)
11.223 Million cell updates/sec

Title: SEQ1
Perfect score: 23
Sequence: 1 dxcxd 5

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 339

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	5	4	US-09-352-548-28
2	23	100.0	5	4	US-09-352-548-35
3	23	100.0	5	4	US-09-352-548-36
4	23	100.0	5	4	US-09-352-548-37
5	23	100.0	5	4	US-09-352-548-38
6	23	100.0	5	4	US-09-352-548-39
7	23	100.0	5	4	US-09-352-548-40
8	23	100.0	6	4	US-09-352-548-27
9	23	100.0	7	4	US-09-352-548-26
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12	23	100.0	9	1	US-08-459-019A-5
13	23	100.0	9	2	US-08-460-428A-5
14	23	100.0	9	3	US-08-458-860A-5
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16	23	100.0	9	3	US-09-258-754-345
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18	23	100.0	9	3	US-09-042-107-331
19	23	100.0	9	3	US-09-042-107-345
20	23	100.0	9	4	US-09-352-548-24
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23	23	100.0	9	4	US-09-341-982-37
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25	23	100.0	9	4	US-09-722-250D-345
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70	23	100.0	18	6	5177197-9	Patent No. 5177197
71	23	100.0	19	3	US-08-584-671-5	Sequence 5, Appl
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113	23	100.0	40	3	US-08-945-983-6	Sequence 6, Appl	186	23	100.0	75	3	US-09-249-472-26	Sequence 26, Appl
114	23	100.0	40	3	US-09-670-827-25	Sequence 25, Appl	187	23	100.0	75	3	US-09-249-472-57	Sequence 26, Appl
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123	23	100.0	45	2	US-08-800-644-106	Sequence 106, App	196	23	100.0	75	4	US-09-249-473-26	Sequence 26, Appl
124	23	100.0	45	3	US-08-990-065-21	Sequence 21, Appl	197	23	100.0	75	4	US-09-249-473-57	Sequence 26, Appl
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126	23	100.0	45	4	US-09-380-532-11	Sequence 11, Appl	199	23	100.0	76	2	US-08-326-110A-55	Sequence 55, Appl
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128	23	100.0	51	2	US-08-870-518-25	Sequence 25, Appl	201	23	100.0	77	2	US-08-465-380-55	Sequence 55, Appl
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131	23	100.0	51	4	US-09-494-151-7	Sequence 7, Appl	204	23	100.0	77	2	US-08-461-965-55	Sequence 55, Appl
132	23	100.0	51	4	US-09-205-258-583	Sequence 583, App	205	23	100.0	77	2	US-08-634-641-55	Sequence 55, Appl
133	23	100.0	51	4	US-09-972-484-7	Sequence 7, Appl	206	23	100.0	77	3	US-09-249-471-55	Sequence 55, Appl
134	23	100.0	52	4	US-09-621-976-6222	Sequence 6222, Ap	207	23	100.0	77	3	US-09-249-472-55	Sequence 55, Appl
135	23	100.0	55	4	US-09-187-789-47	Sequence 47, Appl	208	23	100.0	77	3	US-09-249-451-55	Sequence 55, Appl
136	23	100.0	55	4	US-09-139-600-42	Sequence 42, Appl	209	23	100.0	77	3	US-08-809-455-55	Sequence 55, Appl
137	23	100.0	55	4	US-09-621-976-5065	Sequence 5065, Ap	210	23	100.0	77	3	US-09-249-461-55	Sequence 55, Appl
138	23	100.0	60	4	US-09-381-546-13	Sequence 13, Appl	211	23	100.0	77	3	US-09-249-448-55	Sequence 55, Appl
139	23	100.0	60	4	US-09-381-546-15	Sequence 15, Appl	212	23	100.0	77	3	US-08-061-376-11	Sequence 11, Appl
140	23	100.0	63	4	US-09-381-546-16	Sequence 16, Appl	213	23	100.0	77	3	US-08-866-545-2	Sequence 2, Appl
141	23	100.0	67	4	US-09-543-681A-5213	Sequence 5213, Ap	214	23	100.0	77	4	US-09-249-473-55	Sequence 55, Appl
142	23	100.0	67	4	US-09-543-681A-5326	Sequence 5326, Ap	215	23	100.0	77	4	US-09-627-775-2	Sequence 2, Appl
143	23	100.0	67	4	US-09-543-681A-7265	Sequence 7265, Ap	216	23	100.0	78	2	US-08-465-380-28	Sequence 28, Appl
144	23	100.0	67	4	US-09-543-681A-7534	Sequence 7534, Ap	217	23	100.0	78	2	US-08-465-380-47	Sequence 47, Appl
145	23	100.0	67	4	US-09-540-236-2014	Sequence 2014, Ap	218	23	100.0	78	2	US-08-465-380-53	Sequence 53, Appl
146	23	100.0	68	4	US-09-107-532A-4291	Sequence 4291, Ap	219	23	100.0	78	2	US-08-465-380-54	Sequence 54, Appl
147	23	100.0	70	4	US-09-352-548-44	Sequence 44, Appl	220	23	100.0	78	2	US-08-465-380-56	Sequence 56, Appl
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149	23	100.0	70	4	US-09-352-548-46	Sequence 46, Appl	222	23	100.0	78	2	US-08-486-397-28	Sequence 28, Appl
150	23	100.0	70	4	US-09-352-548-49	Sequence 49, Appl	223	23	100.0	78	2	US-08-486-397-47	Sequence 47, Appl
151	23	100.0	70	4	US-09-352-548-50	Sequence 50, Appl	224	23	100.0	78	2	US-08-486-397-54	Sequence 54, Appl
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153	23	100.0	70	4	US-09-352-548-52	Sequence 52, Appl	226	23	100.0	78	2	US-08-486-398-28	Sequence 28, Appl
154	23	100.0	70	4	US-09-352-548-53	Sequence 53, Appl	227	23	100.0	78	2	US-08-486-399-53	Sequence 53, Appl
155	23	100.0	70	4	US-09-107-532A-6358	Sequence 6358, Ap	228	23	100.0	78	2	US-08-486-399-55	Sequence 55, Appl
156	23	100.0	71	4	US-09-543-681A-4174	Sequence 4174, Ap	229	23	100.0	78	2	US-08-486-399-53	Sequence 53, Appl
157	23	100.0	72	4	US-09-543-681A-8206	Sequence 8206, Ap	230	23	100.0	78	2	US-08-486-399-54	Sequence 54, Appl
158	23	100.0	74	2	US-08-465-380-42	Sequence 42, Appl	231	23	100.0	78	2	US-08-486-399-56	Sequence 56, Appl
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163	23	100.0	74	3	US-09-249-471-42	Sequence 42, Appl	236	23	100.0	78	2	US-08-461-965-56	Sequence 56, Appl
164	23	100.0	74	3	US-09-249-472-42	Sequence 42, Appl	237	23	100.0	78	2	US-08-326-110A-57	Sequence 57, Appl
165	23	100.0	74	3	US-09-249-451-42	Sequence 42, Appl	238	23	100.0	78	2	US-08-634-641-28	Sequence 28, Appl
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170	23	100.0	74	4	US-09-479-729B-20	Sequence 20, Appl	243	23	100.0	78	3	US-09-249-471-28	Sequence 28, Appl
171	23	100.0	74	4	US-09-366-887A-25	Sequence 25, Appl	244	23	100.0	78	3	US-09-249-471-47	Sequence 47, Appl
172	23	100.0	74	4	US-09-249-473-42	Sequence 42, Appl	245	23	100.0	78	3	US-09-249-471-53	Sequence 53, Appl
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280 23 100.0 79 3 US-09-027-376-14 Sequence 14, Appl
281 23 100.0 79 3 US-09-027-376-16 Sequence 16, Appl
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285 23 100.0 80 2 US-08-584-671-15 Sequence 15, Appl
286 23 100.0 80 3 US-09-027-376-15 Sequence 15, Appl
287 23 100.0 81 4 US-08-939-107-38 Sequence 38, Appl
288 23 100.0 81 4 US-09-352-548-2 Sequence 2, Appl
289 23 100.0 81 4 US-09-686-583B-17 Sequence 17, Appl
290 23 100.0 81 4 US-09-543-681A-7102 Sequence 7102, Ap
291 23 100.0 82 4 US-09-228-986-85 Sequence 85, Appl
292 23 100.0 83 2 US-08-465-380-52 Sequence 52, Appl
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295 23 100.0 83 2 US-08-461-965-52 Sequence 52, Appl
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303 23 100.0 83 3 US-09-249-448-52 Sequence 52, Appl
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305 23 100.0 84 4 US-09-621-976-4389 Sequence 4389, Ap
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307 23 100.0 85 2 US-08-467-389-18 Sequence 18, Appl
308 23 100.0 85 2 US-08-779-319-18 Sequence 18, Appl
309 23 100.0 85 2 US-08-469-219-18 Sequence 18, Appl
310 23 100.0 85 3 US-09-228-152-17 Sequence 17, Appl
311 23 100.0 87 4 US-09-371-671B-4 Sequence 4, Appl
312 23 100.0 89 4 US-09-858-664A-33 Sequence 33, Appl
313 23 100.0 89 4 US-10-274-978-34 Sequence 34, Appl
314 23 100.0 91 4 US-09-235-451-45 Sequence 45, Appl
315 23 100.0 92 4 US-08-939-107-36 Sequence 36, Appl
316 23 100.0 93 4 US-09-615-192A-346 Sequence 346, App
317 23 100.0 93 4 US-09-621-976-4652 Sequence 4652, Ap
318 23 100.0 94 1 US-08-226-264-22 Sequence 22, Appl
319 23 100.0 94 2 US-08-465-380-22 Sequence 22, Appl
320 23 100.0 94 2 US-08-480-478-51 Sequence 51, Appl
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323 23 100.0 94 2 US-08-461-965-22 Sequence 22, Appl
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325 23 100.0 94 2 US-08-634-641-22 Sequence 22, Appl
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329 23 100.0 94 3 US-08-809-455-22 Sequence 22, Appl
330 23 100.0 94 3 US-09-249-461-22 Sequence 22, Appl
331 23 100.0 94 3 US-09-249-448-22 Sequence 22, Appl
332 23 100.0 94 4 US-09-249-473-22 Sequence 22, Appl
333 23 100.0 95 1 US-07-987-272A-9 Sequence 65, Appl
334 23 100.0 95 4 US-09-399-913-65 Sequence 9, Appl
335 23 100.0 96 3 US-09-230-637-44 Sequence 44, Appl
336 23 100.0 96 4 US-09-489-039A-10646 Sequence 10646, A
337 23 100.0 96 4 US-09-621-976-4327 Sequence 4327, Ap
338 23 100.0 97 4 US-09-366-887A-27 Sequence 27, Appl
339 23 100.0 97 4 US-09-545-894-8 Sequence 8, Appli
; Sequence 28, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-D6
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-28
Query Match 100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
Db 1 DVCQD 5
RESULT 2
US-09-352-548-35
; Sequence 35, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 35
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-(A3)-D6
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-35

Query Match          100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DACQD 5

RESULT 3
US-09-352-548-36
; Sequence 36, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-(I3)-D6
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-36

Query Match          100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DACQD 5

RESULT 4
US-09-352-548-37
; Sequence 37, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-(L3)-D6
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-37

Query Match          100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DACQD 5

RESULT 5
US-09-352-548-38
; Sequence 38, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-(S5)-D6
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-38

Query Match          100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 60.0%; Pred. No. 3e+05;
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Qy 1 DXCXD 5
Db 1 DVCSD 5

RESULT 6
US-09-352-548-39
; Sequence 39, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-(E5)-D6
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-39

Query Match          100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
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Db      1 DVCED 5
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      |.:|:|

RESULT 7
US-09-352-548-40
; Sequence 40, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-(D5)-D6
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-40

Query Match      100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DXCXD 5
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Db      1 DVCDD 5

RESULT 8
US-09-352-548-27
; Sequence 27, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-C7
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-27

Query Match      100.0%; Score 23; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DXCXD 5
      |.:|:|
Db      1 DVCQD 5

RESULT 9
US-09-352-548-26
; Sequence 26, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-18
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-26

Query Match      100.0%; Score 23; DB 4; Length 7;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DXCXD 5
      |.:|:|
Db      1 DVCQD 5

RESULT 10
US-09-352-548-25
; Sequence 25, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-Q9
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-25

Query Match      100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DXCXD 5
      |.:|:|
Db      1 DVCQD 5

RESULT 11
US-08-109-391A-5
; Sequence 5, Application US/08109391A
; Patent No. 5639876
; GENERAL INFORMATION:
; APPLICANT: Tripp, Cynthia A.
; APPLICANT: Frank, Glenn R.
; APPLICANT: Grievie, Robert B.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING NOVEL
; TITLE OF INVENTION: PARASITIC HELMINTH PROTEINS
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; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/109,391A
; FILING DATE: 19-AUG-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-109-391A-5
;
; Query Match 100.0%; Score 23; DB 1; Length 9;
; Best Local Similarity 60.0%; Pred. No. 3e+05;
; Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 DXCXD 5
; DB 1 DDCGD 5
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; RESULT 12
; US-08-459-019A-5
; Sequence 5, Application US/08459019A
; Patent No. 5686080
; GENERAL INFORMATION:
; APPLICANT: Tripp, Cynthia A.
; APPLICANT: Frank, Glenn R.
; APPLICANT: Grieve, Robert B.
; TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P4 PROTEINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, #3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,019A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 33,020
; REFERENCE/DOCKET NUMBER: 2618-13-1
; TELECOMMUNICATION INFORMATION:
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; Query Match 100.0%; Score 23; DB 2; Length 9;
; Best Local Similarity 60.0%; Pred. No. 3e+05;
; Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 DXCXD 5
; DB 1 DDCGD 5
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; RESULT 13
; US-08-460-428A-5
; Sequence 5, Application US/08460428A
; Patent No. 5912337
; GENERAL INFORMATION:
; APPLICANT: Tripp, Cynthia A.
; APPLICANT: Frank, Glenn R.
; APPLICANT: Grieve, Robert B.
; TITLE OF INVENTION: NOVEL PARASITIC HELMINTH
; TITLE OF INVENTION: P22U PROTEINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,428A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-13-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-460-428A-5
;
; Query Match 100.0%; Score 23; DB 2; Length 9;
; Best Local Similarity 60.0%; Pred. No. 3e+05;
; Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 DXCXD 5
; DB 1 DDCGD 5
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; RESULT 14
; US-08-460-428A-5
; Sequence 5, Application US/08460428A
; Patent No. 5912337
; GENERAL INFORMATION:
; APPLICANT: Tripp, Cynthia A.
; APPLICANT: Frank, Glenn R.
; APPLICANT: Grieve, Robert B.
; TITLE OF INVENTION: NOVEL PARASITIC HELMINTH
; TITLE OF INVENTION: P22U PROTEINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,428A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-13-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-460-428A-5
;
; Query Match 100.0%; Score 23; DB 2; Length 9;
; Best Local Similarity 60.0%; Pred. No. 3e+05;
; Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 DXCXD 5
; DB 1 DDCGD 5
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; RESULT 14
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US-08-458-860A-5
; Sequence 5, Application US/08458860A
; Patent No. 6100390
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Tripp, Cynthia A.
; APPLICANT: Griewe, Robert B.
; TITLE OF INVENTION: NOVEL PARASITIC HELMINTH
; TITLE OF INVENTION: P22U NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,860A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-13-2
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-860A-5

Query Match 100.0%; Score 23; DB 3; Length 9;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DDCGD 5

RESULT 15
US-09-258-754-331
; Sequence 31, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 331
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (4)
; OTHER INFORMATION: Unsure
; FEATURE:
; OTHER INFORMATION: Unsure
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-331

Query Match 100.0%; Score 23; DB 3; Length 9;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DDCGD 5

RESULT 15
US-09-258-754-331
; Sequence 31, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 331
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; ORGANISM: Artificial Sequence
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; LOCATION: (4)
; OTHER INFORMATION: Unsure
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; OTHER INFORMATION: Unsure
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-331

Query Match 100.0%; Score 23; DB 3; Length 9;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DDCGD 5

RESULT 15
US-09-258-754-331
; Sequence 31, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
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US-09-258-754-331

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Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DDCGD 5

RESULT 15
US-09-258-754-331
; Sequence 31, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 331
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; NAME/KEY: UNSURE
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; OTHER INFORMATION: Unsure
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US-09-258-754-331

Query Match 100.0%; Score 23; DB 3; Length 9;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DDCGD 5

RESULT 15
US-09-258-754-331
; Sequence 31, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 331
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; LOCATION: (4)
; OTHER INFORMATION: Unsure
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; OTHER INFORMATION: Unsure
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-331

Query Match 100.0%; Score 23; DB 3; Length 9;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DDCGD 5

RESULT 15
US-09-258-754-331
; Sequence 31, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-331

Query Match 100.0%; Score 23; DB 3; Length 9;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DDCGD 5

RESULT 15
US-09-258-754-331
; Sequence 31, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 331
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (4)
; OTHER INFORMATION: Unsure
; FEATURE:
; OTHER INFORMATION: Unsure
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-331

Query Match 100.0%; Score 23; DB 3; Length 9;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DDCGD 5

RESULT 15
US-09-258-754-331
; Sequence 31, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 331
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (4)
; OTHER INFORMATION: Unsure
; FEATURE:
; OTHER INFORMATION: Unsure
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-331

Query Match 100.0%; Score 23; DB 3; Length 9;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DDCGD 5

RESULT 15
US-09-258-754-331
; Sequence 31, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/
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/ OPERATING SYSTEM: DOS
/ SOFTWARE: Wordperfect 6.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,290
/ FILING DATE: 21-JAN-1988
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB8914020.6
/ FILING DATE: 19-JUN-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/GB90/00933
/ FILING DATE: 18-JUN-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/659,343
/ FILING DATE: 21-WAR-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/963,127
/ FILING DATE: 19-OCT-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/816,922
/ FILING DATE: 12-WAR-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams, Ph.D., Kathleen A
/ REGISTRATION NUMBER: 34,380
/ REFERENCE/DOCKET NUMBER: 3998/73503
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-227-7111
/ TELEFAX: 617-227-4399
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ US-09-010-290-7

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Query Match 100.0%; Score 23; DB 3; Length 9;
Best Local Similarity 60.0%; Pred. NO.3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels

Qy	1	DXCD	5
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Db	3	DSCR	7

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RESULT 18
US-09-042-107-331
; Sequence 331, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042.107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 331
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-331

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Query Match 100.0%; Score 23; DB 3; Length 9;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels

Qy	1	DXCxD	5
		: :	

Db 1 DRCLD 5

RESULT 19
US-09-042-107-345
; Sequence 345, Application US/09042107
; Patent No. 6233287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Paqualini, Renata
; TITLE OF INVENTION: Molecules that H
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/04
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 345
; LENGTH: 9
; TYPE: PRT
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; LOCATION: (2)
; OTHER INFORMATION: Unsure
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (4)
; OTHER INFORMATION: Unsure
; FEATURE:
; OTHER INFORMATION: Description of A
US-09-042-107-345

Query Match	100.0%;	Score 23;	DB 3;	Length 9;
Best Local	Similarity	100.0%;	Pred. No. 3e+05;	
Matches	5;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

Qy	1	DXCD	5
pb	1	DXCD	5

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RESULT 20
US-09-352-548-24
; Sequence 24, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: NO. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-M10
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-24

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Query Match 100.0%; Score 23; DB 4; Length 9;
Best Local Similarity 60.0%; Pred.No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels

Qy	1	DXCD	5
		: :	
Db	1	DVCD	5

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RESULT 21
US-09-341-982-19
; Sequence 19, Application US/09341982
; Patent No. 6558671
; GENERAL INFORMATION:
; APPLICANT: SLINGLUFF, Craig L.
; APPLICANT: HUNT, Donald F.
; APPLICANT: ENGELHARD, Victor H.
; APPLICANT: KITTLESEN, David
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
; TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR
; FILE REFERENCE: SLINGLUFF=3B
; CURRENT APPLICATION NUMBER: US/09/341,982
; CURRENT FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: PCT/US98/01592
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/037,781
; EARLIER FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: human protein
US-09-341-982-19

Query Match      100.0%; Score 23; DB 4; Length 9;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
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Db 3 DICTD 7

RESULT 22
US-09-341-982-70
; Sequence 70, Application US/09341982
; Patent No. 6558671
; GENERAL INFORMATION:
; APPLICANT: SLINGLUFF, Craig L.
; APPLICANT: HUNT, Donald F.
; APPLICANT: ENGELHARD, Victor H.
; APPLICANT: KITTLESEN, David
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
; TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR
; FILE REFERENCE: SLINGLUFF=3B
; CURRENT APPLICATION NUMBER: US/09/341,982
; CURRENT FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: PCT/US98/01592
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/037,781
; EARLIER FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant
US-09-341-982-70

Query Match      100.0%; Score 23; DB 4; Length 9;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 3 DICTD 7

RESULT 23
US-09-341-982-73
; Sequence 73, Application US/09341982
; Patent No. 6558671
; GENERAL INFORMATION:
; APPLICANT: SLINGLUFF, Craig L.
; APPLICANT: HUNT, Donald F.
; APPLICANT: ENGELHARD, Victor H.
; APPLICANT: KITTLESEN, David
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
; TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR
; FILE REFERENCE: SLINGLUFF=3B
; CURRENT APPLICATION NUMBER: US/09/341,982
; CURRENT FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: PCT/US98/01592
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/037,781
; EARLIER FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant
US-09-341-982-73

Query Match      100.0%; Score 23; DB 4; Length 9;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 3 DICTD 7

RESULT 24
US-09-722-250D-331
; Sequence 331, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 331
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-331

Query Match      100.0%; Score 23; DB 4; Length 9;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 1 DRCLD 5
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RESULT 25
US-09-722-250D-345
; Sequence 345, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruslanti, Erkki
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR FILING DATE: US 09/042,107
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 345
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (2)
; OTHER INFORMATION: Unsure
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (4)
; OTHER INFORMATION: Unsure
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-345

Query Match 100.0%; Score 23; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
Db 1 DXCXD 5

RESULT 26
US-08-482-880-27
; Sequence 27, Application US/08482880
; Patent No. 5736122
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Thrombus Imaging
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/482,880
; APPLICATION NUMBER: 424
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5736122nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,216-L
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: /label= Apc
; OTHER INFORMATION: /note= "The sidechain sulfur atom is covalently
; OTHER INFORMATION: linked to a [3-aminopropyl] group to form a
; OTHER INFORMATION: thioether"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /label= Apc
; OTHER INFORMATION: /note= "The sidechain sulfur atom is covalently
; OTHER INFORMATION: linked to a [3-aminopropyl] group to form a
; OTHER INFORMATION: thioether"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /label= Amide
; OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
; OTHER INFORMATION: amide"
US-08-482-880-27

Query Match 100.0%; Score 23; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
Db 4 DVCXD 8

RESULT 27
US-08-273-274-27
; Sequence 27, Application US/08273274
; Patent No. 5849260
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Thrombus Imaging
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/273,274
; APPLICATION NUMBER: 436
; FILING DATE: 21-MAY-1992
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5849260nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,216

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /label= Apc
OTHER INFORMATION: /note= "The sidechain sulfur atom is covalently linked to a [3-aminopropyl] group to form a thioether"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= Apc
OTHER INFORMATION: /note= "The sidechain sulfur atom is covalently linked to a [3-aminopropyl] group to form a thioether"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /label= Amide
OTHER INFORMATION: /note= "The carboxyl terminus is modified to an amide"
US-08-273-274-27

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 4 DVCGD 8

RESULT 28
US-08-475-041-27
Sequence 27, Application US/08475041
Patent No. 5879658
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Lister-James, John
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Thrombus Imaging
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,041
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5879658nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,216-M
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /label= Apc
OTHER INFORMATION: /note= "The sidechain sulfur atom is covalently linked to a [3-aminopropyl] group to form a thioether"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= Apc
OTHER INFORMATION: /note= "The sidechain sulfur atom is covalently linked to a [3-aminopropyl] group to form a thioether"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /label= Amide
OTHER INFORMATION: /note= "The carboxyl terminus is modified to an amide"
US-08-475-041-27

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 4 DVCGD 8

RESULT 29
US-08-335-832-45
Sequence 45, Application US/08335832
Patent No. 5925331
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Lister-James, John
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Thrombus Imaging
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,832
FILING DATE: 05-JAN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5925331nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,216-I
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317

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/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 1
/ OTHER INFORMATION: /label= BAT
/ OTHER INFORMATION: /note= "The amino terminus is modified by covalent
/ OTHER INFORMATION: linkage to a BAT group."
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 2
/ OTHER INFORMATION: /label= Apc
/ OTHER INFORMATION: /note= "The sidechain sulfur atom is covalently
/ OTHER INFORMATION: linked to a [3-aminopropyl] group to form a
/ OTHER INFORMATION: thioether"
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 6
/ OTHER INFORMATION: /label= Apc
/ OTHER INFORMATION: /note= "The sidechain sulfur atom is covalently
/ OTHER INFORMATION: linked to a [3-aminopropyl] group to form a
/ OTHER INFORMATION: thioether"
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 10
/ OTHER INFORMATION: /label= Amide
/ OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
/ OTHER INFORMATION: amide"
/ US-08-335-832-45

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
Db 4 DVCGD 8

RESULT 30
US-08-484-773-27
/ Sequence 27, Application US/08484773
/ Patent No. 5968476
/ GENERAL INFORMATION:
/ APPLICANT: Dean, Richard T
/ APPLICANT: Lister-James, John
/ TITLE OF INVENTION: Technetium-99m Labeled Peptides for
/ TITLE OF INVENTION: Thrombus Imaging
/ NUMBER OF SEQUENCES: 33
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Banner & Allegretti, Ltd.
/ STREET: 10 South Wacker Drive Suite 3000
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/484,773
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 5968476nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 92,216-0
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/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-715-1000
/ TELEFAX: 312-715-1234
/ TELEX: 910-221-5317
/ INFORMATION FOR SEQ ID NO: 27:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 2
/ OTHER INFORMATION: /label= Apc
/ OTHER INFORMATION: /note= "The sidechain sulfur atom is covalently
/ OTHER INFORMATION: linked to a [3-aminopropyl] group to form a
/ OTHER INFORMATION: thioether"
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 6
/ OTHER INFORMATION: /label= Apc
/ OTHER INFORMATION: /note= "The sidechain sulfur atom is covalently
/ OTHER INFORMATION: linked to a [3-aminopropyl] group to form a
/ OTHER INFORMATION: thioether"
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 10
/ OTHER INFORMATION: /label= Amide
/ OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
/ OTHER INFORMATION: amide"
/ US-08-484-773-27
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Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
Db 4 DVCGD 8
```

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RESULT 31
US-09-352-548-21
/ Sequence 21, Application US/09352548
/ Patent No. 6500431
/ GENERAL INFORMATION:
/ APPLICANT: Gill, Parkash S.
/ APPLICANT: Parkash S. Gill, M.D., Inc.
/ TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
/ FILE REFERENCE: 017986-0004100S
/ CURRENT APPLICATION NUMBER: US/09/352,548
/ CURRENT FILING DATE: 1999-07-12
/ EARLIER APPLICATION NUMBER: US 60/092,647
/ EARLIER FILING DATE: 1998-07-13
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 21
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:D2-V11
/ OTHER INFORMATION: anti-angiogenic polypeptide
/ US-09-352-548-21
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Query Match 100.0%; Score 23; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
Db 1 DVCQD 5
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```

RESULT 32
US-09-341-982-37
; Sequence 37, Application US/09341982
; Patent No. 6558671
; GENERAL INFORMATION:
; APPLICANT: SLINGLUFF, Craig L.
; APPLICANT: HUNT, Donald F.
; APPLICANT: ENGELHARD, Victor H.
; APPLICANT: KITTLESEN, David
; TITLE OF INVENTION: CYSTINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
; TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR
; FILE REFERENCE: SLINGLUFF-38
; CURRENT APPLICATION NUMBER: US/09/341,982
; CURRENT FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: PCT/US98/01592
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/037,781
; EARLIER FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: human protein
US-09-341-982-37

Query Match 100.0%; Score 23; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 4 DICTD 8

RESULT 33
5177197-4
; Patent No. 5177197
; APPLICANT: KANZAKI, TETSUO;OLOFSSON, ANDERS;MOREN, ANITA;
; WERNSTEDT, CHRISTER;HELLMAN, ULF;MIYAZONO, KOHEI;CLAESSON-WELSH,
; LENA;HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
; NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
; SEQ ID NO:4;
; LENGTH: 10
5177197-4

Query Match 100.0%; Score 23; DB 6; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 1 DQCED 5

RESULT 34
US-09-149-476-649
; Sequence 649, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11

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EARLIER APPLICATION NUMBER: 60/043,674
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,669
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,312
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,313
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,672
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 100.0%; Score 23; DB 4; Length 11;
Best Local Similarity 60.0%; Pred. No. 4.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5

Db 5 DPCGD 9

RESULT 35

US-09-352-548-19
Sequence 19, Application US/09352548
Patent No. 6500431
GENERAL INFORMATION:
APPLICANT: Gill, Parkash S.
APPLICANT: Parkash S. Gill, M.D., Inc.
TITLE OF INVENTION: NO. 6500431el Inhibitors of Angiogenesis and Tumor Growth
FILE REFERENCE: 017986-000410US
CURRENT APPLICATION NUMBER: US/09/352,548
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: US 60/092,647
EARLIER FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19

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; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:G1-V11
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-19

Query Match          100.0%; Score 23; DB 4; Length 11;
Best Local Similarity 60.0%; Pred. No. 4.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 2 DVCQD 6

RESULT 36
US-09-352-548-33
; Sequence 33, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:G1-(S7)-V11
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-33

Query Match          100.0%; Score 23; DB 4; Length 11;
Best Local Similarity 60.0%; Pred. No. 4.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 2 DVCQD 6

RESULT 37
US-08-482-228-100
; Sequence 100, Application US/08482228
; Patent No. 5968753
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgerson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,528
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,228
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-08-482-228-100

Query Match          100.0%; Score 23; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 1 DQCID 5

RESULT 38
US-08-482-528-100
; Sequence 100, Application US/08482528
; Patent No. 6017719
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgerson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,528
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
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; MOLECULE TYPE: peptide
US-08-482-528-100

Query Match      100.0%; Score 23; DB 3; Length 12;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 1 DQCID 5

RESULT 39
US-09-341-982-10
; Sequence 10, Application US/09341982
; Patent No. 6558671
; GENERAL INFORMATION:
; APPLICANT: SLINGLUFF, Craig L.
; APPLICANT: HUNT, Donald F.
; APPLICANT: ENGELHARD, Victor H.
; APPLICANT: KITTELSEN, David
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
; FILE REFERENCE: SLINGLUFF=3B
; CURRENT APPLICATION NUMBER: US/09/341,982
; EARLIER FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: PCT/US98/01592
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/037,781
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: human protein
US-09-341-982-10

Query Match      100.0%; Score 23; DB 4; Length 12;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 6 DICTD 10

RESULT 40
US-09-341-982-76
; Sequence 76, Application US/09341982
; Patent No. 6558671
; GENERAL INFORMATION:
; APPLICANT: SLINGLUFF, Craig L.
; APPLICANT: HUNT, Donald F.
; APPLICANT: ENGELHARD, Victor H.
; APPLICANT: KITTELSEN, David
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
; FILE REFERENCE: SLINGLUFF=3B
; CURRENT APPLICATION NUMBER: US/09/341,982
; EARLIER FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: PCT/US98/01592
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/037,781
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence: Mutant
; OTHER INFORMATION: human protein
US-09-341-982-76

Query Match      100.0%; Score 23; DB 4; Length 12;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 6 DICTD 10

RESULT 41
US-09-341-982-79
; Sequence 79, Application US/09341982
; Patent No. 6558671
; GENERAL INFORMATION:
; APPLICANT: SLINGLUFF, Craig L.
; APPLICANT: HUNT, Donald F.
; APPLICANT: ENGELHARD, Victor H.
; APPLICANT: KITTELSEN, David
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
; FILE REFERENCE: SLINGLUFF=3B
; CURRENT APPLICATION NUMBER: US/09/341,982
; EARLIER FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: PCT/US98/01592
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/037,781
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant
; OTHER INFORMATION: human protein
US-09-341-982-79

Query Match      100.0%; Score 23; DB 4; Length 12;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 6 DICTD 10

RESULT 42
US-08-335-832-26
; Sequence 26, Application US/08335832
; Patent No. 5925331
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Thrombus Imaging
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,832
; FILING DATE: 05-JAN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5925331nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,216-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: /label= Apc
; OTHER INFORMATION: /note= "The sidechain sulfur atom is covalently
; OTHER INFORMATION: linked to a [3-aminopropyl] group to form a
; OTHER INFORMATION: thioether"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /label= Apc
; OTHER INFORMATION: /note= "The sidechain sulfur atom is covalently
; OTHER INFORMATION: linked to a [3-aminopropyl] group to form a
; OTHER INFORMATION: thioether"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /label= Acm
; OTHER INFORMATION: /note= "This cysteine residue is blocked at the
; OTHER INFORMATION: sidechain sulfur by covalent linkage to an
; OTHER INFORMATION: acetamido group"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /label= Acm
; OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
; OTHER INFORMATION: amide"
; US-08-335-832-26
;
; Query Match 100.0%; Score 23; DB 2; Length 13;
; Best Local Similarity 60.0%; Pred. No. 4.8e+02;
; Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 DXCD 5
; 1:|:|
;
; Db 4 DVCGD 8
;
; RESULT 43
; US-08-335-832-27
; Sequence 27, Application US/08335832
; Patent No. 5925331
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Thrombus Imaging
; NUMBER OF SEQUENCES: 53

```

```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,832
; FILING DATE: 05-JAN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5925331nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,216-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetyl
; OTHER INFORMATION: /note= "The amino terminus is modified by covalent
; OTHER INFORMATION: linkage to an mercaptoacetyl group."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: /label= Apc
; OTHER INFORMATION: /note= "The sidechain sulfur atom is covalently
; OTHER INFORMATION: linked to a [3-aminopropyl] group to form a
; OTHER INFORMATION: thioether"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /label= Apc
; OTHER INFORMATION: /note= "The sidechain sulfur atom is covalently
; OTHER INFORMATION: linked to a [3-aminopropyl] group to form a
; OTHER INFORMATION: thioether"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /label= Acm
; OTHER INFORMATION: /note= "This cysteine residue is blocked at the
; OTHER INFORMATION: sidechain sulfur by covalent linkage to an
; OTHER INFORMATION: acetamido group"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /label= Acm
; OTHER INFORMATION: /note= "This cysteine residue is blocked at the
; OTHER INFORMATION: sidechain sulfur by covalent linkage to an
; OTHER INFORMATION: acetamido group"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /label= Amide
; OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
; OTHER INFORMATION: amide"
; US-08-335-832-27

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Query Match

100.0%; Score 23; DB 2; Length 13;


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Db      1  DOCID 5

RESULT 46
US-08-482-528-99
; Sequence 99, Application US/08482528
; Patent No. 6017719
; GENERAL INFORMATION:
; APPLICANT: Teeng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgeson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,528
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-08-482-528-99

Query Match      100.0%; Score 23; DB 3; Length 13;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1  DXCXD 5
Db      1  DOCID 5

RESULT 47
US-09-258-754-437
; Sequence 437, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452

Query Match      100.0%; Score 23; DB 4; Length 13;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1  DXCXD 5
Db      1  DOCID 5

RESULT 48
US-10-158-847-107
; Sequence 107, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-107

Query Match      100.0%; Score 23; DB 4; Length 13;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1  DXCXD 5
Db      2  DWCFD 6

RESULT 49
US-10-158-847-109
; Sequence 109, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-109

Query Match      100.0%; Score 23; DB 4; Length 13;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1  DXCXD 5
```

Db |:|:|
 2 DFCFD 6

RESULT 50
US-08-584-671-4
; Sequence 4, Application US/08584671
; Patent No. 5910568
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,671
; FILING DATE:
; CLASSIFICATION: 435
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
; US-08-584-671-4

Query Match 100.0%; Score 23; DB 2; Length 15;
Best Local Similarity 60.0%; Pred.No. 5.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
 |:|:|
Db 9 DVCQD 13

RESULT 51
US-09-027-376-4
; Sequence 4, Application US/09027376
; Patent No. 6004586
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA

 |:|:|
 2 DFCFD 6

RESULT 50
US-08-584-671-4
; Sequence 4, Application US/08584671
; Patent No. 5910568
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,376
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/584,671
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
; US-09-027-376-4

Query Match 100.0%; Score 23; DB 3; Length 15;
Best Local Similarity 60.0%; Pred.No. 5.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
 |:|:|
Db 9 DVCQD 13

RESULT 52
US-09-094-192-4
; Sequence 4, Application US/09094192
; Patent No. 6103483
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM TO EGG SURFACES AND PROCI
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,192
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15

; SEQ ID NO 54
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(4)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
; OTHER INFORMATION: present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)-
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)-
; OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (13)..(16)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 13-16 may
; OTHER INFORMATION: be present or absent
US-09-352-548-54

Query Match 100.0%; Score 23; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 7 DVCQD 11

RESULT 57
US-09-352-548-55
; Sequence 55, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(4)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
; OTHER INFORMATION: present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)-
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)-
; OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (14)..(16)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 14-16 may
; OTHER INFORMATION: be present or absent
US-09-352-548-56

Query Match 100.0%; Score 23; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5

; LOCATION: (6)
; OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (13)..(16)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 13-16 may
; OTHER INFORMATION: be present or absent
US-09-352-548-55

Query Match 100.0%; Score 23; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 7 DVCQD 11

RESULT 58
US-09-352-548-56
; Sequence 56, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(4)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
; OTHER INFORMATION: present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)-
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)-
; OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (14)..(16)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 14-16 may
; OTHER INFORMATION: be present or absent
US-09-352-548-56

Query Match 100.0%; Score 23; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 7 DVCQD 11

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-(4)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
; OTHER INFORMATION: present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)-
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)-
; OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)-(14)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (16)-
; OTHER INFORMATION: Xaa = any amino acid, Xaa at position 16 may be
; OTHER INFORMATION: present or absent
; US-09-352-548-58
;
; Query Match 100.0%; Score 23; DB 4; Length 16;
; Best Local Similarity 60.0%; Pred. No. 5.8e+02;
; Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 DXCXD 5
DB 7 DVCQD 11
;
RESULT 61
US-09-352-548-59
; Sequence 59, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-(4)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
; OTHER INFORMATION: present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)-
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)-
; OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
; FEATURE:

```

```
; NAME/KEY: MOD.RES
; LOCATION: (12)..(15)
; OTHER INFORMATION: Xaa = any amino acid
US-09-352-548-59

Query Match      100.0%; Score 23; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
   |:|:|
Db 7 DVCQD 11

RESULT 62
US-10-158-847-63
; Sequence 63, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 16
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-63

Query Match      100.0%; Score 23; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
   |:|:|
Db 11 DYCQD 15

RESULT 63
US-10-158-847-71
; Sequence 71, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 16
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-71

Query Match      100.0%; Score 23; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
   |:|:|
Db 11 DYCQD 15

RESULT 64
US-10-158-847-71
; Sequence 71, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 16
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-71

Query Match      100.0%; Score 23; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
   |:|:|
Db 11 DYCQD 15

RESULT 65
US-08-163-919A-11
; Sequence 11, Application US/08163919A
; Patent No. 6180771
; GENERAL INFORMATION:
; APPLICANT: THOMAS, Wayne R., CHUA, Kaw-Yan, ROGERS, Bruce L., and
; APPLICANT: KUO, Mei-Chang
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING A HOUSE DUST MITE
; TITLE OF INVENTION: ALLERGEN, DER P III, AND USES THEREFOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Labive & Cockfield
; STREET: 60 State Street suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/163,919A
; FILING DATE: 08-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-072 (IMI-041)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-163-919A-11
```

Query Match 100.0%; Score 23; DB 3; Length 17;
Best Local Similarity 60.0%; Pred. No. 6.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
DB 13 DSCQD 17

RESULT 66

PCT-US94-14073-11
; Sequence 11, Application PC/TUS9414073
; GENERAL INFORMATION:
; APPLICANT: THOMAS, Wayne R., CHUA, Kaw-Yan, ROGERS, Bruce L., and
; APPLICANT: KUO, Mei-Chang
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING A HOUSE DUST MITE
; TITLE OF INVENTION: ALLERGEN, DER P III, AND USES THEREFOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14073
; FILING DATE: 08-DEC-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-072 (IMI-041)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal

PCT-US94-14073-11

Query Match 100.0%; Score 23; DB 5; Length 17;
Best Local Similarity 60.0%; Pred. No. 6.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
DB 13 DSCQD 17

RESULT 67

US-08-126-016-26
; Sequence 26, Application US/08126016
; Patent No. 5811261
; GENERAL INFORMATION:
; APPLICANT: WALLACH, DAVID
; APPLICANT: NOPAR, YARON
; APPLICANT: KEMPER, OLIVER
; APPLICANT: ENGELMANN, HARTMUT
; APPLICANT: BRAKEBUSCH, CORD

; APPLICANT: ADERKA, DAN
; TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
; TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-I)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/126,016
; FILING DATE: 24-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/625668
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-126-016-26

Query Match 100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 6.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
DB 7 DSCD 11

RESULT 68

US-09-583-638-5
; Sequence 5, Application US/09583638
; Patent No. 6635421
; GENERAL INFORMATION:
; APPLICANT: KLAGSBRUN, MICHAEL
; APPLICANT: SOKER, SHAY
; APPLICANT: MIAO, HUA-QUAN
; APPLICANT: TAKASHIMA, SEIJI
; TITLE OF INVENTION: NEUROPILINS AND USE THEREOF IN METHODS FOR
; TITLE OF INVENTION: DIAGNOSIS AND PROGNOSIS OF CANCER
; FILE REFERENCE: 701039-48800
; CURRENT APPLICATION NUMBER: US/09/583,638
; CURRENT FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: PCT/US98/26127
; PRIOR FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: 60/069,155
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: 60/069,687
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 18

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-583-638-5

Query Match      100.0%; Score 23; DB 4; Length 18;
Best Local Similarity 60.0%; Pred. No. 6.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 4 DECGD 8

RESULT 69
5177197-9
; Patent No. 5177197
; APPLICANT: KANZAKI, TETSUO;OLOFSSON, ANDERS;MOREN, ANITA;
; WERNSTEDT, CHRISTER;HELLMAN, ULF;MIYAZONO, KOHEI;CLAESSON-WELSH,
; LENA;HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
; NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
; SEQ ID NO: 9;
; LENGTH: 18
5177197-9

Query Match      100.0%; Score 23; DB 6; Length 18;
Best Local Similarity 60.0%; Pred. No. 6.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 6 DHCD 10

RESULT 70
US-08-584-671-5
; Sequence 5, Application US/08584671
; Patent No. 5910568
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,671
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-08-584-671-5

Query Match      100.0%; Score 23; DB 3; Length 19;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 8 DVCQD 12

RESULT 71
US-09-027-376-5
; Sequence 5, Application US/09027376
; Patent No. 6004586
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,376
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/584,671
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-09-027-376-5

Query Match      100.0%; Score 23; DB 3; Length 19;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 8 DVCQD 12

RESULT 72
```

```
US-09-094-192-5
; Sequence 5, Application US/09094192
; Patent No. 6103483
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM TO EGG SURFACES AND PROC
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,192
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-863-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-09-094-192-5
Query Match 100.0%; Score 23; DB 3; Length 19;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
Db 8 DVCQD 12

RESULT 73
US-08-142-449B-1
; Sequence 1, Application US/08142449B
; Patent No. 5668104
; GENERAL INFORMATION:
; APPLICANT: Nakahata, Tatsutoshi
; APPLICANT: Kawano, Genji
; APPLICANT: Sudo, Tetsuo
; APPLICANT: Kojima, Katsuki
; TITLE OF INVENTION: Physiologically Active Protein and
; TITLE OF INVENTION: Hematopoietic Stem Cell Growth Agent
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nels T. Lippert, White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

US-09-094-192-5
Query Match 100.0%; Score 23; DB 3; Length 19;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
Db 8 DVCQD 12

RESULT 73
US-08-142-449B-1
; Sequence 1, Application US/08142449B
; Patent No. 5668104
; GENERAL INFORMATION:
; APPLICANT: Nakahata, Tatsutoshi
; APPLICANT: Kawano, Genji
; APPLICANT: Sudo, Tetsuo
; APPLICANT: Kojima, Katsuki
; TITLE OF INVENTION: Physiologically Active Protein and
; TITLE OF INVENTION: Hematopoietic Stem Cell Growth Agent
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nels T. Lippert, White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

US-09-094-192-5
Query Match 100.0%; Score 23; DB 3; Length 20;
Best Local Similarity 60.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
Db 6 DSCFD 10

RESULT 74
US-08-468-347-12
; Sequence 12, Application US/08468347
; Patent No. 5783421
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; TITLE OF INVENTION: INHIBITORY ACTIVITY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,347
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/225,442
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
```

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US-08-142-449B-1
; APPLICATION NUMBER: US/08/142,449B
; FILING DATE: 24-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lippert, Nels T.
; REGISTRATION NUMBER: 25,888
; REFERENCE/DOCKET NUMBER: 1145358-304
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-819-8582
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
US-08-142-449B-1
Query Match 100.0%; Score 23; DB 1; Length 20;
Best Local Similarity 60.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
Db 6 DSCFD 10

RESULT 74
US-08-468-347-12
; Sequence 12, Application US/08468347
; Patent No. 5783421
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; TITLE OF INVENTION: INHIBITORY ACTIVITY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,347
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/225,442
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; FRAGMENT TYPE: N-terminal
US-08-468-347-12

Query Match          100.0%; Score 23; DB 1; Length 20;
Best Local Similarity 60.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 8 DPCED 12

RESULT 75
US-08-468-347-13
; Sequence 13, Application US/08468347
; Patent No. 5783421
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468.347
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/225,442
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-468-347-13

Query Match          100.0%; Score 23; DB 1; Length 20;
Best Local Similarity 60.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 8 DPCED 12

RESULT 76
US-08-226-264-9
; Sequence 9, Application US/08226264
; Patent No. 5801017

; GENERAL INFORMATION:
; APPLICANT: Werber, Moshe M.
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/226,264
; FILING DATE: 08-APR-94
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-226-264-9

Query Match          100.0%; Score 23; DB 1; Length 20;
Best Local Similarity 60.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 8 DPCED 12

RESULT 77
US-08-467-389-12
; Sequence 12, Application US/08467389
; Patent No. 5824841
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
```


Query Match 100.0%; Score 23; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:|
Db 8 DPCED 12

RESULT 80

US-08-779-379-13
; Sequence 13, Application US/08779379
; Patent No. 5858970

; GENERAL INFORMATION:

; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; TITLE OF INVENTION: INHIBITORY ACTIVITY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,379
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/225,442
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-779-379-13

Query Match 100.0%; Score 23; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:|
Db 8 DPCED 12

RESULT 81

US-08-469-219-12
; Sequence 12, Application US/08469219
; Patent No. 5863534

; GENERAL INFORMATION:

; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; TITLE OF INVENTION: INHIBITORY ACTIVITY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,219
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/225,442
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-469-219-12

Query Match 100.0%; Score 23; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:|
Db 8 DPCED 12

RESULT 82

US-08-469-219-13
; Sequence 13, Application US/08469219
; Patent No. 5863534

; GENERAL INFORMATION:

; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; TITLE OF INVENTION: INHIBITORY ACTIVITY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,219
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,442
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-664-0520
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-469-219-13

Query Match 100.0%; Score 23; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
DB 8 DPCED 12

RESULT 83

US-08-934-915-13
Sequence 13, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUTCH
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:

TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-13

Query Match 100.0%; Score 23; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
DB 2 DGCED 6

RESULT 84

US-09-228-152-12
Sequence 12, Application US/09228152
Patent No. 6211341
GENERAL INFORMATION:
APPLICANT: Zeelon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa INHIBITORY ACTIVITY
FILE REFERENCE: 43020aya
CURRENT APPLICATION NUMBER: US/09/228,152
CURRENT FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: N-terminal
OTHER INFORMATION: sequence.
US-09-228-152-12

Query Match 100.0%; Score 23; DB 3; Length 20;
Best Local Similarity 60.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
DB 8 DPCED 12

RESULT 85

US-08-749-852-49
Sequence 49, Application US/08749852
Patent No. 5874222
GENERAL INFORMATION:
APPLICANT: JIRTLE, RANDY L.
APPLICANT: DE SOUZA, ANGUS T.
APPLICANT: HANKINS, GERALD R.
TITLE OF INVENTION: TUMOR SUPPRESSOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/749,852
;; FILING DATE: 15-NOV-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WILSON, MARY J.
;; REGISTRATION NUMBER: 32,955
;; REFERENCE/DOCKET NUMBER: 1579-104
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4000
;; TELEFAX: (703) 816-4100
;; INFORMATION FOR SEQ ID NO: 49:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: linear
US-08-749-852-49

Query Match 100.0%; Score 23; DB 2; Length 24;
Best Local Similarity 60.0%; Pred. No. 8.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 16 DLCPD 20

RESULT 86
US-08-749-852-51
;; Sequence 51, Application US/08749852
;; Patent No. 5874222
;; GENERAL INFORMATION:
;; APPLICANT: JIRTLE, RANDY L.
;; APPLICANT: DE SOUZA, ANGUS T.
;; APPLICANT: HANKINS, GERALD R.
;; TITLE OF INVENTION: TUMOR SUPPRESSOR
;; NUMBER OF SEQUENCES: 59
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NIXON & VANDERHVE P.C.
;; STREET: 1100 NORTH GLEBE ROAD
;; CITY: ARLINGTON
;; STATE: VIRGINIA
;; COUNTRY: U.S.A.
;; ZIP: 22201-4714
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/749,852
;; FILING DATE: 15-NOV-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WILSON, MARY J.
;; REGISTRATION NUMBER: 32,955
;; REFERENCE/DOCKET NUMBER: 1579-104
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4000
;; TELEFAX: (703) 816-4100
;; INFORMATION FOR SEQ ID NO: 51:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: linear
US-08-749-852-51

Query Match 100.0%; Score 23; DB 2; Length 24;
Best Local Similarity 60.0%; Pred. No. 8.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 16 DLCPD 20

RESULT 87
US-09-149-476-737
;; Sequence 737, Application US/09149476
;; Patent No. 6420526
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: 186 Human Secreted proteins
;; FILE REFERENCE: PZ002P1
;; CURRENT APPLICATION NUMBER: US/09/149,476
;; CURRENT FILING DATE: 1998-09-08
;; EARLIER APPLICATION NUMBER: PCT/US98/04493
;; EARLIER FILING DATE: 1998-03-06
;; EARLIER APPLICATION NUMBER: 60/040,162
;; EARLIER FILING DATE: 1997-03-07
;; EARLIER APPLICATION NUMBER: 60/040,333
;; EARLIER FILING DATE: 1997-03-07
;; EARLIER APPLICATION NUMBER: 60/038,621
;; EARLIER FILING DATE: 1997-03-07
;; EARLIER APPLICATION NUMBER: 60/040,626
;; EARLIER FILING DATE: 1997-03-07
;; EARLIER APPLICATION NUMBER: 60/040,334
;; EARLIER FILING DATE: 1997-03-07
;; EARLIER APPLICATION NUMBER: 60/040,336
;; EARLIER FILING DATE: 1997-03-07
;; EARLIER APPLICATION NUMBER: 60/040,163
;; EARLIER FILING DATE: 1997-03-07
;; EARLIER APPLICATION NUMBER: 60/047,600
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,615
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,597
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,502
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,633
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,583
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,617
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,618
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,503
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,592
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,581
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,584
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,500
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,587
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,492
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,598
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,613
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,582
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,596

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,674
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,669
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,312
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,313
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,672
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
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EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 100.0%; Score 23; DB 4; Length 24;
Best Local Similarity 60.0%; Pred. No. 8.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCD 5
|:|:

```
Db          15 DTCSD 19

RESULT 88
US-09-084-303B-248
; Sequence 248, Application US/09084303B
; Patent No. 6627746
; GENERAL INFORMATION:
; APPLICANT: Doberstein, Stephen
; APPLICANT: Reddy, Bindu
; APPLICANT: Platt, Darren
; APPLICANT: Ferguson, Kimberly
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF C. ELEGANS INSULIN-LIKE GENES AND
; FILE REFERENCE: 7326-069-999
; CURRENT APPLICATION NUMBER: US/09/084,303B
; CURRENT FILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 248
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-084-303B-248

Query Match          100.0%; Score 23; DB 4; Length 25;
Best Local Similarity 60.0%; Pred. No. 8.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DXCXD 5
Db      12 DACSD 16

RESULT 89
US-09-224-785-40
; Sequence 40, Application US/09224785A
; Patent No. 6197526
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: Dyax-008 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/224,785A
; CURRENT FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-224-785-40

Query Match          100.0%; Score 23; DB 3; Length 26;
Best Local Similarity 60.0%; Pred. No. 8.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DXCXD 5
Db      14 DHCHD 18

RESULT 90
US-09-756-594-40
; Sequence 40, Application US/09756594
; Patent No. 6492105
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: Dyax-008 US Div. 1 sequence listing
; CURRENT APPLICATION NUMBER: US/09/756,594
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-756-594-40

Query Match          100.0%; Score 23; DB 4; Length 26;
Best Local Similarity 60.0%; Pred. No. 8.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DXCXD 5
Db      14 DHCHD 18

RESULT 91
US-08-945-983-8
; Sequence 8, Application US/08945983
; Patent No. 6225527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Colwyn M
; APPLICANT: Balint-Kurti, Peter J
; APPLICANT: Jones, David A
; APPLICANT: Jones, Jonathan DG
; TITLE OF INVENTION: Plant pathogen resistance genes and uses
; TITLE OF INVENTION: thereof
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 6225527th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/08/945,983
; FILING DATE: 12-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01155
; FILING DATE: 13-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9509575.8
; FILING DATE: 11-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ms Mary J Wilson
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 620-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
```

; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-945-983-8

Query Match 100.0%; Score 23; DB 3; Length 30;
Best Local Similarity 60.0%; Pred. No. 1.e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 12 DYCVD 16

RESULT 92
5208144-17
; Patent No. 5208144
; APPLICANT: SMITH, JOHN A.; RAYCHOWDHURY, RAKTIMA; NILES, JOHN L.
; TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN DNA
; CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/396,697
; FILING DATE: 22-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 313,682
; FILING DATE: 22-FEB-1989
; APPLICATION NUMBER: 235,211
; FILING DATE: 23-AUG-1988
; SEQ ID NO: 17
; LENGTH: 32
5208144-17

Query Match 100.0%; Score 23; DB 6; Length 32;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 24 DDCHD 28

RESULT 93
US-08-445-520B-4
; Sequence 4, Application US/08445520B
; Patent No. 5866323
; GENERAL INFORMATION:
; APPLICANT: Markowitz, Sanford D.
; APPLICANT: Brattain, Michael G.
; APPLICANT: Willson, James K.V.
; TITLE OF INVENTION: CANCER DIAGNOSIS, PROGNOSIS AND
; THERAPY BASED ON MUTATION OF RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,520B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/417,867

; FILING DATE: 07-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske, Laurence H
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 082361-0101
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-445-520B-4

Query Match 100.0%; Score 23; DB 2; Length 34;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 14 DECND 18

RESULT 94
US-09-239-864A-4
; Sequence 4, Application US/09239864A
; Patent No. 6291237
; GENERAL INFORMATION:
; APPLICANT: Markowitz, Sanford D
; APPLICANT: Brattain, Michael G
; APPLICANT: Willson, James K.V.
; TITLE OF INVENTION: CANCER DIAGNOSIS, PROGNOSIS AND THERAPY BASED ON
; MUTATION OF RECEPTOR
; FILE REFERENCE: 062361.0108
; CURRENT APPLICATION NUMBER: US/09/239,864A
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 08/417,867
; PRIOR FILING DATE: 1995-04-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 4
; LENGTH: 34
; TYPE: PRT
; ORGANISM: human
US-09-239-864A-4

Query Match 100.0%; Score 23; DB 3; Length 34;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
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Db 14 DECND 18

RESULT 95
US-09-366-887A-22
; Sequence 22, Application US/09366887A
; Patent No. 6403782
; GENERAL INFORMATION:
; APPLICANT: LUSTER, ANDREW D.
; APPLICANT: LEIDER, PHILIP
; APPLICANT: ROTHENBERG, MARC
; APPLICANT: GARCIA, EDUARDO
; TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT
; FILE REFERENCE: 00383/025002
; CURRENT APPLICATION NUMBER: US/09/366,887A
; CURRENT FILING DATE: 1999-08-04

; PRIOR APPLICATION NUMBER: 60/000,449
 ; PRIOR FILING DATE: 1995-06-22
 ; PRIOR APPLICATION NUMBER: 08/522,713
 ; PRIOR FILING DATE: 1995-09-01
 ; PRIOR APPLICATION NUMBER: 08/522,713
 ; PRIOR FILING DATE: 1998-06-16
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 22
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ;
 US-09-366-887A-22

Query Match 100.0%; Score 23; DB 4; Length 34;
 Best Local Similarity 60.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
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 Db 8 DICAD 12

RESULT 96
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 ; Sequence 4, Application US/09878905
 ; Patent No. 6630326
 ; GENERAL INFORMATION:
 ; APPLICANT: Markowitz, Sanford D
 ; APPLICANT: Brattson, Michael G
 ; APPLICANT: Willson, James K.V
 ; TITLE OF INVENTION: CANCER DIAGNOSIS, PROGNOSIS AND THERAPY BASED ON
 ; FILE REFERENCE: MUTATION OF RECEPTOR
 ; FILE REFERENCE: 062361.0108
 ; CURRENT APPLICATION NUMBER: US/09/878,905
 ; CURRENT FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: 08/417,867
 ; PRIOR FILING DATE: 1995-04-07
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: human
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 US-09-878-905-4

Query Match 100.0%; Score 23; DB 4; Length 34;
 Best Local Similarity 60.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
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 Db 14 DECND 18

RESULT 97
 US-08-487-890A-21
 ; Sequence 21, Application US/08487890A
 ; Patent No. 5708149
 ; GENERAL INFORMATION:
 ; APPLICANT: Loosmore, Sheena
 ; APPLICANT: Harkness, Robin
 ; APPLICANT: Schryvers, Anthony
 ; APPLICANT: Chong, Pele
 ; APPLICANT: Gray-Owen, Scott
 ; APPLICANT: Yang, Yan-Ping
 ; APPLICANT: Murdin, Andrew
 ; APPLICANT: Klein, Michel
 ; TITLE OF INVENTION: Transferrin Receptor Genes
 ; NUMBER OF SEQUENCES: 147
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sim & McBurney
 ; STREET: 6th Floor, 330 University Avenue

; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5G 1R7
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,890A
 ; FILING DATE: 07-JUN-1993
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/175,116
 ; FILING DATE: 29-DEC-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/148,968
 ; FILING DATE: 08-NOV-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stewart, Michael I
 ; REGISTRATION NUMBER: 24,973
 ; REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 595-1155
 ; TELEFAX: (416) 595-1163
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 36 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ;
 US-08-487-890A-21

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QY 1 DXCXD 5
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 Db 15 DECLD 19

RESULT 98
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 ; Sequence 21, Application US/08478435
 ; Patent No. 5922323
 ; GENERAL INFORMATION:
 ; APPLICANT: Loosmore, Sheena
 ; APPLICANT: Harkness, Robin
 ; APPLICANT: Schryvers, Anthony
 ; APPLICANT: Chong, Pele
 ; APPLICANT: Gray-Owen, Scott
 ; APPLICANT: Yang, Yan-Ping
 ; APPLICANT: Murdin, Andrew
 ; APPLICANT: Klein, Michel
 ; TITLE OF INVENTION: Transferrin Receptor Genes
 ; NUMBER OF SEQUENCES: 147
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sim & McBurney
 ; STREET: Suite 701, 330 University Avenue
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5G 1R7
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/478,435
 ; FILING DATE: 07-JUN-1995


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/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/337,483
/ FILING DATE: 08-NOV-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/175,116
/ FILING DATE: 29-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/148,968
/ FILING DATE: 08-NOV-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stewart, Michael I
/ REGISTRATION NUMBER: 24,973
/ REFERENCE/DOCKET NUMBER: 1038-462 MIS:vg
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (416) 595-1155
/ TELEFAX: (416) 595-1163
/ INFORMATION FOR SEQ ID NO: 21:
/ Sequence 21, Application US/08337483
/ Patent No. 5922562
/ GENERAL INFORMATION:
/ APPLICANT: Loosmore, Sheena
/ APPLICANT: Harkness, Robin
/ APPLICANT: Schryvers, Anthony
/ APPLICANT: Chong, Pele
/ APPLICANT: Gray-Owen, Scott
/ APPLICANT: Yang, Yan-Ping
/ APPLICANT: Murdin, Andrew
/ APPLICANT: Klein, Michel
/ TITLE OF INVENTION: Transferrin Receptor Genes
/ NUMBER OF SEQUENCES: 147
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sim & McBurney
/ STREET: Suite 701, 330 University Avenue
/ CITY: Toronto
/ STATE: Ontario
/ COUNTRY: Canada
/ ZIP: M5G 1R7
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/337,483
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/175,116
/ FILING DATE: 29-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/148,968
/ FILING DATE: 08-NOV-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stewart, Michael I
/ REGISTRATION NUMBER: 24,973
/ REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (416) 595-1155
/ TELEFAX: (416) 595-1163

Query Match 100.0%; Score 23; DB 2; Length 36;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 15 DECLD 19

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US-08-337-483-21
; Sequence 21, Application US/08337483
; Patent No. 5922562
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,483
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
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/ INFORMATION FOR SEQ ID NO: 21:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-337-483-21

Query Match 100.0%; Score 23; DB 2; Length 36;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 15 DECLD 19

RESULT 100
US-08-478-373-21
; Sequence 21, Application US/08478373
; Patent No. 5922841
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,373
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
/ US-08-478-373-21
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Query Match 100.0%; Score 23; DB 2; Length 36;
 Best Local Similarity 60.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |::|
 Db 15 DECLD 19

Search completed: May 6, 2004, 10:47:52
 Job time : 25 secs

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OM'protein - protein search, using sw model

Run on: May 6, 2004, 10:41:10 ; Search time 54 Seconds
(without alignments)
26.162 Million cell updates/sec

Title: SEQ1

Perfect score: 23

Sequence: 1 dxcxd 5

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1158

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 1000 summaries

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2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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133	23	100.0	11	3	AAV58705	Human	161	206	23	100.0	16	6	ABRS5635	Angiotens	
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135	23	100.0	11	5	AAU80444	Positive		208	23	100.0	16	6	ABRS56643	Angiotens	
136	23	100.0	11	5	ABG95509	Human nov		209	23	100.0	17	3	AAAB21517	Cone snai	
137	23	100.0	12	2	AAAR90479	Antibody		210	23	100.0	17	3	AAAB21517	Cone snai	
138	23	100.0	12	2	AAW71237	Fragment		211	23	100.0	17	3	AAAB21515	Cone snai	
139	23	100.0	12	2	AAV55206	Anti CD34		212	23	100.0	17	5	AAU80450	Positive	
140	23	100.0	12	3	AAV86952	Human hae		213	23	100.0	17	5	ABP47340	SPOT exem	
141	23	100.0	13	2	AAV89293	GP IIB/II		214	23	100.0	17	7	ADE65970	Human 161	
142	23	100.0	13	2	AAV89311	GP IIB/II		215	23	100.0	18	4	AAG73098	Protease	
143	23	100.0	13	2	AAV89310	GP IIB/II		216	23	100.0	18	4	AAG73164	Protease	
144	23	100.0	13	2	AAV90478	Antibody		217	23	100.0	18	4	AAG73163	Protease	
145	23	100.0	13	2	AAV55205	Anti CD34		218	23	100.0	18	4	AAG73082	Protease	
146	23	100.0	13	2	AAV48811	Membrane		219	23	100.0	18	4	AAG73100	Protease	
147	23	100.0	13	3	AAV86951	Human hae		220	23	100.0	18	4	AAG73090	Protease	
148	23	100.0	13	3	AAV57806	TRAM-inte		221	23	100.0	18	4	AAG73094	Protease	
149	23	100.0	13	6	ADA03311	Angiotens		222	23	100.0	18	4	AAG73093	Protease	
150	23	100.0	13	6	ADA03309	Angiotens		223	23	100.0	18	4	AAG73089	Protease	
151	23	100.0	13	6	ABRS56681	Angiotens		224	23	100.0	18	4	AAG73091	Protease	
152	23	100.0	13	6	ABRS56679	Angiotens		225	23	100.0	18	4	AAG73092	Protease	
153	23	100.0	14	1	AAV60041	Sequence		226	23	100.0	18	4	AAG73086	Protease	
154	23	100.0	14	1	AAV91930	Junction		227	23	100.0	18	4	AAG73095	Protease	
155	23	100.0	14	5	AAU80448	Positive		228	23	100.0	18	5	ABJ00634	B lymphoc	
156	23	100.0	15	2	AAW18587	Universal		229	23	100.0	18	5	ABJ00647	B lymphoc	
157	23	100.0	15	2	AAW78310	Fragment		230	23	100.0	18	5	ABG33495	B lymphoc	
158	23	100.0	15	3	AAV58685	Antiangio		231	23	100.0	18	5	ABG33508	B lymphoc	
159	23	100.0	15	4	ABBA45087	Rat album		232	23	100.0	19	2	AAW86789	Feline Ig	
160	23	100.0	15	4	ABBA45086	Rat album		233	23	100.0	19	2	AAW18588	Universal	
161	23	100.0	15	4	ABBA45088	Rat album		234	23	100.0	19	2	AAG73154	Protease	
162	23	100.0	15	4	ABBA45082	Rat album		235	23	100.0	19	4	AAG73151	Protease	
163	23	100.0	15	4	ABBA45083	Rat album		236	23	100.0	19	4	AAG73152	Protease	
164	23	100.0	15	4	ABBA45085	Rat album		237	23	100.0	19	4	AAG73153	Protease	
165	23	100.0	15	4	ABBA45084	Rat album		238	23	100.0	19	4	AAG73152	Protease	
166	23	100.0	15	5	AAW49274	Human RNA		239	23	100.0	19	4	AAG73162	Protease	
167	23	100.0	15	7	ADE70274	Human 161		240	23	100.0	19	4	AAG73155	Protease	
168	23	100.0	15	7	ADE70715	Human 161		241	23	100.0	19	4	AAG73161	Protease	
169	23	100.0	15	7	ADE70882	Human 161		242	23	100.0	19	4	AAG73167	Protease	
170	23	100.0	15	7	ADE70884	Human 161		243	23	100.0	19	4	AAG73160	Protease	
171	23	100.0	15	7	ADE70885	Human 161		244	23	100.0	19	4	AAG73169	Protease	
													AAG73168	Protease	

245	23	100.0	19	7	ADE65971	Ad65971 Human 161	318	23	100.0	30	4	ABB29940	Abb29940 Peptide #
246	23	100.0	20	2	AAR15535	Aar15535 Immunopcp	319	23	100.0	30	4	AAM68312	Aam68312 Human bon
247	23	100.0	20	2	AAR62518	Aar62518 N-termina	320	23	100.0	30	4	AAM55946	Aam55946 Human bra
248	23	100.0	20	2	AW68543	Aw68543 Fragment	321	23	100.0	30	4	ABG49977	Abg49977 Human liv
249	23	100.0	20	2	AW92363	Aw92363 H. medici	322	23	100.0	30	5	ABG37862	Abg37862 Human pep
250	23	100.0	20	2	AW92362	Aw92362 H. medici	323	23	100.0	30	5	AAU84875	Aau84875 Human Trp
251	23	100.0	20	2	AY02387	AY02387 Heat stab	324	23	100.0	30	5	AAU84904	Aau84904 Human Tyr
252	23	100.0	20	2	AY29609	AY29609 Versinia	325	23	100.0	30	5	AAU84941	Aau84941 Human Trp
253	23	100.0	20	2	AY06973	AY06973 Versinia	326	23	100.0	30	5	AAU84905	Aau84905 Human Trp
254	23	100.0	20	2	AAW73596	Aaw73596 Factor Xa	327	23	100.0	30	5	AAU84940	Aau84940 Human Trp
255	23	100.0	20	2	AY02399	AY02399 Heat stab	328	23	100.0	31	2	AAW58575	Aaw58575 ACE11 Zn2
256	23	100.0	20	3	AB03522	Ab03522 HLA Class	329	23	100.0	31	5	ABP29071	Abp29071 Streptoco
257	23	100.0	20	4	AB44955	Ab44955 Rabbit al	330	23	100.0	31	5	AAO14371	Aao14371 Human met
258	23	100.0	20	4	AAE00749	Aae00749 N-termina	331	23	100.0	32	2	AAO20527	Aao20527 Human neu
259	23	100.0	20	5	ABG66276	Abg66276 IGE Fceps	332	23	100.0	32	3	AAO3525	Aao3525 HLA Class
260	23	100.0	21	4	AG66970	Ag66970 Mutant pr	333	23	100.0	34	4	AAAB68409	Aab68409 Heparin-b
261	23	100.0	21	5	ABG66562	Abg66562 IGE Fceps	334	23	100.0	32	6	ADA49370	Ada49370 Human Fn1
262	23	100.0	21	5	ABG66380	Abg66380 IGE Fceps	335	23	100.0	33	2	AAW97507	Aaw97507 Antigenic
263	23	100.0	21	5	ABG66368	Abg66368 IGE Fceps	336	23	100.0	33	6	ABP58162	Abp58162 Mouse DAK
264	23	100.0	21	5	ABG66342	Abg66342 IGE Fceps	337	23	100.0	33	6	ABR43571	Ab43571 Mouse bet
265	23	100.0	21	5	AAU89134	Aau89134 Insulin/i	338	23	100.0	34	3	AAAB12348	Aab12348 TGF-beta
266	23	100.0	21	6	ADA03960	Ada03960 IGP-1R re	339	23	100.0	34	4	AAAB82998	Aab82998 TGF-beta
267	23	100.0	21	7	ADE65967	Ad65967 Human 161	340	23	100.0	34	5	ABB80909	Abb80909 Human sot
268	23	100.0	21	7	ADE65968	Ad65968 Human 161	341	23	100.0	34	5	ABB80866	Abb80866 Type II T
269	23	100.0	22	4	AB71673	Ab71673 Human col	342	23	100.0	35	2	AAAR73932	Aar73932 Peptide f
270	23	100.0	22	6	ABR42049	Ab42049 Brine shr	343	23	100.0	35	2	AAW20284	Aaw20284 H. pylori
271	23	100.0	22	7	ADG37012	Adg37012 Binding a	344	23	100.0	35	4	AAU21194	Aau21194 Human nov
272	23	100.0	23	6	AAE30318	Aae30318 Human LP2	345	23	100.0	35	5	ABB88841	Abb88841 Conus mag
273	23	100.0	23	6	AAE30217	Aae30217 Human LP2	346	23	100.0	35	5	ABB88628	Abb88628 Conus mag
274	23	100.0	23	6	AAE30219	Aae30219 Human LP2	347	23	100.0	35	5	AAU83462	Aau83462 Human pan
275	23	100.0	23	6	AAE30316	Aae30316 Human LP2	348	23	100.0	35	6	ABU61346	Abu61346 Human A d
276	23	100.0	24	2	AAW17762	Aaw17762 M6P/IGF-I	349	23	100.0	35	6	ABU61258	Abu61258 Human A d
277	23	100.0	24	3	AAW72103	Aaw72103 Peptide f	350	23	100.0	35	6	ABU61221	Abu61221 Human A d
278	23	100.0	24	5	ABG30794	Abg30794 Human ser	351	23	100.0	35	6	ABU61261	Abu61261 Human A d
279	23	100.0	24	5	ABE17925	Ab17925 Human gen	352	23	100.0	35	6	ABU61275	Abu61275 Human A d
280	23	100.0	24	5	ABG95597	Abg95597 Human nov	353	23	100.0	35	6	ABU61291	Abu61291 Human A d
281	23	100.0	24	6	ABO34791	Ab034791 Fragment	354	23	100.0	35	6	ABU61219	Abu61219 Human A d
282	23	100.0	25	4	ABB43291	Abb43291 Peptide #	355	23	100.0	35	6	ABU61335	Abu61335 Human A d
283	23	100.0	25	4	AAW31135	Aaw31135 Peptide #	356	23	100.0	35	6	ABU61204	Abu61204 Human A d
284	23	100.0	25	4	AAW77025	Aaw77025 Human bon	357	23	100.0	35	6	ABU61253	Abu61253 Human A d
285	23	100.0	25	4	AAW64199	Aaw64199 Human bra	358	23	100.0	35	6	ABU61411	Abu61411 Low densi
286	23	100.0	25	4	ABG58686	Abg58686 Human liv	359	23	100.0	35	6	ABU61366	Abu61366 Human A d
287	23	100.0	25	5	ABG46103	Abg46103 Human pep	360	23	100.0	35	6	ABU61378	Abu61378 Human A d
288	23	100.0	26	1	AAW90029	Aaw90029 Antigenic	361	23	100.0	35	6	ABU61316	Abu61316 Human A d
289	23	100.0	26	3	AB15274	Ab15274 Specific	362	23	100.0	35	6	ABU61318	Abu61318 Human A d
290	23	100.0	26	7	ABW01431	Abw01431 Murine TA	363	23	100.0	35	6	ABU61215	Abu61215 Human A d
291	23	100.0	27	4	AB48916	Ab48916 Human ace	364	23	100.0	35	6	ABU61231	Abu61231 Human A d
292	23	100.0	27	4	AB41654	Ab41654 Peptide #	365	23	100.0	35	6	ABR43520	Ab43520 Mouse bet
293	23	100.0	27	4	AAW35450	Aaw35450 Peptide #	366	23	100.0	35	6	ABR43519	Ab43519 Human bet
294	23	100.0	27	4	AAW50034	Aaw50034 Acetylcho	367	23	100.0	36	2	AAAR77905	Aar77905 Antigenic
295	23	100.0	27	4	AAW75336	Aaw75336 Human bon	368	23	100.0	36	2	AAW46098	Aaw46098 Predicted
296	23	100.0	27	4	AAW62526	Aaw62526 Human bra	369	23	100.0	36	2	AAW51703	Aaw51703 H. influe
297	23	100.0	27	4	ABG57094	Abg57094 Human liv	370	23	100.0	36	2	AAW53058	Aaw53058 Tbp1 anti
298	23	100.0	28	4	AAW20023	Aaw20023 Peptide #	371	23	100.0	36	3	AAW76281	Aaw76281 Fragment
299	23	100.0	28	4	AAW61649	Aaw61649 TRP2 pept	372	23	100.0	36	3	AAW80400	Aaw80400 H. influe
300	23	100.0	28	4	AB40132	Ab40132 Peptide #	373	23	100.0	36	4	ABG79287	Abg79287 Amino aci
301	23	100.0	28	4	AAW33772	Aaw33772 Peptide #	374	23	100.0	36	5	ABG47298	Abg47298 Human pep
302	23	100.0	28	4	AB24596	Ab24596 Protein #	375	23	100.0	36	5	ABG47298	Abg47298 Human pep
303	23	100.0	28	4	AAW73577	Aaw73577 Human bon	376	23	100.0	36	5	ABB88829	Abb88829 Conus lyn
304	23	100.0	28	4	AAW60894	Aaw60894 Human bra	377	23	100.0	36	5	ABB88871	Abb88871 Conus epi
305	23	100.0	28	4	ABG55306	Abg55306 Human liv	378	23	100.0	36	5	ABB88871	Abb88871 Conus epi
306	23	100.0	28	5	ABG43443	Abg43443 Human pep	379	23	100.0	36	5	ABB88831	Abb88831 Conus lyn
307	23	100.0	29	4	AB43269	Ab43269 Peptide #	380	23	100.0	36	5	ABB88688	Abb88688 Conus lyn
308	23	100.0	29	4	AAW37112	Aaw37112 Peptide #	381	23	100.0	36	5	ABB88682	Abb88682 Conus lyn
309	23	100.0	29	4	AAW77004	Aaw77004 Human bon	382	23	100.0	36	5	ABB88692	Abb88692 Conus epi
310	23	100.0	29	4	AAW64176	Aaw64176 Human bra	383	23	100.0	36	5	ABB88775	Abb88775 Conus epi
311	23	100.0	29	4	ABG58666	Abg58666 Human liv	384	23	100.0	36	5	ABB88686	Abb88686 Conus lyn
312	23	100.0	29	4	ABG66979	Abg66979 Mutant pr	385	23	100.0	36	5	ABB88832	Abb88832 Conus lyn
313	23	100.0	29	4	ABG66968	Abg66968 Mutant pr	386	23	100.0	36	5	ABB88834	Abb88834 Conus lyn
314	23	100.0	29	4	ABG66967	Abg66967 Castor oi	387	23	100.0	36	6	ABU61299	Abu61299 Human A d
315	23	100.0	29	7	ABE65972	Ab65972 Human 161	388	23	100.0	36	6	ABU61406	Abu61406 Low densi
316	23	100.0	30	2	AAW25848	Aaw25848 Human sec	389	23	100.0	36	6	ABU61284	Abu61284 Human A d
317	23	100.0	30	4	ABB35123	Abb35123 Peptide #	390	23	100.0	36	6	ABU61302	Abu61302 Human A d

391	23	100.0	36	6	ABU61367	Human A d	464	23	100.0	41	4	AAM71515	Human bon
392	23	100.0	36	6	ABU61369	Human A d	465	23	100.0	41	4	AAM69632	Human bon
393	23	100.0	36	6	ABU61351	Human A d	466	23	100.0	41	4	AAM59837	Human bra
394	23	100.0	36	6	ABU61364	Human A d	467	23	100.0	41	4	AAM57230	Human bra
395	23	100.0	36	6	ABU61300	Human A d	468	23	100.0	41	4	ABG51312	Human liv
396	23	100.0	36	6	ABU61295	Human A d	469	23	100.0	41	4	ABG53208	Human liv
397	23	100.0	36	6	ABU61310	Human A d	470	23	100.0	41	4	AAM05125	Peptide #
398	23	100.0	36	6	ABU61352	Human A d	471	23	100.0	41	5	ABG39254	Human pep
399	23	100.0	36	7	ADE11923	Human sec	472	23	100.0	41	5	ABG41327	Human pep
400	23	100.0	37	4	ABG12573	Novel hum	473	23	100.0	41	5	AAU83470	Bee venom
401	23	100.0	37	4	AAU20741	Human nov	474	23	100.0	42	4	AAM22107	Peptide #
402	23	100.0	37	5	ABB88701	Conus ema	475	23	100.0	42	4	ABB44512	Peptide #
403	23	100.0	37	5	ABB88817	Conus ema	476	23	100.0	42	4	AAM38560	Peptide #
404	23	100.0	37	6	ABU61308	Human A d	477	23	100.0	42	4	ABB27341	Protein #
405	23	100.0	37	6	ABU61379	Human A d	478	23	100.0	42	4	AAM78313	Human bon
406	23	100.0	37	6	ABU61340	Human A d	479	23	100.0	42	4	AAM65698	Human bra
407	23	100.0	37	6	ABU61362	Human A d	480	23	100.0	42	4	ABG59818	Human bra
408	23	100.0	37	6	ABU61377	Human A d	481	23	100.0	42	4	ABG59921	Human liv
409	23	100.0	37	6	ABU61380	Human A d	482	23	100.0	42	5	ABG47339	Human pep
410	23	100.0	37	6	ABU61344	Human A d	483	23	100.0	42	7	ADD84729	Human spa
411	23	100.0	37	6	ABU61309	Human A d	484	23	100.0	43	2	AAR95472	V39, mono
412	23	100.0	37	6	ABU61349	Human A d	485	23	100.0	43	4	AAM19749	Peptide #
413	23	100.0	37	6	ABU61248	Human A d	486	23	100.0	43	4	ABB39504	Peptide #
414	23	100.0	37	6	ABU61376	Human A d	487	23	100.0	43	4	AAM33046	Peptide #
415	23	100.0	37	6	ABU61399	Peptide #	488	23	100.0	43	4	AAM86967	Human imm
416	23	100.0	38	4	ABB34995	Peptide #	489	23	100.0	43	4	ABB24254	Protein #
417	23	100.0	38	4	AAM28501	Peptide #	490	23	100.0	43	4	ABG72816	Human bon
418	23	100.0	38	4	ABB20403	Protein #	491	23	100.0	43	4	AAM60196	Human bon
419	23	100.0	38	4	AAM58176	Human bon	492	23	100.0	43	4	AAM60196	Human liv
420	23	100.0	38	4	AAM58802	Human bra	493	23	100.0	43	4	ABG54520	Human liv
421	23	100.0	38	4	ABG49828	Human liv	494	23	100.0	43	5	ABG42644	Human pep
422	23	100.0	38	4	AAM03734	Peptide #	495	23	100.0	43	7	ADD44508	Polypepti
423	23	100.0	38	6	ABU61289	Human A d	496	23	100.0	44	2	AAU25808	Human sec
424	23	100.0	38	6	ABU61304	Human A d	497	23	100.0	44	4	AAU04702	Human ace
425	23	100.0	38	6	ABU61328	Human A d	498	23	100.0	44	4	AAU65949	Human ace
426	23	100.0	38	6	ABU61328	Human A d	499	23	100.0	45	2	AAR86788	Feline Ig
427	23	100.0	39	2	AAR77010	Alternati	500	23	100.0	45	2	AAW74586	Amino aci
428	23	100.0	39	3	AAB21602	Cone snai	501	23	100.0	45	2	AAW48800	C-termina
429	23	100.0	39	3	AAB21604	Cone snai	502	23	100.0	45	2	AAW68144	Human ACH
430	23	100.0	39	3	AAB21636	Cone snai	503	23	100.0	45	3	AAU76905	Xenopus I
431	23	100.0	39	3	AAG10878	Arabidops	504	23	100.0	45	4	ABG19530	Peptide #
432	23	100.0	39	4	AAM18874	Peptide #	505	23	100.0	45	4	ABG39062	Peptide #
433	23	100.0	39	4	ABB37994	Peptide #	506	23	100.0	45	4	AAM32553	Peptide #
434	23	100.0	39	4	AAM31408	Peptide #	507	23	100.0	45	4	ABG23988	Protein #
435	23	100.0	39	4	ABE23232	Protein #	508	23	100.0	45	4	AAU72294	Human bra
436	23	100.0	39	4	AAU71117	Human bon	509	23	100.0	45	4	AAM58201	Human bon
437	23	100.0	39	4	AAM58621	Human bra	510	23	100.0	45	4	AAU59714	Human bra
438	23	100.0	39	4	ABG52841	Human liv	511	23	100.0	45	4	ABG52358	Human liv
439	23	100.0	39	5	ABG40922	Human pep	512	23	100.0	45	5	ABG33980	Human liv
440	23	100.0	39	6	ABR43588	Human bet	513	23	100.0	45	5	ABG42109	Human pep
441	23	100.0	40	3	ABU51857	Human sec	514	23	100.0	46	2	ABG83978	Rat Binlb
442	23	100.0	40	3	AAU32251	Human Clq	515	23	100.0	46	4	AAU10973	Polyclona
443	23	100.0	40	3	AAE21624	Cone snai	516	23	100.0	46	4	AAM90371	Human imm
444	23	100.0	40	4	AAE22386	Alternati	517	23	100.0	46	6	ABU48113	Consensus
445	23	100.0	40	4	AAE48915	Human ace	518	23	100.0	47	4	AAU20451	Protein e
446	23	100.0	40	4	AAE50033	Acetylcho	519	23	100.0	47	4	AAM13785	Peptide #
447	23	100.0	40	4	AAU73873	Protein t	520	23	100.0	47	4	AAM13785	Peptide #
448	23	100.0	40	5	AAU81065	Human alp	521	23	100.0	47	4	ABG32719	Peptide #
449	23	100.0	40	5	AAU81048	Human alp	522	23	100.0	47	4	ABU41250	Peptide #
450	23	100.0	40	5	AAU98023	Human syn	523	23	100.0	47	4	AAM26183	Peptide #
451	23	100.0	40	6	ABP71131	E10 CARD	524	23	100.0	47	4	AAM35034	Peptide #
452	23	100.0	40	6	ABU25342	SAC isola	525	23	100.0	47	4	ABG27560	Human pep
453	23	100.0	40	6	ABG74487	Tyrosine	526	23	100.0	47	4	ABU18205	Protein #
454	23	100.0	41	4	AAM17448	Peptide #	527	23	100.0	47	4	ABG25246	Protein #
455	23	100.0	41	4	AAM19167	Peptide #	528	23	100.0	47	4	ABG65918	Human bon
456	23	100.0	41	4	ABE38376	Peptide #	529	23	100.0	47	4	AAM74919	Human bon
457	23	100.0	41	4	ABE36468	Peptide #	530	23	100.0	47	4	AAM53537	Human bra
458	23	100.0	41	4	AAM29965	Peptide #	531	23	100.0	47	4	AAM62115	Human bra
459	23	100.0	41	4	AAM31815	Peptide #	532	23	100.0	47	4	ABG56695	Human liv
460	23	100.0	41	4	AAM87384	Human imm	533	23	100.0	47	4	ABG47574	Human liv
461	23	100.0	41	4	ABE31260	Peptide #	534	23	100.0	47	4	AAM01530	Peptide #
462	23	100.0	41	4	ABE23554	Protein #	535	23	100.0	47	5	ABG44674	Human pep
463	23	100.0	41	4	ABE21811	Protein #	536	23	100.0	48	2	AAU03460	Intracell

537	23	100.0	48	4	AAM39584	Human pol	Aam39584	Human pol	610	23	100.0	55	6	ABM63547	Propionib
538	23	100.0	48	4	AAO08848	Human pol	Aao08848	Human pol	611	23	100.0	55	7	ABJ39193	Fragment
539	23	100.0	48	6	ABR42048	Brine shr	Ab42048	Brine shr	612	23	100.0	56	3	AB45029	Human sec
540	23	100.0	48	7	ABD47923	Novel hum	Abd47923	Novel hum	613	23	100.0	56	4	ABB40966	Peptide #
541	23	100.0	50	4	AM21713	Peptide #	Aam21713	Peptide #	614	23	100.0	56	4	AM34740	Peptide #
542	23	100.0	50	4	ABB44081	Peptide #	Abb44081	Peptide #	615	23	100.0	56	4	AM74627	Human bon
543	23	100.0	50	4	AM38026	Peptide #	Aam38026	Peptide #	616	23	100.0	56	4	AAU51158	Propionib
544	23	100.0	50	4	ABB26972	Protein #	Abb26972	Protein #	617	23	100.0	56	4	AAU51158	Propionib
545	23	100.0	50	4	AAU58879	Propionib	Aau58879	Propionib	618	23	100.0	56	4	ABW71668	Human bra
546	23	100.0	50	4	AM651102	Human bra	Aam651102	Human bra	619	23	100.0	56	4	ABG56412	Human col
547	23	100.0	50	4	ABG59463	Human liv	Abg59463	Human liv	620	23	100.0	56	5	ABG44455	Human pep
548	23	100.0	50	6	ABM55398	Propionib	Abm55398	Propionib	621	23	100.0	56	6	ABM47677	Propionib
549	23	100.0	50	6	ADA23270	Zea may	Ada23270	Zea may	622	23	100.0	57	4	AAU50758	Propionib
550	23	100.0	51	1	AAU50546	Protein a	Aap50546	Protein a	623	23	100.0	57	4	AAU50758	Propionib
551	23	100.0	51	1	AAU50546	Protein a	Aap50546	Protein a	624	23	100.0	57	5	ABG99662	Conus ep
552	23	100.0	51	3	AB32842	Eucalyptu	Ab32842	Eucalyptu	625	23	100.0	57	6	ABM47277	Propionib
553	23	100.0	51	4	AB506335	Human sec	Ab506335	Human sec	626	23	100.0	58	3	AB21460	Cone snai
554	23	100.0	51	4	AAU46337	Propionib	Aau46337	Propionib	627	23	100.0	58	4	AB21460	Cone snai
555	23	100.0	51	6	ABM42856	Propionib	Abm42856	Propionib	628	23	100.0	58	5	ABP06674	Human ORF
556	23	100.0	51	6	ABO44892	Novel hum	Abm44892	Novel hum	629	23	100.0	58	5	ABP31284	Human ORF
557	23	100.0	51	7	ABO26372	Protein a	Abm26372	Protein a	630	23	100.0	59	4	AAU14545	Peptide #
558	23	100.0	52	3	AG044498	Arabidops	Aag044498	Arabidops	631	23	100.0	59	4	AB33502	Peptide #
559	23	100.0	52	4	AM89686	Human imm	Aam89686	Human imm	632	23	100.0	59	4	AB26962	Peptide #
560	23	100.0	52	4	AM80423	Human hae	Aam80423	Human hae	633	23	100.0	59	4	AM81373	Human hae
561	23	100.0	52	4	AM81064	Human hae	Aam81064	Human hae	634	23	100.0	59	4	AB28326	Human pep
562	23	100.0	52	4	AM81528	Human hae	Aam81528	Human hae	635	23	100.0	59	4	AB18962	Protein #
563	23	100.0	52	4	AAU60779	Propionib	Aau60779	Propionib	636	23	100.0	59	4	ABM66677	Human bon
564	23	100.0	52	6	ABM57298	Propionib	Abm57298	Propionib	637	23	100.0	59	4	AAU45986	Propionib
565	23	100.0	53	2	AM62265	Subtilase	Aaw62265	Subtilase	638	23	100.0	59	4	AAU58966	Propionib
566	23	100.0	53	3	AAU54253	Insert of	Aay54253	Insert of	639	23	100.0	59	4	AAU58966	Propionib
567	23	100.0	53	4	AAU48466	Propionib	Aau48466	Propionib	640	23	100.0	59	4	AAU54282	Human bra
568	23	100.0	53	4	AAU45013	Propionib	Aau45013	Propionib	641	23	100.0	59	4	ABG48348	Human liv
569	23	100.0	53	4	AAU67818	Propionib	Aau67818	Propionib	642	23	100.0	59	5	ABP02996	Human ORF
570	23	100.0	53	4	ABG03003	Novel hum	Abg03003	Novel hum	643	23	100.0	59	5	ABG36331	Human pep
571	23	100.0	53	4	AAU04299	Bovine ac	Aau04299	Bovine ac	644	23	100.0	59	6	ABM55485	Propionib
572	23	100.0	53	4	AG65953	Bovine ac	Aag65953	Bovine ac	645	23	100.0	59	6	ABM43505	Propionib
573	23	100.0	53	6	ABM41532	Propionib	Abm41532	Propionib	646	23	100.0	59	6	ABU24323	Protein e
574	23	100.0	53	6	ABM44337	Propionib	Abm44337	Propionib	647	23	100.0	60	2	AAW76654	Elapidae
575	23	100.0	53	6	ABM44385	Propionib	Abm44385	Propionib	648	23	100.0	60	2	AAW76654	Elapidae
576	23	100.0	54	3	AG58372	Arabidops	Aag58372	Arabidops	649	23	100.0	60	3	AAU02165	Human sec
577	23	100.0	54	4	AAU41874	Propionib	Aau41874	Propionib	650	23	100.0	60	3	AAU02165	Human sec
578	23	100.0	54	4	AAU67384	Propionib	Aau67384	Propionib	651	23	100.0	60	4	AM80703	Human hae
579	23	100.0	54	4	AAU04703	Rabbit ac	Aau04703	Rabbit ac	652	23	100.0	61	4	ABP80573	N. gonorr
580	23	100.0	54	4	AG65950	Rabbit ac	Aag65950	Rabbit ac	653	23	100.0	61	4	AAU13458	Human pol
581	23	100.0	54	6	ABM38393	Propionib	Abm38393	Propionib	654	23	100.0	61	4	AAU09094	Human pol
582	23	100.0	54	6	ABM63303	Propionib	Abm63303	Propionib	655	23	100.0	61	4	AAU62825	Propionib
583	23	100.0	54	6	ABP75827	Human sec	Abp75827	Human sec	656	23	100.0	61	4	AAU58612	Propionib
584	23	100.0	55	3	AG60384	Arabidops	Aag60384	Arabidops	657	23	100.0	61	5	ABP08503	Human ORF
585	23	100.0	55	3	AG56375	Arabidops	Aag56375	Arabidops	658	23	100.0	61	5	ABP30566	Streptoco
586	23	100.0	55	4	AM17684	Peptide #	Aam17684	Peptide #	659	23	100.0	61	6	ABM55131	Propionib
587	23	100.0	55	4	AB36706	Peptide #	Abb36706	Peptide #	660	23	100.0	61	6	ABM59344	Propionib
588	23	100.0	55	4	AM30198	Peptide #	Aam30198	Peptide #	661	23	100.0	62	3	AAU00128	Human sec
589	23	100.0	55	4	AB31493	Peptide #	Ab31493	Peptide #	662	23	100.0	62	4	AAU00128	Human sec
590	23	100.0	55	4	AB222039	Protein #	Ab222039	Protein #	663	23	100.0	62	4	AAU00128	Human sec
591	23	100.0	55	4	AM69858	Human bon	Aam69858	Human bon	664	23	100.0	62	4	AAU00128	Human sec
592	23	100.0	55	4	AAU79292	Amino aci	Aag79292	Amino aci	665	23	100.0	62	4	AAU00128	Human hae
593	23	100.0	55	4	AAU67028	Propionib	Aau67028	Propionib	666	23	100.0	62	4	AAU00128	Human hae
594	23	100.0	55	4	AAU52270	Propionib	Aau52270	Propionib	667	23	100.0	62	4	AAU00128	Human hae
595	23	100.0	55	4	AAU49962	Propionib	Aau49962	Propionib	668	23	100.0	62	4	AAU49962	Propionib
596	23	100.0	55	4	AAU45150	Propionib	Aau45150	Propionib	669	23	100.0	62	4	AAU45150	Propionib
597	23	100.0	55	4	AAU39134	Propionib	Aau39134	Propionib	670	23	100.0	62	4	ABG05569	Novel hum
598	23	100.0	55	4	AM57463	Human bra	Aam57463	Human bra	671	23	100.0	62	5	ABP08784	Human ORF
599	23	100.0	55	4	ABG51557	Human liv	Abg51557	Human liv	672	23	100.0	62	6	ABM41443	Propionib
600	23	100.0	55	4	AM05345	Peptide #	Aam05345	Peptide #	673	23	100.0	62	6	ABM45320	Propionib
601	23	100.0	55	4	AB15865	Human ner	Ab15865	Human ner	674	23	100.0	62	6	ABP75920	Human sec
602	23	100.0	55	5	ABG39490	Human pep	Abg39490	Human pep	675	23	100.0	63	2	AAW76657	Elapidae
603	23	100.0	55	5	ABG77235	Selected	Abg77235	Selected	676	23	100.0	63	3	AAU59384	Arabidops
604	23	100.0	55	5	ABJ11106	Yeast sel	Abj11106	Yeast sel	677	23	100.0	63	3	AAU59384	Arabidops
605	23	100.0	55	6	ABP80559	N. gonorr	Abp80559	N. gonorr	678	23	100.0	63	4	AAU63047	Propionib
606	23	100.0	55	6	ABM41669	Propionib	Abm41669	Propionib	679	23	100.0	63	5	AAU63047	Propionib
607	23	100.0	55	6	ABM46481	Propionib	Abm46481	Propionib	680	23	100.0	63	6	ABM59566	Propionib
608	23	100.0	55	6	ABM48789	Propionib	Abm48789	Propionib	681	23	100.0	63	6	ABU41171	Protein e
609	23	100.0	55	6	ABM35653	Propionib	Abm35653	Propionib	682	23	100.0	64	4	ABM4580	Amino aci

683	23	100.0	64	4	AAB84579	Aab84579 Amino aci	756	23	100.0	71	5	AAU91255	Aau91255 Nucleic a
684	23	100.0	64	4	AAU56743	Aau56743 Propionib	757	23	100.0	71	5	AB888627	Ab888627 Conus meg
685	23	100.0	64	4	ABG08328	Abg08328 Novel hum	758	23	100.0	71	6	ABM48249	Abm48249 Propionib
686	23	100.0	64	4	ABG14055	Abg14055 Novel hum	759	23	100.0	71	6	AAU40799	Aau40799 Propionib
687	23	100.0	64	5	ABP08525	Abp08525 Human ORF	760	23	100.0	72	2	AAU12720	Aau12720 Human 5'
688	23	100.0	64	5	ABP29133	Abp29133 Streptoco	761	23	100.0	72	3	AAG60757	Aag60757 Arabidops
689	23	100.0	64	5	ABP52391	Abp52391 JAK famil	762	23	100.0	72	3	AAG55109	Aag55109 Arabidops
690	23	100.0	64	6	ABM53262	Abm53262 Propionib	763	23	100.0	72	4	AAU05966	Aau05966 Human pol
691	23	100.0	65	2	AAU41318	Aau41318 Human sec	764	23	100.0	72	4	AAU53087	Aau53087 Propionib
692	23	100.0	65	4	AAU58288	Aau58288 Propionib	765	23	100.0	72	4	AB888764	Ab888764 Conus epi
693	23	100.0	65	4	AAU61425	Aau61425 Propionib	766	23	100.0	72	5	AB888774	Ab888774 Conus epi
694	23	100.0	65	4	ABM15243	Abm15243 Human ner	767	23	100.0	72	6	ABM49606	Abm49606 Propionib
695	23	100.0	65	6	ABM57944	Abm57944 Propionib	768	23	100.0	73	4	AAU19515	Aau19515 Human dia
696	23	100.0	65	6	ABM54807	Abm54807 Propionib	769	23	100.0	73	4	ABG11192	Abg11192 Novel hum
697	23	100.0	66	3	ABM34327	Abm34327 Human sec	770	23	100.0	73	5	ABP07699	Abp07699 Human ORF
698	23	100.0	66	4	AAU52583	Aau52583 Propionib	771	23	100.0	73	5	AB888700	Ab888700 Conus ema
699	23	100.0	66	4	AAU48052	Aau48052 Propionib	772	23	100.0	73	5	ABP31160	Abp31160 Human ORF
700	23	100.0	66	5	ABP07662	Abp07662 Human ORF	773	23	100.0	73	7	ADE80854	Ad80854 Botaxin c
701	23	100.0	66	5	ABP01438	Abp01438 Human ORF	774	23	100.0	73	7	ABE80877	Ab80877 BOTAXIN c
702	23	100.0	66	5	ABP52400	Abp52400 JAK famil	775	23	100.0	74	2	AAU30415	Aau30415 Mature ne
703	23	100.0	66	6	ABM44571	Abm44571 Propionib	776	23	100.0	74	3	AAU69023	Aau69023 Amino aci
704	23	100.0	66	6	ABM49102	Abm49102 Propionib	777	23	100.0	74	3	AAU69023	Aau69023 Amino aci
705	23	100.0	67	2	AAR58597	Aar58597 Brain fun	778	23	100.0	74	3	AAU69023	Aau69023 Amino aci
706	23	100.0	67	2	AAU08496	Aau08496 Acetylcho	779	23	100.0	74	3	AAU69023	Aau69023 Amino aci
707	23	100.0	67	4	ABM50037	Abm50037 Human MCP	780	23	100.0	74	3	AAU69023	Aau69023 Amino aci
708	23	100.0	67	4	ABM17839	Abm17839 Human MCP	781	23	100.0	74	3	AAU69023	Aau69023 Amino aci
709	23	100.0	67	4	ABG29967	Abg29967 Novel hum	782	23	100.0	74	3	AAU69023	Aau69023 Amino aci
710	23	100.0	67	5	ABP01643	Abp01643 Human ORF	783	23	100.0	74	3	AAU69023	Aau69023 Amino aci
711	23	100.0	67	5	AAU78396	Aau78396 Human/mou	784	23	100.0	74	3	AAU69023	Aau69023 Amino aci
712	23	100.0	67	5	AAU68359	Aau68359 Chimeric	785	23	100.0	74	3	AAU69023	Aau69023 Amino aci
713	23	100.0	67	6	ABM99539	Abm99539 Amino aci	786	23	100.0	74	3	AAU69023	Aau69023 Amino aci
714	23	100.0	67	7	ADC98692	Adc98692 Human MCP	787	23	100.0	74	3	AAU69023	Aau69023 Amino aci
715	23	100.0	68	4	AAU92333	Aau92333 Human dig	788	23	100.0	74	3	AAU69023	Aau69023 Amino aci
716	23	100.0	68	4	AAU49289	Aau49289 Propionib	789	23	100.0	74	3	AAU69023	Aau69023 Amino aci
717	23	100.0	68	4	ABM61808	Abm61808 Murine MD	790	23	100.0	74	3	AAU69023	Aau69023 Amino aci
718	23	100.0	68	5	AAU81051	Aau81051 Human alp	791	23	100.0	74	3	AAU69023	Aau69023 Amino aci
719	23	100.0	68	5	ABG31332	Abg31332 GFP-fused	792	23	100.0	74	3	AAU69023	Aau69023 Amino aci
720	23	100.0	68	5	ABM93977	Abm93977 Rat Binib	793	23	100.0	74	3	AAU69023	Aau69023 Amino aci
721	23	100.0	68	5	AAU78392	Aau78392 Mouse che	794	23	100.0	74	3	AAU69023	Aau69023 Amino aci
722	23	100.0	68	5	AAU68335	Aau68335 Murine ch	795	23	100.0	74	3	AAU69023	Aau69023 Amino aci
723	23	100.0	68	5	ABP33041	Abp33041 Human ORF	796	23	100.0	74	3	AAU69023	Aau69023 Amino aci
724	23	100.0	68	6	ABM45808	Abm45808 Propionib	797	23	100.0	74	3	AAU69023	Aau69023 Amino aci
725	23	100.0	68	6	ABM99535	Abm99535 Amino aci	798	23	100.0	74	3	AAU69023	Aau69023 Amino aci
726	23	100.0	68	7	ADC98688	Adc98688 Human mmp	799	23	100.0	74	3	AAU69023	Aau69023 Amino aci
727	23	100.0	68	7	ADC94664	Adc94664 E. faeciu	800	23	100.0	74	3	AAU69023	Aau69023 Amino aci
728	23	100.0	69	2	AAU18129	Aau18129 Clone 3 o	801	23	100.0	74	3	AAU69023	Aau69023 Amino aci
729	23	100.0	69	3	AAU28166	Aau28166 Arabidops	802	23	100.0	74	3	AAU69023	Aau69023 Amino aci
730	23	100.0	69	4	AAU08304	Aau08304 Human pol	803	23	100.0	74	3	AAU69023	Aau69023 Amino aci
731	23	100.0	69	4	AAU50528	Aau50528 Propionib	804	23	100.0	74	3	AAU69023	Aau69023 Amino aci
732	23	100.0	69	4	AAU42264	Aau42264 Propionib	805	23	100.0	74	3	AAU69023	Aau69023 Amino aci
733	23	100.0	69	6	ABM36200	Abm36200 Propionib	806	23	100.0	74	3	AAU69023	Aau69023 Amino aci
734	23	100.0	69	6	ABM47047	Abm47047 Propionib	807	23	100.0	74	3	AAU69023	Aau69023 Amino aci
735	23	100.0	69	6	ABM38783	Abm38783 Propionib	808	23	100.0	74	3	AAU69023	Aau69023 Amino aci
736	23	100.0	69	6	ABM66163	Abm66163 Propionib	809	23	100.0	74	3	AAU69023	Aau69023 Amino aci
737	23	100.0	69	6	ABM66163	Abm66163 Propionib	810	23	100.0	74	3	AAU69023	Aau69023 Amino aci
738	23	100.0	70	3	AAG36901	Aag36901 Arabidops	811	23	100.0	74	3	AAU69023	Aau69023 Amino aci
739	23	100.0	70	4	AAU08338	Aau08338 Human pol	812	23	100.0	74	3	AAU69023	Aau69023 Amino aci
740	23	100.0	70	4	AAU43039	Aau43039 Propionib	813	23	100.0	74	3	AAU69023	Aau69023 Amino aci
741	23	100.0	70	5	ABP01663	Abp01663 Human ORF	814	23	100.0	74	3	AAU69023	Aau69023 Amino aci
742	23	100.0	70	5	ABG61978	Abg61978 Human tum	815	23	100.0	74	3	AAU69023	Aau69023 Amino aci
743	23	100.0	70	5	ABG61981	Abg61981 Human tum	816	23	100.0	74	3	AAU69023	Aau69023 Amino aci
744	23	100.0	70	5	ABG61979	Abg61979 Human tum	817	23	100.0	74	3	AAU69023	Aau69023 Amino aci
745	23	100.0	70	5	ABG61980	Abg61980 Human tum	818	23	100.0	74	3	AAU69023	Aau69023 Amino aci
746	23	100.0	70	5	AB888691	Ab888691 Conus lyn	819	23	100.0	74	3	AAU69023	Aau69023 Amino aci
747	23	100.0	70	5	AB888687	Ab888687 Conus lyn	820	23	100.0	74	3	AAU69023	Aau69023 Amino aci
748	23	100.0	70	5	AB888685	Ab888685 Conus lyn	821	23	100.0	74	3	AAU69023	Aau69023 Amino aci
749	23	100.0	70	5	AB888681	Ab888681 Conus lyn	822	23	100.0	74	3	AAU69023	Aau69023 Amino aci
750	23	100.0	70	5	ABP66659	Abp66659 Human bre	823	23	100.0	74	3	AAU69023	Aau69023 Amino aci
751	23	100.0	70	5	ABM39538	Abm39538 Propionib	824	23	100.0	74	3	AAU69023	Aau69023 Amino aci
752	23	100.0	70	7	ADC96731	Adc96731 E. faeciu	825	23	100.0	74	3	AAU69023	Aau69023 Amino aci
753	23	100.0	71	3	AAG00489	Aag00489 Human sec	826	23	100.0	74	3	AAU69023	Aau69023 Amino aci
754	23	100.0	71	4	AAU51730	Aau51730 Propionib	827	23	100.0	74	3	AAU69023	Aau69023 Amino aci
755	23	100.0	71	4	AAU44280	Aau44280 Propionib	828	23	100.0	74	3	AAU69023	Aau69023 Amino aci

829	23	100.0	77	4	AAU25296	Human pro	902	23	100.0	81	4	AAU66788	Propionib
830	23	100.0	77	4	AAO03507	Human pol	903	23	100.0	81	4	AGP92203	C glutami
831	23	100.0	77	4	AAU65949	Propionib	904	23	100.0	81	5	ABP00935	Human ORF
832	23	100.0	77	4	ABG29109	Novel hum	905	23	100.0	81	5	AAU81064	Human alp
833	23	100.0	77	4	ABG69193	Human TNF	906	23	100.0	81	5	AAE24070	Flea peri
834	23	100.0	77	5	ABF08160	Human ORF	907	23	100.0	81	6	ABP78091	N. gonorr
835	23	100.0	77	5	ABP08941	Human ORF	908	23	100.0	81	6	ABM53052	Propionib
836	23	100.0	77	5	ABP31167	Human ORF	909	23	100.0	81	6	ABM63431	Propionib
837	23	100.0	77	6	ABM62468	Propionib	910	23	100.0	81	6	ABM61398	Propionib
838	23	100.0	78	2	AAW44766	TVHURT hu	911	23	100.0	81	6	ABM63307	Propionib
839	23	100.0	78	2	AAU30402	Nematode	912	23	100.0	81	7	ABU12495	Novel hum
840	23	100.0	78	2	AAU30426	Mature ne	913	23	100.0	81	7	ADB34355	NADH dehy
841	23	100.0	78	2	AAU30427	Mature ne	914	23	100.0	82	2	AAW44721	Amino aci
842	23	100.0	78	2	AAU30420	Mature ne	915	23	100.0	82	3	AAU25117	Eucalyptu
843	23	100.0	78	2	AAU30429	Mature ne	916	23	100.0	82	3	AAU52266	Arabidops
844	23	100.0	78	3	AAU15314	A. duoden	917	23	100.0	82	4	ABM63697	Peptide #
845	23	100.0	78	3	AAU15305	A. caninu	918	23	100.0	82	4	AAU71775	Human olf
846	23	100.0	78	3	AAU15296	A. duoden	919	23	100.0	82	4	ABM22032	Protein #
847	23	100.0	78	4	AAU55712	Propionib	920	23	100.0	82	4	AAU69853	Human bon
848	23	100.0	78	4	AAU31584	Novel hum	921	23	100.0	82	4	AAU52266	Propionib
849	23	100.0	78	6	ABM52231	Propionib	922	23	100.0	82	4	AAU47366	Propionib
850	23	100.0	78	6	ABR41688	Human DIT	923	23	100.0	82	4	AAU49422	Propionib
851	23	100.0	79	3	AAU54421	Human pan	924	23	100.0	82	4	ABG51547	Human liv
852	23	100.0	79	3	AAU40344	Arabidops	925	23	100.0	82	4	ABG25924	Novel hum
853	23	100.0	79	3	AAU57689	Arabidops	926	23	100.0	82	5	ABP09031	Human ORF
854	23	100.0	79	4	AAU85975	Human imm	927	23	100.0	82	5	ABP04826	Human ORF
855	23	100.0	79	4	AAU13302	Human pol	928	23	100.0	82	5	AAO26497	Human cyc
856	23	100.0	79	4	AAU66787	Propionib	929	23	100.0	82	6	ABM43885	Propionib
857	23	100.0	79	4	AAU56555	Propionib	930	23	100.0	82	6	ABM45941	Propionib
858	23	100.0	79	4	AAU61166	Propionib	931	23	100.0	82	6	ABM65690	Propionib
859	23	100.0	79	5	ABP03243	Human ORF	932	23	100.0	82	6	ABM48785	Propionib
860	23	100.0	79	5	ABP03243	Human ORF	933	23	100.0	83	2	AAU30425	Mature ne
861	23	100.0	79	6	ABM48751	Propionib	934	23	100.0	83	3	AAU45011	Human sec
862	23	100.0	79	6	ABM48751	Propionib	935	23	100.0	83	3	AAU45012	Human sec
863	23	100.0	79	6	ABM57685	Propionib	936	23	100.0	83	3	AAU45823	Arabidops
864	23	100.0	79	6	ABM53074	Propionib	937	23	100.0	83	3	AAU45823	Arabidops
865	23	100.0	79	7	ADC97252	E. faeciu	938	23	100.0	83	3	AAU32709	Zea mays
866	23	100.0	80	2	AAU42822	rECF 84.	939	23	100.0	83	3	AAU45823	Arabidops
867	23	100.0	80	4	AAU14173	Peptide #	940	23	100.0	83	3	AAU45823	Arabidops
868	23	100.0	80	4	ABM33120	Peptide #	941	23	100.0	83	3	AAU13890	Peptide #
869	23	100.0	80	4	AAU26583	Peptide #	942	23	100.0	83	4	AAU17547	Peptide #
870	23	100.0	80	4	AAU484385	Human imm	943	23	100.0	83	4	AAU14000	Peptide #
871	23	100.0	80	4	ABM12243	Human ren	944	23	100.0	83	4	ABM31929	Amino aci
872	23	100.0	80	4	ABM27948	Human pep	945	23	100.0	83	4	ABM32835	Peptide #
873	23	100.0	80	4	AAU96692	Human rep	946	23	100.0	83	4	ABM32945	Peptide #
874	23	100.0	80	4	AAU95792	Human rep	947	23	100.0	83	4	ABM36568	Peptide #
875	23	100.0	80	4	AAU84568	Amino aci	948	23	100.0	83	4	AAU26406	Peptide #
876	23	100.0	80	4	AAU84567	Amino aci	949	23	100.0	83	4	AAU30068	Peptide #
877	23	100.0	80	4	ABM18585	Protein #	950	23	100.0	83	4	AAU91059	Human imm
878	23	100.0	80	4	AAU66304	Human bon	951	23	100.0	83	4	ABM27665	Human pep
879	23	100.0	80	4	AAU46057	Propionib	952	23	100.0	83	4	ABM27774	Human pep
880	23	100.0	80	4	AAU50947	Propionib	953	23	100.0	83	4	ABM31365	Peptide #
881	23	100.0	80	4	AAU53917	Human bra	954	23	100.0	83	4	ABM18317	Protein #
882	23	100.0	80	4	ABG47971	Human liv	955	23	100.0	83	4	ABM21907	Protein #
883	23	100.0	80	4	ABM96323	Human tes	956	23	100.0	83	4	AAU69733	Human bon
884	23	100.0	80	4	ABM96591	Human tes	957	23	100.0	83	4	AAU66021	Human bon
885	23	100.0	80	4	AAU01911	Peptide #	958	23	100.0	83	4	AAU66129	Human bon
886	23	100.0	80	4	ABG01418	Novel hum	959	23	100.0	83	4	AAU50135	Propionib
887	23	100.0	80	5	AAU81049	Human alp	960	23	100.0	83	4	AAU53746	Human bra
888	23	100.0	80	5	AAU81043	Human alp	961	23	100.0	83	4	ABG47797	Human liv
889	23	100.0	80	5	ABG35952	Human pep	962	23	100.0	83	4	ABG47687	Human liv
890	23	100.0	80	6	ABM42576	Propionib	963	23	100.0	83	4	ABG51417	Human liv
891	23	100.0	80	6	ABM47466	Propionib	964	23	100.0	83	4	AAU01741	Peptide #
892	23	100.0	81	2	AAU05877	Rat macro	965	23	100.0	83	4	AAU05217	Peptide #
893	23	100.0	81	3	AAU29624	Cat flea	966	23	100.0	83	4	AAU01633	Peptide #
894	23	100.0	81	3	AAU04565	Arabidops	967	23	100.0	83	4	AAU30280	Novel hum
895	23	100.0	81	3	AAU45784	Arabidops	968	23	100.0	83	5	ABG39355	Human pep
896	23	100.0	81	3	AAU45824	Arabidops	969	23	100.0	83	5	ABG35779	Human pep
897	23	100.0	81	3	AAU09400	Arabidops	970	23	100.0	83	5	ABG35669	Human pep
898	23	100.0	81	4	ABG03201	Human mus	971	23	100.0	83	6	ABM46654	Propionib
899	23	100.0	81	4	AAU66912	Propionib	972	23	100.0	84	2	AAU42821	rECF 84.
900	23	100.0	81	4	AAU56533	Propionib	973	23	100.0	84	4	AAU24296	Human EST
901	23	100.0	81	4	AAU64879	Propionib	974	23	100.0	84	4	ABM43375	Peptide #

CC 'vascular adhesions and hypertrophic scars

XX Sequence 5 AA;

SQ Query Match 100.0%; Score 23; DB 3; Length 5;

Best Local Similarity 60.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 2;

QY 1 DXCXD 5

DB 1 DICQD 5

RESULT 3

AAAY58709

ID AAY58709 standard; peptide; 5 AA.

XX AC AAY58709;

XX DT 25-APR-2000 (first entry)

XX DE Antiangiogenic peptide derived from saposin B.

XX KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;

XX KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO200002902-A1.

XX PD 20-JAN-2000.

XX PF 12-JUL-1999; 99WO-US015772.

XX PR 13-JUL-1998; 98US-0092647P.

XX (GILL/) GILL P S.

XX PI Gill PS;

XX WPI; 2000-171128/15.

XX Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.

PS Disclosure; Page 19; 78pp; English.

XX The present sequence is that of a novel peptide, based on a human saposin B derived peptide, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumour activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars

SQ Sequence 5 AA;

Query Match

Best Local Similarity 100.0%; Score 23; DB 3; Length 5;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5

DB 1 DLQCD 5

RESULT 4

AAAY58711

ID AAY58711 standard; peptide; 5 AA.

XX AC AAY58711;

XX DT 25-APR-2000 (first entry)

XX DE Antiangiogenic peptide derived from saposin B.

XX KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;

XX KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO200002902-A1.

XX PD 20-JAN-2000.

XX PF 12-JUL-1999; 99WO-US015772.

XX PR 13-JUL-1998; 98US-0092647P.

XX (GILL/) GILL P S.

XX PI Gill PS;

XX WPI; 2000-171128/15.

XX Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.

PS Disclosure; Page 19; 78pp; English.

XX The present sequence is that of a novel peptide, based on a human saposin B derived peptide, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumour activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars

SQ Sequence 5 AA;

Query Match

Best Local Similarity 100.0%; Score 23; DB 3; Length 5;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5

DB 1 DVCED 5

RESULT 5

AAAY58684

ID AAY58684 standard; peptide; 5 AA.

XX AC AAY58684;

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XX 25-APR-2000 (first entry)
XX DT
XX DE
XX DE Antiangiogenic peptide derived from saposin B.
XX KW
XX KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
XX KW Antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200002902-A1.
XX XX
XX XX 20-JAN-2000.
XX PD
XX PD Misc-difference 2 /note= "any amino acid, preferably Val"
XX FT
XX FT Misc-difference 4 /note= "any amino acid, preferably Gln"
XX FT
XX FT Misc-difference 4 /note= "any amino acid, preferably Gln"
XX FT
XX FN WO200002902-A1.
XX XX
XX XX 20-JAN-2000.
XX PD
XX PD 12-JUL-1999; 99WO-US015772.
XX PF
XX PF 13-JUL-1998; 98US-0092647P.
XX PR
XX PR (GILL/) GILL P S.
XX PA
XX PA Gill PS;
XX PI
XX PI WPI; 2000-171128/15.
XX DR
XX DR Saposin B derived peptides, useful as inhibitors of angiogenesis and
XX PT tumor growth.
XX PT
XX PS Claim 1; Page 57; 78pp; English.
XX PS
XX CC The present sequence is a generic sequence of novel peptides derived from
XX CC saposin B having potent antiangiogenic and antitumour activity. The
XX CC invention is based on the discovery that saposin B (see AAY58716),
XX CC previously known to be involved in the hydrolysis of sphingolipids, has
XX CC potent antiangiogenic and antitumour activity, and also has
XX CC antiproliferative and antimigratory activity against endothelial cells.
XX CC This activity against tumour and endothelial cells is conserved in
XX CC cryptic polypeptides as small as 5 amino acids. These small polypeptides
XX CC (see AAY58684-715) can be synthetically prepared and used in vitro or in
XX CC vivo as antiangiogenic and antitumour agents. They are of use in the
XX CC treatment of undesired angiogenesis and tumor growth, especially Kaposi's
XX CC sarcoma (claimed). They can also be used in conjunction with cytotoxic
XX CC moieties to selectively kill certain cell types for treatment of cancer,
XX CC angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion
XX CC fracture, arthritis and other connective tissue disorders, Osler-Weber
XX CC syndrome, atherosclerotic plaque, psoriasis, corneal graft
XX CC neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic
XX CC retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and
XX CC hypertrophic scars
XX XX
XX SQ Sequence 5 AA;
XX Query Match 100.0%; Score 23; DB 3; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 DXCXD 5
XX Db 1 DXCXD 5
XX |||||
XX 1 DXCXD 5
XX 1 DXCXD 5
XX RESULT 6
XX AAY58712
XX ID AAY58712 standard; peptide; 5 AA.
XX AC
XX AC AAY58712;
XX XX
XX XX 25-APR-2000 (first entry)
XX DT

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XX Antiangiogenic peptide derived from saposin B.
XX DE
XX DE Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
XX KW Antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
XX KW
XX OS
XX OS Synthetic.
XX OS Homo sapiens.
XX PN
XX PN WO200002902-A1.
XX XX
XX XX 20-JAN-2000.
XX PD
XX PD 12-JUL-1999; 99WO-US015772.
XX PF
XX PF 13-JUL-1998; 98US-0092647P.
XX PR
XX PR (GILL/) GILL P S.
XX PA
XX PA Gill PS;
XX PI
XX PI WPI; 2000-171128/15.
XX DR
XX DR Saposin B derived peptides, useful as inhibitors of angiogenesis and
XX PT tumor growth.
XX PT
XX PS Disclosure; Page 20; 78pp; English.
XX PS
XX CC The present sequence is that of a novel peptide, based on a human saposin
XX CC B derived peptide, that has antiangiogenic activity. The invention is
XX CC based on the discovery that saposin B (see AAY58716), previously known to
XX CC be involved in the hydrolysis of sphingolipids, has potent antiangiogenic
XX CC and antitumour activity, and also has antiproliferative and antimigratory
XX CC activity against endothelial cells. This activity is conserved in cryptic
XX CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
XX CC synthetically prepared and used in vitro or in vivo for the treatment of
XX CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
XX CC (claimed). The polypeptides can also be used in conjunction with
XX CC cytotoxic moieties to selectively kill certain cell types, e.g. for
XX CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
XX CC malformation, nonunion fracture, arthritis and other connective tissue
XX CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
XX CC corneal graft neovascularization, pyogenic granuloma, retrolental
XX CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
XX CC vascular adhesions and hypertrophic scars
XX XX
XX SQ Sequence 5 AA;
XX Query Match 100.0%; Score 23; DB 3; Length 5;
XX Best Local Similarity 60.0%; Pred. No. 1.4e+06;
XX Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 DXCXD 5
XX Db 1 DXCXD 5
XX |||||
XX 1 DXCXD 5
XX 1 DXCXD 5
XX RESULT 7
XX AAY58700
XX ID AAY58700 standard; peptide; 5 AA.
XX AC
XX AC AAY58700;
XX XX
XX XX 25-APR-2000 (first entry)
XX DT
XX DT Antiangiogenic peptide derived from saposin B.
XX DE
XX DE Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
XX KW Antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
XX KW
XX OS
XX OS Homo sapiens.
XX XX
XX XX WO200002902-A1.
XX PN

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XX PD 20-JAN-2000.
XX PF 12-JUL-1999; 99WO-US015772.
XX PR 13-JUL-1998; 98US-0092647P.
XX PA (GILL/) GILL P S.
XX PI Gill PS;
XX PT Saposin B derived peptides, useful as inhibitors of angiogenesis and
XX tumor growth.
XX PS Claim 4; Page 57; 78pp; English.
XX CC The present sequence is that of a claimed peptide, derived from human
XX saposin B, that has antiangiogenic activity. The invention is based on
XX the discovery that saposin B (see AAY58716), previously known to be
XX involved in the hydrolysis of sphingolipids, has potent antiangiogenic
XX and antitumor activity, and also has antiproliferative and antimigratory
XX activity against endothelial cells. This activity is conserved in cryptic
XX polypeptides as small as 5 amino acids (see AAY58684-715), which can be
XX synthetically prepared and used in vitro or in vivo for the treatment of
XX undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
XX (claimed). The polypeptides can also be used in conjunction with
XX cytotoxic moieties to selectively kill certain cell types, e.g. for
XX treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
XX malformation, nonunion fracture, arthritis and other connective tissue
XX disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
XX corneal graft neovascularization, pyogenic granuloma, retrolental
XX fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
XX vascular adhesions and hypertrophic scars
XX SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 3; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 1 DVCQD 5

Sequence 5 AA;

RESULT 8
AAY58707
ID AAY58707 standard; peptide; 5 AA.
XX AC AAY58707;
XX DT 25-APR-2000 (first entry)
XX DE Antiangiogenic peptide derived from saposin B.
XX KW Antiangiogenic; angiogenesis inhibitor; antitumor; antiproliferative;
XX antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO200002902-A1.
XX PD 20-JAN-2000.
XX PF 12-JUL-1999; 99WO-US015772.
XX PR 13-JUL-1998; 98US-0092647P.
XX PA (GILL/) GILL P S.
XX PT Identifying a voltage gated sodium channel (VGSC) modulator for producing

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PI Gill PS;
XX DR WPI; 2000-171128/15.
XX PT Saposin B derived peptides, useful as inhibitors of angiogenesis and
XX tumor growth.
XX PS Disclosure; Page 19; 78pp; English.
XX CC The present sequence is that of a novel peptide, based on a human saposin
XX B derived peptide, that has antiangiogenic activity. The invention is
XX based on the discovery that saposin B (see AAY58716), previously known to
XX be involved in the hydrolysis of sphingolipids, has potent antiangiogenic
XX and antitumor activity, and also has antiproliferative and antimigratory
XX activity against endothelial cells. This activity is conserved in cryptic
XX polypeptides as small as 5 amino acids (see AAY58684-715), which can be
XX synthetically prepared and used in vitro or in vivo for the treatment of
XX undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
XX (claimed). The polypeptides can also be used in conjunction with
XX cytotoxic moieties to selectively kill certain cell types, e.g. for
XX treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
XX malformation, nonunion fracture, arthritis and other connective tissue
XX disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
XX corneal graft neovascularization, pyogenic granuloma, retrolental
XX fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
XX vascular adhesions and hypertrophic scars
XX SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 3; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 1 DACQD 5

Sequence 5 AA;

RESULT 9
ABG76196
ID ABG76196 standard; peptide; 5 AA.
XX AC ABG76196;
XX DT 10-MAY-2003 (first entry)
XX DE Rat small calcium binding protein p11, Nav1.8 binding region #1.
XX KW Rat; voltage gated sodium channel; VGSC; Nav1.8; p11;
XX small calcium binding protein; analgesia; chronic pain; osteoarthritis;
XX rheumatoid arthritis; neuropathic pain; cancer pain;
XX tri geminal neuralgia; hyperalgesia; inflammatory pain; nociceptive pain;
XX tabes dorsalis; phantom limb pain; spinal cord injury pain; central pain;
XX post-herpetic pain; HIV pain; non-cardiac chest pain;
XX irritable bowel syndrome; bowel disorder.
XX OS Rattus norvegicus.
XX PN WO2003016917-A2.
XX PD 27-FEB-2003.
XX PF 20-AUG-2002; 2002WO-GB003852.
XX PR 20-AUG-2001; 2001GB-00020238.
XX PA (UNLO ) UNIV COLLEGE LONDON.
XX PI Okuse K, Baker M, Poon L, Wood JN, Malik-Hall M;
XX DR WPI; 2003-278589/27.
XX PT Identifying a voltage gated sodium channel (VGSC) modulator for producing

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PT analgesia and for relieving chronic pain, e.g. osteoarthritis or HIV
 PT pain, comprises bringing into contact a VGSC, a p11 peptide and a test
 PT compound.

PS Example 6; Page 55; 114pp; English.

XX The invention relates to identifying a modulator of a voltage gated
 CC sodium channel (VGSC) e.g. Nav1.8 comprising: (a) bringing into contact a
 CC VGSC, a p11 peptide (a small calcium binding protein of the S-100 family)
 CC and test compound (tc) so that the VGSC and the p11 peptide can form a
 CC complex in the absence of the (tc); and (b) measuring an activity of the
 CC VGSC, where a change in the activity of the VGSC relative to the activity
 CC in the absence of the (tc) indicates that the (tc) is a modulator of
 CC VGSC. Also included are a method of enhancing the functional expression
 CC of a VGSC in a cell by increasing the level of p11 in the cell, a
 CC compound identified by a method above, a host cell capable of expressing
 CC a VGSC and a p11 peptide (where the VGSC and/or peptide 11 is expressed
 CC from one or more heterologous expression vectors within the cell),
 CC treating a disorder or condition associated with the activity of a
 CC voltage gated sodium channel (by administering with the activity of a
 CC compound identified by the method above, or an inhibitor of p11 activity
 CC or expression). The method is useful for identifying modulators of VGSC.
 CC Compounds identified as modulator of VGSC are useful for manufacturing a
 CC medicament for modulating the functional expression of a voltage gated
 CC sodium channel, for producing analgesia and for relieving chronic pain
 CC such as osteoarthritis, rheumatoid arthritis, neuropathic pain, cancer
 CC pain, trigeminal neuralgia, primary and secondary hyperalgesia,
 CC inflammatory pain, nociceptive pain, tabes dorsalis, phantom limb pain,
 CC spinal cord injury pain, central pain, post-herpetic pain and HIV pain,
 CC non-cardiac chest pain, irritable bowel syndrome and pain associated with
 CC bowel disorders. The present sequence represents a Nav1.8 binding region
 CC of rat p11 (amino acids 60-64)

XX Sequence 5 AA;

Query Match 100.0%; Score 23; DB 6; Length 5;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |.:|
 Db 1 DQCXD 5

RESULT 10
 ID AAR76052
 AC AAR76052 standard; peptide; 6 AA.

AC AAR76052;

XX 24-DEC-1995 (first entry)

XX Netrin domain VI peptide p78(40-45)/p75(27-32).

XX Neural axon out-growth modulator; epidermal growth factor; EGF; netrin-1;
 KW netrin-2; p78; p75; neurodegenerative disease.

XX Gallus sp.

XX WO9513367-A1.

XX 18-MAY-1995.

XX 08-NOV-1994; 94WO-US012913.

XX 12-NOV-1993; 93US-00152019.

XX (REGC) UNIV CALIFORNIA.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Tessier-Lavigne M, Serafini T, Kennedy T, Placzek M, Jessell T;
 PI Dodd J;

DR WPI; 1995-194086/25.

XX Neural axon out-growth modulators derived from EGF-like repeats of netrin
 PT 1 or netrin 2 - comprise peptide(s) capable of selectively increasing
 PT spinal axon out-growth or directing axon orientation.

XX Disclosure; Page 5; 58pp; English.

XX The peptides given in AAR74189-200 and AAR76042-58 have axon outgrowth
 CC and/or orienting activity and are based on domain V, domain VI or the C-
 CC terminal domains of chick p78 and p75 (AAR74186-87)

XX Sequence 6 AA;

Query Match 100.0%; Score 23; DB 2; Length 6;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |.:|
 Db 1 DQCXD 5

RESULT 11

AAAY58699

XX AAAY58699 standard; peptide; 6 AA.

XX AAAY58699;

XX 25-APR-2000 (first entry)

XX Antiangiogenic peptide derived from saposin B.

XX Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
 KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.

XX Homo sapiens.

XX WO200002902-A1.

XX 20-JAN-2000.

XX 12-JUL-1999; 99WO-US015772.

XX 13-JUL-1998; 98US-0092647P.

XX (GILL/) GILL P S.

XX Gill PS;

XX WPI; 2000-171128/15.

XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
 PT tumor growth.

XX Disclosure; Page 19; 78pp; English.

XX The present sequence is that of a novel peptide, derived from human
 CC saposin B, that has antiangiogenic activity. The invention is based on
 CC the discovery that saposin B (see AAY58716), previously known to be
 CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
 CC and antitumour activity, and also has antiproliferative and antimigratory
 CC activity against endothelial cells. This activity is conserved in cryptic
 CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
 CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
 CC (claimed). The polypeptides can also be used in conjunction with
 CC cytotoxic moieties to selectively kill certain cell types, e.g. for
 CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
 CC malformation, nonunion fracture, arthritis and other connective tissue
 CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
 CC corneal graft neovascularization, pyogenic granuloma, retrolental
 CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,

```

CC  vascular adhesions and hypertrophic scars
XX
SQ  Sequence 6 AA;

    Query Match      100.0%; Score 23; DB 3; Length 6;
    Best Local Similarity 60.0%; Pred. No. 1.4e+06;
    Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 DXCXD 5
DB  1 DVCQD 5

RESULT 12
ABB90472
ID  ABB90472 standard; peptide; 6 AA.
XX
AC  ABB90472;
XX
DT  27-MAY-2002 (first entry)
XX
DE  Hominidae LDL receptor related peptide sequence #87.
XX
KW  Hominidae; low density lipoprotein receptor; LDL receptor; LDL-R;
KW  detection; lipid metabolic error; hyperlipaemia; mutation;
KW  arteriosclerosis; ischaemic heart disease; ischaemia.
XX
OS  Hominidae.
OS  Synthetic.
XX
PN  WO200206467-A1.
XX
PD  24-JAN-2002.
XX
PF  17-JUL-2001; 2001WO-JP006153.
XX
PR  18-JUL-2000; 2000JP-00218039.
XX
PA  (BMLB-) BML INC.
PI  Hattori H, Tsuchi M, Okada T, Nagano M, Egaehira T, Ishihara M;
PI  Iwasaki T;
XX
DR  WPI; 2002-179794/23.
XX
PT  Set of specific low density lipoprotein receptor gene mutations for
PT  diagnosis of familial lipid metabolism errors including hyperlipemia.
XX
PS  Example; Fig 34; 123pp; Japanese.
XX
CC  The present invention describes a method for detecting lipid metabolism
CC  errors in patients using as indicators a set of 65 specific low density
CC  lipoprotein (LDL) receptor gene mutations. The method can be used in the
CC  diagnosis of an inherited predisposition to the development of diseases
CC  associated with hyperlipaemia, such as arteriosclerosis and ischaemic
CC  heart disease. ABL91141 encodes the LDL receptor given in ABB90525.
CC  ABL91142 to ABL91183 represent PCR primers used in the amplification of
CC  the receptor gene. ABL90990 to ABL91140 and ABB90445 to ABB90524
CC  represents sequences used in the exemplification of the present invention
XX
SQ  Sequence 6 AA;

    Query Match      100.0%; Score 23; DB 5; Length 6;
    Best Local Similarity 60.0%; Pred. No. 1.4e+06;
    Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 DXCXD 5
DB  2 DECQD 6

RESULT 13
AAY58698

```

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ID  AAY58698 standard; peptide; 7 AA.
XX
AC  AAY58698;
XX
DT  25-APR-2000 (first entry)
XX
DE  Antiangiogenic peptide derived from saposin B.
XX
KW  Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
KW  antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
XX
OS  Homo sapiens.
XX
PN  WO200002902-A1.
XX
PD  20-JAN-2000.
XX
PF  12-JUL-1999; 99WO-US015772.
XX
PR  13-JUL-1998; 98US-0092647P.
XX
PA  (GILL/) GILL P S.
XX
PI  Gill PS;
XX
DR  WPI; 2000-171128/15.
XX
PT  Saposin B derived peptides, useful as inhibitors of angiogenesis and
PT  tumor growth.
XX
PS  Disclosure; Page 19; 78pp; English.
XX
CC  The present sequence is that of a novel peptide, derived from human
CC  saposin B, that has antiangiogenic activity. The invention is based on
CC  the discovery that saposin B (see AAY58716), previously known to be
CC  involved in the hydrolysis of sphingolipids, has potent antiangiogenic
CC  and antitumour activity, and also has antiproliferative and antimigratory
CC  activity against endothelial cells. This activity is conserved in cryptic
CC  polypeptides as small as 5 amino acids (see AAY58684-715), which can be
CC  synthetically prepared and used in vitro or in vivo for the treatment of
CC  undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
CC  (claimed). The polypeptides can also be used in conjunction with
CC  cytotoxic moieties to selectively kill certain cell types, e.g. for
CC  treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
CC  malformation, nonunion fracture, arthritis and other connective tissue
CC  disorders. Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
CC  corneal graft neovascularization, pyogenic granuloma, retrolental
CC  fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
CC  vascular adhesions and hypertrophic scars
XX
SQ  Sequence 7 AA;

    Query Match      100.0%; Score 23; DB 3; Length 7;
    Best Local Similarity 60.0%; Pred. No. 1.4e+06;
    Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 DXCXD 5
DB  1 DVCQD 5

RESULT 14
ADC21082
ID  ADC21082 standard; peptide; 7 AA.
XX
AC  ADC21082;
XX
DT  18-DEC-2003 (first entry)
XX
DE  Hair growth promoting peptide #6.
XX
KW  epimorphin coiled coil domain; pep 7; hair growth; vulnary; cytostatic;
KW  antiarteriosclerotic; antianginal; endothelial cell growth;

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cardiovascular regeneration; liver regeneration; pancreatic endothelium;
cardiovascular endothelial cell; periodontic disease; fracture;
bone tumour; burn; wound; hair loss;
chronic obstructive arteriosclerosis; Buerger's disease;
severe angina pectoris; bone deficiency; lung branching morphogenesis;
crypt-villus morphogenesis; gallbladder epithelium;
mammary luminal morphogenesis; pulmonary fibrosis.

Synthetic.
OS Homo sapiens.
OS Mus sp.
US2003086893-A1.
08-MAY-2003.
23-MAY-2002; 2002US-00155922.
05-JUN-2000; 2000JP-00166903.
04-JUN-2001; 2001WO-JP004691.
13-NOV-2001; 2001JP-00347338.
13-NOV-2001; 2001JP-00347340.
05-DEC-2001; 2001JP-00371175.
05-DEC-2001; 2001JP-00371366.
(HIRA/) HIRAI Y.
(OKAY/) OKA Y.
(TAKE/) TAKEBE K.
(TSUD/) TSUDA H.
(TOCH/) TOCHIGI K.
(SHIN/) SHINAGAWA T.
(MURA/) MURAKAMI K.
(KOSH/) KOSHIDA S.

Hirai Y, Oka Y, Takebe K, Tsuda H, Tochigi K, Shinagawa T;
Murakami K, Koshida S;
WPI; 2003-786930/74.

Novel isolated oligopeptide having hair growth promoting activity, useful
for treating burns, wounds.

Claim 70; SEQ ID NO 8; 64pp; English.

The invention relates to an isolated oligopeptide having hair growth
promoting activity. The peptides are mutants or derivatives of the pep7
peptide from mouse and/or human epimorphin coiled coil domain. A general
formula for the peptides is given in the specification. Also included are
an oligopeptide polymer which is obtained by cross-linking the peptides
(if that the polymer is not a homopolymer of human epimorphin coiled coil
domain or the murine epimorphin coiled coil domain), a monoclonal
antibody or its fragments which specifically recognises an antigen of
about 220 kDa present in epithelial new follicles, a monoclonal antibody
or its fragments produced by the hybridoma deposited with the Patent and
Bio-Resource Center of National Institute of Advanced Industrial Science
and Technology and having an Accession number of FERM P-18578, an antigen
or its fragment recognised by the antibody; a hybridoma producing the
antibody, and a host cell comprising a nucleic acid encoding the
oligopeptides. Compositions comprising the peptides are useful for
promoting hair growth in a mammal. The peptides are useful for evaluating
hair growth promoting activity involves incubating skin tissue derived
from a mammal in the presence of a substance to be tested under suitable
conditions and for a time effective to promote hair growth, recovering
the skin tissue from above step, reacting the skin tissue with the
antibody and detecting the monoclonal antibody or their fragment that
reacted with skin tissue. The peptides are useful for treating and/or
amelioration of symptoms of diseases or disorders of abnormal
morphogenesis of pancreatic endothelium, cardiovascular endothelial cell,
periodontics, fracture, bone tumour, burns or wounds, preventing hair
loss, chronic obstructive arteriosclerosis, Buerger's disease, severe
angina pectoris, bone deficiency, lung branching morphogenesis, crypt-
villus morphogenesis, gallbladder epithelium, mammary luminal
morphogenesis and also useful for regeneration of liver, pulmonary

fibrosis. The present sequence hair growth promoting peptide of the
invention.

Sequence 7 AA;

Query Match 100.0%; Score 23; DB 7; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 3 DQCCD 7

RESULT 15

ADC21139
ID ADC21139 standard; peptide; 7 AA.

XX

AC ADC21139;

XX

DT 18-DEC-2003 (first entry)

XX

DE Hair growth promoting peptide #63.

XX epimorphin coiled coil domain; pep 7; hair growth; vulnery; cytostatic;
KW antiarteriosclerotic; antiangular; endothelial cell growth;
KW cardiovascular regeneration; liver regeneration; pancreatic endothelium;
KW cardiovascular endothelial cell; periodontic disease; fracture;
KW bone tumour; burn; wound; hair loss;
KW chronic obstructive arteriosclerosis; Buerger's disease;
KW severe angina pectoris; bone deficiency; lung branching morphogenesis;
KW crypt-villus morphogenesis; gallbladder epithelium;
KW mammary luminal morphogenesis; pulmonary fibrosis.

XX Synthetic.

OS Homo sapiens.

OS Mus sp.

XX

PN US2003086893-A1.

XX

PD 08-MAY-2003.

XX

PF 23-MAY-2002; 2002US-00155922.

XX

PR 05-JUN-2000; 2000JP-00166903.

PR 04-JUN-2001; 2001WO-JP004691.

PR 13-NOV-2001; 2001JP-00347338.

PR 13-NOV-2001; 2001JP-00347340.

PR 05-DEC-2001; 2001JP-00371175.

XX

XX (HIRA/) HIRAI Y.

PA (OKAY/) OKA Y.

PA (TAKE/) TAKEBE K.

PA (TSUD/) TSUDA H.

PA (TOCH/) TOCHIGI K.

PA (SHIN/) SHINAGAWA T.

PA (MURA/) MURAKAMI K.

XX (KOSH/) KOSHIDA S.

XX Hirai Y, Oka Y, Takebe K, Tsuda H, Tochigi K, Shinagawa T;

PI Murakami K, Koshida S;

XX WPI; 2003-786930/74.

XX Novel isolated oligopeptide having hair growth promoting activity, useful
for treating burns, wounds.

XX Claim 70; SEQ ID NO 65; 64pp; English.

XX The invention relates to an isolated oligopeptide having hair growth
promoting activity. The peptides are mutants or derivatives of the pep7
peptide from mouse and/or human epimorphin coiled coil domain. A general

CC formula for the peptides is given in the specification. Also included are
 CC an oligopeptide polymer which is obtained by cross-linking the peptides
 CC (if that the polymer is not a homopolymer of human epimorphin coiled coil
 CC domain or the murine epimorphin coiled coil domain), a monoclonal
 CC antibody or its fragments which specifically recognises an antigen of
 CC about 220 kDa present in epithelial new follicles, a monoclonal antibody
 CC or its fragments produced by the hybridoma deposited with the Patent and
 CC Bio-Resource Center of National Institute of Advanced Industrial Science
 CC and technology and having an Accession number of FERM P-18578, an antigen
 CC or its fragment recognised by the antibody; a hybridoma producing the
 CC antibody, and a host cell comprising a nucleic acid encoding the
 CC oligopeptides. Compositions comprising the peptides are useful for
 CC promoting hair growth in a mammal. The peptides are useful for evaluating
 CC hair growth promoting activity involves incubating skin tissue derived
 CC from a mammal in the presence of a substance to be tested under suitable
 CC conditions and for a time effective to promote hair growth, recovering
 CC the skin tissue from above step, reacting the skin tissue with the
 CC antibody and detecting the monoclonal antibody or their fragment that
 CC reacted with skin tissue. The peptides are useful for treating and/or
 CC amelioration of symptoms of diseases or disorders of abnormal
 CC morphogenesis of pancreatic endothelium, cardiovascular endothelial cell,
 CC periodontics, fracture, bone tumour, burns or wounds, preventing hair
 CC loss, chronic obstructive arteriosclerosis, Buerger's disease, severe
 CC angina pectoris, bone deficiency, lung branching morphogenesis, crypt-
 CC villus morphogenesis, gallbladder epithelium, mammary luminal
 CC morphogenesis and also useful for regeneration of liver, pulmonary
 CC fibrosis. The present sequence hair growth promoting peptide of the
 CC invention.

XX
 CC
 SQ Sequence 7 AA;

Query Match 100.0%; Score 23; DB 7; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 | : | : |
 DB 3 DOCCD 7

RESULT 16
 AA58697
 ID AA58697 standard; peptide; 8 AA.

AC AA58697;
 DT 25-APR-2000 (first entry)
 XX
 DE Antiangiogenic peptide derived from saposin B.

KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
 KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.

XX Homo sapiens.

OS WO200002902-A1.

PN 20-JAN-2000.

XX 12-JUL-1999; 99WO-US015772.

XX 13-JUL-1996; 98US-0092647P.

XX (GILL/) GILL P S.

XX Gill PS;

XX WPI; '2000-171128/15.

XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
 PT tumor growth.

XX Disclosure; Page 19; 78pp; English.

XX The present sequence is that of a novel peptide, derived from human
 CC saposin B, that has antiangiogenic activity. The invention is based on
 CC the discovery that saposin B (see AA58716), previously known to be
 CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
 CC and antitumour activity, and also has antiproliferative and antimigratory
 CC activity against endothelial cells. This activity is conserved in cryptic
 CC polypeptides as small as 5 amino acids (see AA58684-715), which can be
 CC synthetically prepared and used in vitro or in vivo for the treatment of
 CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
 CC (claimed). The polypeptides can also be used in conjunction with
 CC cytotoxic moieties to selectively kill certain cell types, e.g. for
 CC treatment of cancer, angioblastoma, neovascular glaucoma, arteriovenous
 CC malformation, nonunion fracture, arthritis and other connective tissue
 CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
 CC corneal graft neovascularization, pyogenic granuloma, retrolental
 CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
 CC vascular adhesions and hypertrophic scars

XX Sequence 8 AA;

Query Match 100.0%; Score 23; DB 3; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 | : | : |
 DB 1 DVCQD 5

RESULT 17
 AA25185
 ID AA25185 standard; peptide; 8 AA.

XX AA25185;

XX 30-OCT-2002 (first entry)

XX S. hindustanus ble gene product peptide (residues 32-39) variant #5.

KW Optimisation; drug; ble gene product; BRP; bleomycin; mutant; mutein;
 KW variant.

XX Streptoalloteichus hindustanus.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 3 /note= "Wild type Val substituted with Cys"

XX WO200244361-A2.

XX 06-JUN-2002.

XX 28-NOV-2001; 2001WO-US044600.

XX 28-NOV-2000; 2000US-00724762.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION INC.

XX Huse WD;

XX WPI; 2002-519586/55.

XX New cell composition having population of non-yeast eukaryotic cells
 PT containing diverse population of variant nucleic acids that are expressed
 PT in different cell and located within each cell at identical site in
 PT genome.

XX Example 9; Page 143; 157pp; English.

XX The present invention relates to a cell composition having population of
 CC non-yeast eukaryotic cells containing a diverse population of ten or more

CC variant nucleic acids or heterologous nucleic acid fragments comprising
 CC distinct species of nucleic acid fragments, each of the variant nucleic
 CC acids or heterologous nucleic acid fragments being expressed in different
 CC cells and located within each cell at an identical site in the genome.
 CC The composition is useful to identify polypeptides exhibiting optimised
 CC activity. It is also useful for identifying a binding ligand. It is also
 CC useful for identifying specific ligands to desired target molecules. Such
 CC ligands can be developed as potential drug candidates or alternatively
 CC used as lead compounds for the generation and identification of ligand
 CC variants which exhibit enhanced activity of the desired binding property.
 CC The methods can similarly be applied to identify a nucleic acid having an
 CC optimised activity by screening for an activity associated with a parent
 CC nucleic acid. The present sequence is *S. hindustanus* (Sh) *ble* gene
 CC product (BRP) peptide (residues 32-39) variant. BRP is involved in
 CC bleomycin binding. This sequence is used in the exemplification of the
 CC invention

SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 5; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 | : | : |
 Db 1 DFCED 5

RESULT 18

ABW00645
 ID ABW00645 standard; peptide; 8 AA.

AC ABW00645;

XX 15-JAN-2004 (first entry)

DE Bleomycin resistance protein (BRP) variant peptide, 1.5.

XX Bleomycin resistance protein; BRP; variant.

XX Unidentified.

XX US2003096401-A1.

XX 22-MAY-2003.

XX 28-NOV-2001; 2001US-00997209.

XX 28-NOV-2000; 2000US-0367370P.

XX (HUSE/) HUSE W D.

XX Huse WD;

XX WPI; 2003-786991/74.

XX Cell composition comprises non-yeast eukaryotic cells having diverse
 PT population of variant nucleic acids or heterologous nucleic acid
 PT fragments, useful for identifying polypeptide with optimized activity.

PS Example 9; Page 35; Opp; English.

XX The invention relates to a cell composition comprising a population of
 CC non-yeast eukaryotic cells containing diverse population of variant
 CC nucleic acids, or heterologous nucleic acid fragments with distinct
 CC species of nucleic acid fragments, where each of the variant nucleic
 CC acids or heterologous nucleic acid fragments are expressed in different
 CC cell and located within each cell at an identical site in the genome. The
 CC invention is useful for identifying polypeptide with optimised activity
 CC and for identifying a polypeptide receptor for a ligand. The present
 CC sequence is bleomycin resistance protein (BRP) variant peptide. This
 CC sequence is used in the exemplification of the invention

SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 7; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 | : | : |
 Db 1 DFCED 5

RESULT 19

AAW38411
 ID AAW38411 standard; peptide; 9 AA.

XX AAW38411;

XX 08-APR-1998 (first entry)

XX HLA-A1 restricted CTL epitope.

XX Melanoma; immunogen; cytotoxic T lymphocyte; CTL;
 KW human leukocyte antigen-A1; HLA-A1; human leukocyte antigen-A3; HLA-A3;
 KW epitope; pMEL-17; tyrosinase; vaccine; protection.

XX Homo sapiens.

XX WO9734613-A1.

XX 25-SEP-1997.

XX 17-MAR-1997; 97WO-US004958.

XX 19-MAR-1996; 96US-0013972P.

XX 04-OCT-1996; 96US-0027627P.

XX (UYVI-) UNIV VIRGINIA PATENT FOUND.

XX Slingluff CL, Hunt DF, Shabanowitz J, Cox AL, Engelhard VH;
 PI Kittlesen D, Skipper J, Hendrikson RC;

XX WPI; 1997-479982/44.

XX Melanoma-specific immunogens of pMEL-17 and tyrosinase - useful in
 PT vaccination for producing melanoma-specific cytotoxic T lymphocytes.

XX Claim 10; Page 84; 106pp; English.

XX A novel melanoma specific immunogen comprises at least 1 melanoma
 CC specific cytotoxic T lymphocyte (CTL) epitope, where at least 1 of the
 CC epitopes is substantially homologous to a human leukocyte antigen-A1 (HLA
 CC -A1) and HLA-A3 restricted epitope of a melanoma antigen, either pMEL-17
 CC or tyrosinase, e.g. the present sequence. The immunogen can be used in
 CC vaccines for protection against melanoma in mammals

SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 | : | : |
 Db 3 DICTD 7

RESULT 20

AA48947
 ID AA48947 standard; peptide; 9 AA.

XX AA48947;

XX 20-MAR-2003 (revised)

CC saposin B, that has antiangiogenic activity. The invention is based on
 CC the discovery that saposin B (see AAY58716), previously known to be
 CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
 CC and antitumour activity, and also has antiproliferative and antimigratory
 CC activity against endothelial cells. This activity is conserved in cryptic
 CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
 CC synthetically prepared and used in vitro or in vivo for the treatment of
 CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
 CC (claimed). The polypeptides can also be used in conjunction with
 CC cytotoxic moieties to selectively kill certain cell types, e.g. for
 CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
 CC malformation, nonunion fracture, arthritis and other connective tissue
 CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
 CC corneal graft neovascularization, pyogenic granuloma, retrolental
 CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
 CC vascular adhesions and hypertrophic scars

SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 3; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:-|
 Db 1 DVCQD 5

RESULT 23

ID ABG79058 standard; peptide; 9 AA.

AC ABG79058;

DT 15-NOV-2002 (first entry)

XX Human PSM class I HLA melanocyte cancer antigen peptide #2.

XX Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
 KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
 KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
 KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
 KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
 KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
 KW cytostatic; human.

XX Homo sapiens.

XX WO200264057-A2.

XX 22-AUG-2002.

XX 15-FEB-2002; 2002WO-US005212.

XX 15-FEB-2001; 2001US-0268687P.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Wang R;

XX WPI; 2002-627577/67.

XX Novel composition for treating a disease in an animal, comprises an
 PT immune effector cell and cell penetrating peptide associated with an
 PT antigen or antibody.

PS Disclosure; Page 16; 6lpp; English.

XX The invention relates to a composition (1) comprising an immune effector
 CC cell and a cell penetrating peptide (CPP) associated with an antigen or
 CC antibody. Also included are (1) a vaccine comprising (1), CPP associated
 CC with an antigen, and a pharmaceutically acceptable carrier and (2)
 CC preparing a composition for a disease, by providing (1) and CPP

CC associated with an antigen for disease, and introducing the antigen-
 CC associated CPP to (1), where antigen enters into the cell. The antigens
 CC are, for example, tumour antigen derived epitopes recognised by tumour
 CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
 CC or II. The composition is useful for enhancing immunity in an animal to a
 CC disease, by administering a mature dendritic cell comprising CPP
 CC associated with an antigen to disease, to the animal, such that following
 CC the administration, animal is protected from disease, where the animal
 CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
 CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
 CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
 CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
 CC The animal is further subjected to a cancer treatment including surgery,
 CC radiation, chemotherapy or gene therapy. The administration of (1),
 CC preferably dendritic cell is prior to, subsequent to or concurrent with,
 CC the cancer treatment. The present sequence is a tumour antigen derived
 CC epitope for inclusion in the composition of the invention

XX Sequence 9 AA;

Query Match 100.0%; Score 23; DB 5; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:-|
 Db 3 DICTD 7

RESULT 24

AAO17094

ID AAO17094 standard; peptide; 9 AA.

XX AAO17094;

DT 06-JUN-2002 (first entry)

XX Tyrosinase analogue antigen SEQ ID NO: 14.

XX Cryopreserved mature dendritic cell; antigen; vaccine; cytostatic;
 KW virucide; cancer; hepatitis B virus.

XX Unidentified.

XX WO200216560-A1.

XX 28-FEB-2002.

XX 24-AUG-2001; 2001WO-EP009790.

XX 24-AUG-2000; 2000DE-01041515.

XX (SCHU/) SCHULER G.

XX Schuler G, Schuler-Thurner B;

XX WPI; 2002-292062/33.

XX Preparation of cryopreserved, mature dendritic cells, useful in vaccines,
 PT comprises culturing immature cells on medium containing cocktail of
 PT maturation factors, then freezing.

PS Disclosure; Fig 28; 87pp; German.

XX The present invention relates to a method for the preparation of ready-
 CC for-use, cryopreserved, mature dendritic cells comprising growing
 CC immature dendritic cells in a culture medium that includes a 'maturation
 CC cocktail' of one or more maturation stimuli and freezing the resulting
 CC matured cells in a freezing medium that does not contain heterologous
 CC serum. When loaded with antigens, the dendritic cells can be used as
 CC vaccines, e.g. against tumours and hepatitis B virus. The present
 CC sequence is an antigen described in the invention

```

XX
SQ Sequence 9 AA;
  Query Match      100.0%; Score 23; DB 5; Length 9;
  Best Local Similarity 60.0%; Pred. No. 1.4e+06;
  Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
  |:|:|
Db 3 DICTD 7

RESULT 25
ABG66774
ID ABG66774 standard; peptide; 9' AA.
XX
AC ABG66774;
XX
DT 24-SEP-2002 (first entry)
XX
DE Tumour antigen Tyrosinase, HLA-A1 epitope.
XX
KW Beta-2 microglobulin; beta-2m; cytotoxic T lymphocyte; CTL; HLA;
KW human leukocyte antigen; fusion protein; epitope; cytostatic; tumour;
KW gastrointestinal tumour; colorectal cancer; gastro-oesophageal cancer;
KW liver cancer; biliary tract cancer; pancreatic cancer; vaccine;
KW prostatic cancer; testicular cancer; lung cancer; breast cancer;
KW malignant melanoma; mesothelioma; brain tumour; ovarian cancer;
KW uterine cancer; cervical cancer; head and neck cancer; bladder cancer;
KW Kaposi's sarcoma; renal carcinoma; leukaemia; lymphoma;
KW acquired immunodeficiency syndrome; AIDS-related lymphoma.
XX
OS Homo sapiens.
XX
PN WO200236146-A2.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-GB004844.
XX
PR 02-NOV-2000; 2000GB-00026812.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
XX Tafuro S, Meier U, McMichael AJ, Bell JI, Layton G, Hunter M;
DR WPI; 2002-508108/54.
XX
PT New polynucleotide capable of expressing an epitope-beta2m fusion protein
PT useful for generating cytotoxic T lymphocyte responses against a tumor
PT and in restoring antigen presentation in the tumor of a host.
XX
PS Disclosure; Page 24; 46pp; English.
XX
CC The invention relates to a new polynucleotide capable of expressing an
CC epitope-beta 2m fusion protein useful for generating cytotoxic T
CC lymphocyte (CTL) responses against a tumor or in restoring antigen
CC presentation in the tumor of a host. Also included are a polynucleotide
CC capable of expressing an epitope-beta 2m fusion protein in combination
CC with a vaccination agent that stimulates a CTL response against the
CC epitope of the fusion protein for simultaneous, separate or sequential
CC use in the treatment of cancer and a method of treating a tumour by
CC administering a capable of expressing an epitope-beta 2m fusion protein,
CC and optionally a vaccination agent that stimulates a CTL response against
CC the epitope of the fusion protein. The polynucleotide is useful for
CC generating CTL responses against tumours, for restoring antigen
CC presentation in the tumour, and subsequently for treating cancers, such
CC as gastrointestinal tumour, prostatic, testicular, lung or breast cancer,
CC malignant melanoma, mesothelioma, brain tumour, ovarian cancer, uterine
CC cancer including cervical cancer, cancer of the head and neck, bladder
CC cancer, Kaposi's sarcoma, AIDS (acquired immunodeficiency syndrome) -
CC related Kaposi's sarcoma, sarcomas, osteosarcoma, renal carcinoma, and
CC haematopoietic malignant tumours such as leukaemia and lymphoma. The

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CC epitope is an HLA (human leukocyte antigen) peptide derived from a viral
CC or tumour antigen. The present sequence is a tumour HLA epitope used in
CC the fusion proteins of the invention
XX
SQ Sequence 9 AA;
  Query Match      100.0%; Score 23; DB 5; Length 9;
  Best Local Similarity 60.0%; Pred. No. 1.4e+06;
  Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
  |:|:|
Db 3 DICTD 7

RESULT 26
ADE68450
ID ADE68450 standard; peptide; 9' AA.
XX
AC ADE68450;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 2455.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX
DR WPI; 2003-441560/41.
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 164; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 9 AA;
  Query Match      100.0%; Score 23; DB 7; Length 9;
  Best Local Similarity 60.0%; Pred. No. 1.4e+06;
  Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
  |:|:|
Db 5 DCCAD 9

```

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RESULT 27
ADE66341
ID ADE66341 standard; peptide; 9 AA.
XX
XX AC ADE66341;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 348.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
XX OS Homo sapiens.
XX
XX PN WO2003040340-A2.
XX
XX PD 15-MAY-2003.
XX
XX PF 07-NOV-2002; 2002WO-US036002.
XX
XX PR 07-NOV-2001; 2001US-00005480.
XX
XX PR 31-JAN-2002; 2002US-00062109.
XX
XX PA (AGEN-) AGENSYS INC.
XX
XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
XX PI Morrison RK, Challita-Eid PM;
XX DR WPI; 2003-441560/41.
XX
XX PF A composition for diagnosing, preventing and treating cancer (e.g.
XX PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
XX PT and polypeptides.
XX
XX PS Claim 13; Page 147; 135pp; English.
XX
XX CC This invention relates to a novel composition which comprises a substance
XX CC that modulates the status of a novel human protein (161P2F10B) and its
XX CC variants having a sequence of 875 amino acids provided in the
XX CC specification. The protein of the invention is over-expressed in certain
XX CC cancers. The compounds of the invention may have cytostatic activity and
XX CC be useful for gene therapy or the development of a vaccine. The
XX CC composition and methods of the invention are useful in diagnosing,
XX CC preventing and treating cancer. The present sequence is the amino acid
XX CC sequence of a peptide which is derived from the sequence of the human
XX CC 161P2F10B protein and which may be used in the development of the
XX CC compounds of the invention.
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 100.0%; Score 23; DB 7; Length 9;
XX Best Local Similarity 60.0%; Pred. No. 1.4e+06;
XX Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DXCXD 5
XX Db 5 DCCAD 9
XX
XX RESULT 28
ADE66581
ID ADE66581 standard; peptide; 9 AA.
XX
XX AC ADE66581;
XX
XX DT 29-JAN-2004 (first entry)
XX
XX DE Human 161P2F10B protein-related peptide 588.
XX
XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.

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XX OS Homo sapiens.
XX
XX PN WO2003040340-A2.
XX
XX PD 15-MAY-2003.
XX
XX PF 07-NOV-2002; 2002WO-US036002.
XX
XX PR 07-NOV-2001; 2001US-00005480.
XX
XX PR 31-JAN-2002; 2002US-00062109.
XX
XX PA (AGEN-) AGENSYS INC.
XX
XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
XX PI Morrison RK, Challita-Eid PM;
XX DR WPI; 2003-441560/41.
XX
XX PF A composition for diagnosing, preventing and treating cancer (e.g.
XX PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
XX PT and polypeptides.
XX
XX PS Claim 13; Page 150; 135pp; English.
XX
XX CC This invention relates to a novel composition which comprises a substance
XX CC that modulates the status of a novel human protein (161P2F10B) and its
XX CC variants having a sequence of 875 amino acids provided in the
XX CC specification. The protein of the invention is over-expressed in certain
XX CC cancers. The compounds of the invention may have cytostatic activity and
XX CC be useful for gene therapy or the development of a vaccine. The
XX CC composition and methods of the invention are useful in diagnosing,
XX CC preventing and treating cancer. The present sequence is the amino acid
XX CC sequence of a peptide which is derived from the sequence of the human
XX CC 161P2F10B protein and which may be used in the development of the
XX CC compounds of the invention.
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 100.0%; Score 23; DB 7; Length 9;
XX Best Local Similarity 60.0%; Pred. No. 1.4e+06;
XX Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DXCXD 5
XX Db 3 DCCAD 7
XX
XX RESULT 29
ADE66821
ID ADE66821 standard; peptide; 9 AA.
XX
XX AC ADE66821;
XX
XX DT 29-JAN-2004 (first entry)
XX
XX DE Human 161P2F10B protein-related peptide 828.
XX
XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
XX OS Homo sapiens.
XX
XX PN WO2003040340-A2.
XX
XX PD 15-MAY-2003.
XX
XX PF 07-NOV-2002; 2002WO-US036002.
XX
XX PR 07-NOV-2001; 2001US-00005480.
XX
XX PR 31-JAN-2002; 2002US-00062109.
XX
XX PA (AGEN-) AGENSYS INC.

```

XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 PI Morrison RK, Challita-Eid PM;
 DR WPI; 2003-441560/41.
 XX
 PT A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX
 PS Claim 13; Page 151; 135pp; English.
 XX
 CC This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
 CC be useful for gene therapy or the development of a vaccine. The
 CC composition and methods of the invention are useful in diagnosing,
 CC preventing and treating cancer. The present sequence is the amino acid
 CC sequence of a peptide which is derived from the sequence of the human
 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 7; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 Db 3 DCCAD 7

RESULT 30
 ADE68264
 ID ADE68264 standard; peptide; 9 AA.
 XX
 AC ADE68264;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human 161P2F10B protein-related peptide 2269.
 XX
 KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040340-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 07-NOV-2002; 2002WO-US036002.
 XX
 PR 07-NOV-2001; 2001US-00005480.
 XX
 PR 31-JAN-2002; 2002US-00062109.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 PI Morrison RK, Challita-Eid PM;
 XX
 DR WPI; 2003-441560/41.
 XX
 PT A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX
 PS Claim 13; Page 162; 135pp; English.
 XX
 CC This invention relates to a novel composition which comprises a substance

CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
 CC be useful for gene therapy or the development of a vaccine. The
 CC composition and methods of the invention are useful in diagnosing,
 CC preventing and treating cancer. The present sequence is the amino acid
 CC sequence of a peptide which is derived from the sequence of the human
 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 7; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 Db 5 DCCAD 9

RESULT 31
 ADE66342
 ID ADE66342 standard; peptide; 9 AA.
 XX
 AC ADE66342;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human 161P2F10B protein-related peptide 349.
 XX
 KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040340-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 07-NOV-2002; 2002WO-US036002.
 XX
 PR 07-NOV-2001; 2001US-00005480.
 XX
 PR 31-JAN-2002; 2002US-00062109.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 PI Morrison RK, Challita-Eid PM;
 XX
 DR WPI; 2003-441560/41.
 XX
 PT A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX
 PS Claim 13; Page 147; 135pp; English.
 XX
 CC This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
 CC be useful for gene therapy or the development of a vaccine. The
 CC composition and methods of the invention are useful in diagnosing,
 CC preventing and treating cancer. The present sequence is the amino acid
 CC sequence of a peptide which is derived from the sequence of the human
 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.
 XX
 SQ Sequence 9 AA;

```
Query Match      100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 3 DCCAD 7

RESULT 32
ADE67312
ID ADE67312 standard; peptide; 9 AA.
XX AC
XX DE
XX AC ADE67312;
XX DT 29-JAN-2004 (first entry)
XX DE
XX DE Human 161P2F10B protein-related peptide 1317.
XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX OS Homo sapiens.
XX XX
XX PN WO2003040340-A2.
XX PD 15-MAY-2003.
XX PF 07-NOV-2002; 2002WO-US036002.
XX PR 07-NOV-2001; 2001US-00005480.
XX PR 31-JAN-2002; 2002US-00062109.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
XX PI Morrison RK, Challita-Eid PM;
XX DR WPI; 2003-441560/41.
XX PF
XX PT A composition for diagnosing, preventing and treating cancer (e.g.
XX PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
XX PT and polypeptides.
XX PS Claim 13; Page 155; 135pp; English.
XX CC
XX CC This invention relates to a novel composition which comprises a substance
XX CC that modulates the status of a novel human protein (161P2F10B) and its
XX CC variants having a sequence of 875 amino acids provided in the
XX CC specification. The protein of the invention is over-expressed in certain
XX CC cancers. The compounds of the invention may have cytostatic activity and
XX CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
XX CC be useful for gene therapy or the development of a vaccine. The
XX CC composition and methods of the invention are useful in diagnosing,
XX CC preventing and treating cancer. The present sequence is the amino acid
XX CC sequence of a peptide which is derived from the sequence of the human
XX CC 161P2F10B protein and which may be used in the development of the
XX CC compounds of the invention.
XX SQ Sequence 9 AA;

Query Match      100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 4 DCCAD 8

RESULT 33
ADE68265
ID ADE68265 standard; peptide; 9 AA.

Query Match      100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 4 DCCAD 8

RESULT 34
ADE68269
ID ADE68269 standard; peptide; 9 AA.
XX AC
XX AC ADE68269;
XX DT 29-JAN-2004 (first entry)
XX DE
XX DE Human 161P2F10B protein-related peptide 2274.
XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX OS Homo sapiens.
XX XX
XX PN WO2003040340-A2.
XX PD
```

```
XX ADE68265;
XX AC
XX DT 29-JAN-2004 (first entry)
XX DE
XX DE Human 161P2F10B protein-related peptide 2270.
XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX OS Homo sapiens.
XX XX
XX PN WO2003040340-A2.
XX PD 15-MAY-2003.
XX PF 07-NOV-2002; 2002WO-US036002.
XX PR 07-NOV-2001; 2001US-00005480.
XX PR 31-JAN-2002; 2002US-00062109.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
XX PI Morrison RK, Challita-Eid PM;
XX DR WPI; 2003-441560/41.
XX PF
XX PT A composition for diagnosing, preventing and treating cancer (e.g.
XX PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
XX PT and polypeptides.
XX PS Claim 13; Page 162; 135pp; English.
XX CC
XX CC This invention relates to a novel composition which comprises a substance
XX CC that modulates the status of a novel human protein (161P2F10B) and its
XX CC variants having a sequence of 875 amino acids provided in the
XX CC specification. The protein of the invention is over-expressed in certain
XX CC cancers. The compounds of the invention may have cytostatic activity and
XX CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
XX CC be useful for gene therapy or the development of a vaccine. The
XX CC composition and methods of the invention are useful in diagnosing,
XX CC preventing and treating cancer. The present sequence is the amino acid
XX CC sequence of a peptide which is derived from the sequence of the human
XX CC 161P2F10B protein and which may be used in the development of the
XX CC compounds of the invention.
XX SQ Sequence 9 AA;

Query Match      100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 3 DCCAD 7

RESULT 34
ADE68269
ID ADE68269 standard; peptide; 9 AA.
XX AC
XX AC ADE68269;
XX DT 29-JAN-2004 (first entry)
XX DE
XX DE Human 161P2F10B protein-related peptide 2274.
XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX OS Homo sapiens.
XX XX
XX PN WO2003040340-A2.
XX PD
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PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
DR WPI; 2003-441560/41.
XX
XX A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
PS Claim 13; Page 163; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC be useful for gene therapy or the development of a vaccine. The
CC sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred.No.1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
Db 4 DCCAD 8
RESULT 35
ADE68898
ID ADE68898 standard; peptide; 9 AA.
XX
AC ADE68898;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 2903.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX
XX WPI; 2003-441560/41.
DR
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XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 167; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC be useful for gene therapy or the development of a vaccine. The
CC sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred.No.1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
Db 3 DCCAD 7
RESULT 36
ADE68351
ID ADE68351 standard; peptide; 9 AA.
XX
AC ADE68351;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 2356.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX
XX WPI; 2003-441560/41.
DR
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
PS Claim 13; Page 163; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC be useful for gene therapy or the development of a vaccine. The
CC sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
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PS Claim 13; Page 157; 135pp; English.

XX This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. NO. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 4 DCCAD 8

RESULT 42

ADE68038
ID ADE68038 standard; peptide; 9 AA.
XX
AC ADE68038;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 2043.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
FN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
XX
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
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PI Jakobovits A, Raitano AB, Paris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX
DR WPI; 2003-441560/41.
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PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 161; 135pp; English.

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CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the

CC compounds of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. NO. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 3 DCCAD 7

RESULT 43

ADE68040
ID ADE68040 standard; peptide; 9 AA.
XX
AC ADE68040;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 2045.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
FN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
XX
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
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PI Jakobovits A, Raitano AB, Paris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
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DR WPI; 2003-441560/41.
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PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 161; 135pp; English.

XX This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. NO. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 4 DCCAD 8

```

RESULT 44
ADE68746
ID ADE68746 standard; peptide; 9 AA.
XX
AC ADE68746;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 2751.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
XX
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX
DR WPI; 2003-441560/41.
XX
PS Claim 13; Page 166; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Claim 13; Page 166; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 9 AA;
XX
Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 3 DCCAD 7

RESULT 45
ADE69068
ID ADE69068 standard; peptide; 9 AA.
XX
AC ADE69068;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 3073.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.

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XX WO2003040340-A2.
XX 15-MAY-2003.
XX 07-NOV-2002; 2002WO-US036002.
XX 07-NOV-2001; 2001US-00005480.
XX 31-JAN-2002; 2002US-00062109.
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
XX Morrison RK, Challita-Eid PM;
XX WPI; 2003-441560/41.
XX A composition for diagnosing, preventing and treating cancer (e.g.
XX prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
XX and polypeptides.
XX Claim 13; Page 168; 135pp; English.
XX This invention relates to a novel composition which comprises a substance
XX that modulates the status of a novel human protein (161P2F10B) and its
XX variants having a sequence of 875 amino acids provided in the
XX specification. The protein of the invention is over-expressed in certain
XX cancers. The compounds of the invention may have cytostatic activity and
XX the sequence of the 161P2F10B protein, and the gene which encodes it, may
XX be useful for gene therapy or the development of a vaccine. The
XX composition and methods of the invention are useful in diagnosing,
XX preventing and treating cancer. The present sequence is the amino acid
XX sequence of a peptide which is derived from the sequence of the human
XX 161P2F10B protein and which may be used in the development of the
XX compounds of the invention.
XX Sequence 9 AA;
XX
Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 1 DCCAD 5

RESULT 46
ADE66824
ID ADE66824 standard; peptide; 9 AA.
XX
AC ADE66824;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 831.
XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX Homo sapiens.
XX WO2003040340-A2.
XX 15-MAY-2003.
XX 07-NOV-2002; 2002WO-US036002.
XX 07-NOV-2001; 2001US-00005480.
XX 31-JAN-2002; 2002US-00062109.
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
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PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX
DR WPI; 2003-441560/41.
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 150; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
Db 3 DCCAD 7
|:|:|
|:|:|

RESULT 52
ADE66763
ID ADE66763 standard; peptide; 9 AA.
XX
AC ADE66763;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 770.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX
DR WPI; 2003-441560/41.
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 157; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
Db 5 DCCAD 9
|:|:|
|:|:|

RESULT 53
ADE67533
ID ADE67533 standard; peptide; 9 AA.
XX
AC ADE67533;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 1538.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
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PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
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DR WPI; 2003-441560/41.
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 157; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
Db 3 DCCAD 7
|:|:|
|:|:|

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CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 4 DCCAD 8

RESULT 54

ADE68997
ID ADE68997 standard; peptide; 9 AA.

XX AC ADE68997;

XX DT 29-JAN-2004 (first entry)

XX DE Human 161P2F10B protein-related peptide 3002.

XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.

XX OS Homo sapiens.

XX PN WO2003040340-A2.

XX PD 15-MAY-2003.

XX PF 07-NOV-2002; 2002WO-US036002.

XX PR 07-NOV-2001; 2001US-00005480.

XX PR 31-JAN-2002; 2002US-00062109.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;

XX DR WPI; 2003-441560/41.

XX PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.

XX PS Claim 13; Page 167; 135pp; English.

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CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
XX

Db 4 DCCAD 8

RESULT 55

ADE67768
ID ADE67768 standard; peptide; 9 AA.

XX AC ADE67768;

XX DT 29-JAN-2004 (first entry)

XX DE Human 161P2F10B protein-related peptide 1773.

XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.

XX OS Homo sapiens.

XX PN WO2003040340-A2.

XX PD 15-MAY-2003.

XX PF 07-NOV-2002; 2002WO-US036002.

XX PR 07-NOV-2001; 2001US-00005480.

XX PR 31-JAN-2002; 2002US-00062109.

XX PA (AGEN-) AGENSYS INC.

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XX DR WPI; 2003-441560/41.

XX PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.

XX PS Claim 13; Page 159; 135pp; English.

XX CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 4 DCCAD 8

RESULT 56

ADE68023
ID ADE68023 standard; peptide; 9 AA.

XX AC ADE68023;

XX DT 29-JAN-2004 (first entry)

XX DE Human 161P2F10B protein-related peptide 2028.

KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
 OS Homo sapiens.
 XX
 PI WO2003040340-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 07-NOV-2002; 2002WO-US036002.
 PF
 XX 07-NOV-2001; 2001US-00005480.
 PR
 PR 31-JAN-2002; 2002US-00062109.
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 XX (AGEN-) AGENSYS INC.
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 XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
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 XX WPI; 2003-441560/41.
 XX
 XX A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX
 XX Claim 13; Page 161; 135pp; English.
 PS
 XX This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC be useful for gene therapy or the development of a vaccine. The
 CC composition and methods of the invention are useful in diagnosing,
 CC preventing and treating cancer. The present sequence is the amino acid
 CC sequence of a peptide which is derived from the sequence of the human
 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 23; DB 7; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DXCXD 5
 Db 3 DCCAD 7
 XX
 RESULT 57
 ADE67067
 ID ADE67067 standard; peptide; 9 AA.
 AC ADE67067;
 XX
 XX 29-JAN-2004 (first entry)
 DT Human 161P2F10B protein-related peptide 1072.
 DE
 XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
 KW Homo sapiens.
 XX
 XX WO2003040340-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 07-NOV-2002; 2002WO-US036002.
 PF
 XX 07-NOV-2001; 2001US-00005480.
 PR
 PR 31-JAN-2002; 2002US-00062109.
 XX
 XX (AGEN-) AGENSYS INC.
 PA
 XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 PI Morrison RK, Challita-Eid PM;
 XX WPI; 2003-441560/41.
 XX
 XX A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX
 XX Claim 13; Page 161; 135pp; English.
 PS
 XX This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC be useful for gene therapy or the development of a vaccine. The
 CC composition and methods of the invention are useful in diagnosing,
 CC preventing and treating cancer. The present sequence is the amino acid
 CC sequence of a peptide which is derived from the sequence of the human
 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 23; DB 7; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DXCXD 5
 Db 3 DCCAD 7
 XX
 RESULT 58
 ADE68349
 ID ADE68349 standard; peptide; 9 AA.
 AC ADE68349;
 XX
 XX 29-JAN-2004 (first entry)
 DT Human 161P2F10B protein-related peptide 2354.
 DE
 XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
 KW Homo sapiens.
 XX
 XX WO2003040340-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 07-NOV-2002; 2002WO-US036002.
 PF
 XX 07-NOV-2001; 2001US-00005480.
 PR
 PR 31-JAN-2002; 2002US-00062109.
 XX
 XX (AGEN-) AGENSYS INC.
 PA
 XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 PI Morrison RK, Challita-Eid PM;
 XX WPI; 2003-441560/41.
 XX
 XX A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX
 XX Claim 13; Page 163; 135pp; English.
 PS
 XX

(AGEN-) AGENSYS INC.
 PA
 XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 PI Morrison RK, Challita-Eid PM;
 XX WPI; 2003-441560/41.
 XX
 XX A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
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 XX
 XX Claim 13; Page 153; 135pp; English.
 PS
 XX This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC be useful for gene therapy or the development of a vaccine. The
 CC composition and methods of the invention are useful in diagnosing,
 CC preventing and treating cancer. The present sequence is the amino acid
 CC sequence of a peptide which is derived from the sequence of the human
 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 23; DB 7; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DXCXD 5
 Db 4 DCCAD 8
 XX
 RESULT 58
 ADE68349
 ID ADE68349 standard; peptide; 9 AA.
 AC ADE68349;
 XX
 XX 29-JAN-2004 (first entry)
 DT Human 161P2F10B protein-related peptide 2354.
 DE
 XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
 KW Homo sapiens.
 XX
 XX WO2003040340-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 07-NOV-2002; 2002WO-US036002.
 PF
 XX 07-NOV-2001; 2001US-00005480.
 PR
 PR 31-JAN-2002; 2002US-00062109.
 XX
 XX (AGEN-) AGENSYS INC.
 PA
 XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 PI Morrison RK, Challita-Eid PM;
 XX WPI; 2003-441560/41.
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 PT and polypeptides.
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 XX Claim 13; Page 163; 135pp; English.
 PS
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CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 4 DCCAD 8
|:|:|

RESULT 59
ADE68623
ID ADE68623 standard; peptide; 9 AA.

XX AC ADE68623;

XX DT 29-JAN-2004 (first entry)

XX DE Human 161P2F10B protein-related peptide 2628.

XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.

XX OS Homo sapiens.

XX PN WO2003040340-A2.

XX PD 15-MAY-2003.

XX PF 07-NOV-2002; 2002WO-US036002.

XX PR 07-NOV-2001; 2001US-00005480.

XX PR 31-JAN-2002; 2002US-00062109.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;

XX PI Morrison RK, Challita-Bid PM;

XX DR WPI; 2003-441560/41.

XX A composition for diagnosing, preventing and treating cancer (e.g.

XX PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides

XX PT and polypeptides.

XX PS Claim 13; Page 165; 135pp; English.

XX This invention relates to a novel composition which comprises a substance
XX that modulates the status of a novel human protein (161P2F10B) and its
XX variants having a sequence of 875 amino acids provided in the
XX specification. The protein of the invention is over-expressed in certain
XX cancers. The compounds of the invention may have cytostatic activity and
XX the sequence of the 161P2F10B protein, and the gene which encodes it, may
XX be useful for gene therapy or the development of a vaccine. The
XX composition and methods of the invention are useful in diagnosing,
XX preventing and treating cancer. The present sequence is the amino acid
XX sequence of a peptide which is derived from the sequence of the human
XX 161P2F10B protein and which may be used in the development of the
XX compounds of the invention.

SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 3 DCCAD 7
|:|:|

RESULT 60

ADE68897
ID ADE68897 standard; peptide; 9 AA.

XX AC ADE68897;

XX DT 29-JAN-2004 (first entry)

XX DE Human 161P2F10B protein-related peptide 2902.

XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.

XX OS Homo sapiens.

XX PN WO2003040340-A2.

XX PD 15-MAY-2003.

XX PF 07-NOV-2002; 2002WO-US036002.

XX PR 07-NOV-2001; 2001US-00005480.

XX PR 31-JAN-2002; 2002US-00062109.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;

XX PI Morrison RK, Challita-Bid PM;

XX DR WPI; 2003-441560/41.

XX A composition for diagnosing, preventing and treating cancer (e.g.

XX PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides

XX PT and polypeptides.

XX PS Claim 13; Page 167; 135pp; English.

XX This invention relates to a novel composition which comprises a substance
XX that modulates the status of a novel human protein (161P2F10B) and its
XX variants having a sequence of 875 amino acids provided in the
XX specification. The protein of the invention is over-expressed in certain
XX cancers. The compounds of the invention may have cytostatic activity and
XX the sequence of the 161P2F10B protein, and the gene which encodes it, may
XX be useful for gene therapy or the development of a vaccine. The
XX composition and methods of the invention are useful in diagnosing,
XX preventing and treating cancer. The present sequence is the amino acid
XX sequence of a peptide which is derived from the sequence of the human
XX 161P2F10B protein and which may be used in the development of the
XX compounds of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 4 DCCAD 8
|:|:|

RESULT 61

ADE66098

```

ID ADE66098 standard; peptide; 9 AA.
AC ADE66098;
XX
DT 29-JAN-2004 (first entry)
DE Human 161P2F10B protein-related peptide 105.
DE 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
KW
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KM;
PI Morrison RK, Challita-Eid PM;
XX
DR WPI; 2003-441560/41.
XX
PS Claim 13; Page 145; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 9 AA;
XX
Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DXCXD 5
Db 4 DCCAD 8
XX
RESULT 62
ADE67070
ID ADE67070 standard; peptide; 9 AA.
XX
AC ADE67070;
XX
DT 29-JAN-2004 (first entry)
DE Human 161P2F10B protein-related peptide 1075.
DE 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
KW
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
XX

ID ADE66098 standard; peptide; 9 AA.
AC ADE66098;
XX
DT 29-JAN-2004 (first entry)
DE Human 161P2F10B protein-related peptide 105.
DE 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
KW
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KM;
PI Morrison RK, Challita-Eid PM;
XX
DR WPI; 2003-441560/41.
XX
PS Claim 13; Page 145; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 9 AA;
XX
Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DXCXD 5
Db 4 DCCAD 8
XX
RESULT 63
ADE68101
ID ADE68101 standard; peptide; 9 AA.
XX
AC ADE68101;
XX
DT 29-JAN-2004 (first entry)
DE Human 161P2F10B protein-related peptide 2106.
DE 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
KW
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KM;
PI Morrison RK, Challita-Eid PM;
XX
XX
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DR WPI; 2003-441560/41.
XX A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX Claim 13; Page 161; 135pp; English.
XX This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC be useful for gene therapy or the development of a vaccine. The
CC sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX Sequence 9 AA;
XX Query Match 100.0%; Score 23; DB 7; Length 9;
XX Best Local Similarity 60.0%; Pred. No. 1.4e+06;
XX Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 DXCXD 5
XX Db 4 DCCWD 8
XX RESULT 64
XX ADE66102
XX ID ADE66102 standard; peptide; 9 AA.
XX AC ADE66102;
XX DT 29-JAN-2004 (first entry)
XX DE Human 161P2F10B protein-related peptide 109.
XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX OS Homo sapiens.
XX PN WO2003040340-A2.
XX PD 15-MAY-2003.
XX PF 07-NOV-2002; 2002WO-US036002.
XX PR 07-NOV-2001; 2001US-00005480.
XX PR 31-JAN-2002; 2002US-00062109.
XX (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
XX PI Morrison RK, Challita-Eid PM;
XX PN WO2003040340-A2.
XX PD 15-MAY-2003.
XX PF 07-NOV-2002; 2002WO-US036002.
XX PR 07-NOV-2001; 2001US-00005480.
XX PR 31-JAN-2002; 2002US-00062109.
XX (AGEN-) AGENSYS INC.
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XX WPI; 2003-441560/41.
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CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and

CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX Sequence 9 AA;
XX Query Match 100.0%; Score 23; DB 7; Length 9;
XX Best Local Similarity 60.0%; Pred. No. 1.4e+06;
XX Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 DXCXD 5
XX Db 5 DCCAD 9
XX RESULT 65
XX ADE67071
XX ID ADE67071 standard; peptide; 9 AA.
XX AC ADE67071;
XX DT 29-JAN-2004 (first entry)
XX DE Human 161P2F10B protein-related peptide 1076.
XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX OS Homo sapiens.
XX PN WO2003040340-A2.
XX PD 15-MAY-2003.
XX PF 07-NOV-2002; 2002WO-US036002.
XX PR 07-NOV-2001; 2001US-00005480.
XX PR 31-JAN-2002; 2002US-00062109.
XX (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
XX PI Morrison RK, Challita-Eid PM;
XX PN WPI; 2003-441560/41.
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CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX Sequence 9 AA;
XX Query Match 100.0%; Score 23; DB 7; Length 9;
XX Best Local Similarity 60.0%; Pred. No. 1.4e+06;
XX Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 DXCXD 5
Db 3 DCCAD 7

RESULT 66
ADE67748
ID ADE67748 standard; peptide; 9 AA.
AC ADE67748;
XX
XX 29-JAN-2004 (first entry)
DT
DE Human 161P2F10B protein-related peptide 1753.
XX
XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
KW
XX Homo sapiens.
OS
XX WO2003040340-A2.
PN
XX 15-MAY-2003.
PD
XX
XX 07-NOV-2002; 2002WO-US036002.
PF
XX
XX 07-NOV-2001; 2001US-00005480.
PR
XX 31-JAN-2002; 2002US-00062109.
XX
XX (AGEN-) AGENSYS INC.
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XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Bid PM;
XX
XX WPI; 2003-441560/41.
DR
XX
XX Claim 13; Page 159; 135pp; English.
PS
XX This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
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CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
XX Sequence 9 AA;
Qy Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 4 DCCAD 8

RESULT 67
ADE67771
ID ADE67771 standard; peptide; 9 AA.
AC ADE67771;
XX
XX 29-JAN-2004 (first entry)
DT

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XX Human 161P2F10B protein-related peptide 1776.
DE
XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
KW
XX Homo sapiens.
OS
XX WO2003040340-A2.
PN
XX 15-MAY-2003.
PD
XX
XX 07-NOV-2002; 2002WO-US036002.
PF
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XX 07-NOV-2001; 2001US-00005480.
PR
XX 31-JAN-2002; 2002US-00062109.
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XX (AGEN-) AGENSYS INC.
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XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Bid PM;
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XX WPI; 2003-441560/41.
DR
XX
XX Claim 13; Page 159; 135pp; English.
PS
XX This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
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CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
XX Sequence 9 AA;
Qy Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 3 DCCAD 7

RESULT 68
ADE68745
ID ADE68745 standard; peptide; 9 AA.
XX
XX ADE68745;
AC
XX 29-JAN-2004 (first entry)
DT
XX
XX Human 161P2F10B protein-related peptide 2750.
DE
XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
KW
XX Homo sapiens.
OS
XX WO2003040340-A2.
PN
XX 15-MAY-2003.
PD
XX
XX 07-NOV-2002; 2002WO-US036002.
PF
XX

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PR 07-NOV-2001; 2001US-00005480.
XX 31-JAN-2002; 2002US-00062109.
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX WPI; 2003-441560/41.
XX A composition for diagnosing, preventing and treating cancer (e.g.
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CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX Sequence 9 AA;
XX Query Match 100.0%; Score 23; DB 7; Length 9;
XX Best Local Similarity 60.0%; Pred. NO. 1.4e+06;
XX Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
DB 4 DCCAD 8
XX RESULT 69
XX ADE66825
XX ID ADE66825 standard; peptide; 9 AA.
XX AC ADE66825;
XX DT 29-JAN-2004 (first entry)
XX DE Human 161P2F10B protein-related peptide 832.
XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX OS Homo sapiens.
XX PN WO2003040340-A2.
XX PD 15-MAY-2003.
XX PF 07-NOV-2002; 2002WO-US036002.
XX PR 07-NOV-2001; 2001US-00005480.
XX PR 31-JAN-2002; 2002US-00062109.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
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CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX Sequence 9 AA.
XX Query Match 100.0%; Score 23; DB 7; Length 9;
XX Best Local Similarity 60.0%; Pred. NO. 1.4e+06;
XX Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
DB 4 DCCAD 8
XX RESULT 70
XX ADE67555
XX ID ADE67555 standard; peptide; 9 AA.
XX AC ADE67555;
XX DT 29-JAN-2004 (first entry)
XX DE Human 161P2F10B protein-related peptide 1560.
XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX OS Homo sapiens.
XX PN WO2003040340-A2.
XX PD 15-MAY-2003.
XX PF 07-NOV-2002; 2002WO-US036002.
XX PR 07-NOV-2001; 2001US-00005480.
XX PR 31-JAN-2002; 2002US-00062109.
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XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
XX PI Morrison RK, Challita-Eid PM;
XX WPI; 2003-441560/41.
XX A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX Claim 13; Page 157; 135pp; English.
XX This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX Sequence 9 AA;
XX Query Match 100.0%; Score 23; DB 7; Length 9;
XX Best Local Similarity 60.0%; Pred. NO. 1.4e+06;
XX Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
DB 4 DCCAD 8
XX RESULT 70
XX ADE67555
XX ID ADE67555 standard; peptide; 9 AA.
XX AC ADE67555;
XX DT 29-JAN-2004 (first entry)
XX DE Human 161P2F10B protein-related peptide 1560.
XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX OS Homo sapiens.
XX PN WO2003040340-A2.
XX PD 15-MAY-2003.
XX PF 07-NOV-2002; 2002WO-US036002.
XX PR 07-NOV-2001; 2001US-00005480.
XX PR 31-JAN-2002; 2002US-00062109.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
XX PI Morrison RK, Challita-Eid PM;
XX WPI; 2003-441560/41.
XX A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
```

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CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 9 AA;

  Query Match      100.0%; Score 23; DB 7; Length 9;
  Best Local Similarity 60.0%; Pred. No. 1.4e+06;
  Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
   |:|
Db 3 DCCAD 7

RESULT 71
ADE68149
ID ADE68149 standard; peptide; 9 AA.
XX
AC ADE68149;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 2154.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
XX
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX
DR WPI; 2003-441560/41.
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 162; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 9 AA;

  Query Match      100.0%; Score 23; DB 7; Length 9;
  Best Local Similarity 60.0%; Pred. No. 1.4e+06;
  Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
   |:|
Db 4 DCCAD 8

RESULT 72
ADE67308
ID ADE67308 standard; peptide; 9 AA.
XX
AC ADE67308;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 1313.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
XX
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX
DR WPI; 2003-441560/41.
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 155; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in the
CC cancers. The compounds of the invention may have cytostatic activity and
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 9 AA;

  Query Match      100.0%; Score 23; DB 7; Length 9;
  Best Local Similarity 60.0%; Pred. No. 1.4e+06;
  Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
   |:|
Db 5 DCCAD 9

RESULT 73
ADE66095
ID ADE66095 standard; peptide; 9 AA.
XX
AC ADE66095;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 102.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX

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OS Homo sapiens.
PN WO2003040340-A2.
XX
XX 15-MAY-2003.
XX
XX 07-NOV-2002; 2002WO-US036002.
XX
XX 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KM;
PI Morrison RK, Challita-Bid PM;
XX
XX WPI; 2003-441560/41.
XX
XX A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PR and polypeptides.
XX
XX Claim 13; Page 145; 135pp; English.
XX
XX This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
Db 3 DCCAD 7

RESULT 74
ADE68452
XX ADE68452 standard; peptide; 9 AA.
XX
XX ADE68452;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human 161P2F10B protein-related peptide 2457.
XX
XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
XX Homo sapiens.
XX
XX WO2003040340-A2.
XX
XX 15-MAY-2003.
XX
XX 07-NOV-2002; 2002WO-US036002.
XX
XX 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
XX (AGEN-) AGENSYS INC.
XX
XX
XX

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PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KM;
PI Morrison RK, Challita-Bid PM;
XX
XX WPI; 2003-441560/41.
XX
XX A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PR and polypeptides.
XX
XX Claim 13; Page 164; 135pp; English.
XX
XX This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 23; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
Db 4 DCCAD 8

RESULT 75
AAR69344
ID AAR69344 standard; peptide; 10 AA.
XX
XX AAR69344;
XX
XX 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)
XX
XX Gp IIB/IIIA receptor ligand used in scintigraphic imaging of thrombi.
XX
XX Scintigraphy; thrombus; thrombi; imaging; specific binding;
XX technetium-99m; radiolabelled; Gp IIB/IIIA.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1 /note= "[BAT]-Gly; in which [BAT] is N6,N9-bis(2-
FT mercapto-2-methylpropyl)-6,9-diaza- nonanoic acid
FT residue"
FT Modified-site 2 /note= "S-(3-aminopropyl)-Cys"
FT Modified-site 6 /note= "S-(3-aminopropyl)-Cys"
FT Modified-site 10 /note= "Lys-amide"
FT Modified-site 10 /note= "Lys-amide"
XX
XX WO9323085-A1.
XX
XX 25-NOV-1993.
PD
XX
XX 21-MAY-1993; 93WO-US004794.
XX
XX 21-MAY-1992; 92US-00886752.
XX
XX (DIAT-) DIATECH INC.
XX
XX

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PI Dean RT, Lister-James J;
 XX WPI; 1993-386229/48.
 XX
 XX Reagent for scintigraphic imaging of thrombi with 99m technetium -
 PT comprises synthetic peptide which binds to thrombus covalently coupled to
 PT metal binding gp., rapidly cleared from blood and tissue.
 XX
 XX Claim 59; Page 49; 61pp; English.
 XX
 CC The invention relates to reagents for scintigraphic imaging of a thrombus
 CC in-vivo, comprising (A) a specific binding compound capable of binding to
 CC at least one component of a thrombus, covalently linked to (B) a
 CC technetium-99m-binding moiety. Specific peptides constituting the
 CC reagents are claimed as new. The present peptide is one such peptide.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 10 AA;
 SQ

Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DXCXD 5
 Db 4 DVCGD 8

RESULT 76
 ID AAY06901 standard; peptide; 10 AA.
 AC AAY06901;
 XX
 XX 18-JUN-1999 (first entry)
 XX
 DE Antiparallel oligopeptide IFNalpha-Ap for Hu-IFN alpha8 protein.
 KW Antiparallel oligopeptide; interferon alpha 8; IFN alpha8; human;
 KW hydrophobic complementary oligopeptide; immunoblotting; antiviral;
 KW viral disease; hepatitis; papillomatosis; herpes; adenoviral; AIDS;
 KW antiproliferative; immunostimulatory; renal carcinoma; melanoma;
 KW non-Hodgkin lymphoma; leukemia; multiple myeloma.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX EP915099-A1.
 XX
 PD 12-MAY-1999.
 XX
 XX 02-NOV-1998; 98EP-00120622.
 XX
 XX 04-NOV-1997; 97IT-B0000655.
 XX
 PA (ALFA-) ALFA WASSERMANN SPA.
 XX
 PI Viscomi CG, Bruno C, Scapol L;
 XX
 XX WPI; 1999-265905/23.
 XX
 PT New antiparallel and hydrophobically complementary oligopeptides useful
 PT for purification and detection of alpha interferon.
 XX
 XX Claim 2; Page 10; 14pp; English.
 XX
 CC The invention relates to antiparallel oligopeptides with affinity for the
 CC human interferon (IFN) alpha8 protein. Matrices on solid supports
 CC containing the antiparallel oligopeptides or hydrophobic complementary
 CC oligopeptides are useful for detection of human IFN alpha8 by ELISA or
 CC immunoblotting and purification by affinity chromatography. Human IFN
 CC alpha8 is an antiviral agent and may be administered to patients
 CC suffering from viral diseases such as hepatitis B, C, D, papillomatosis,

CC herpes and adenoviral infections. Its antiproliferative and
 CC immunostimulatory properties may also be exploited by administering the
 CC protein to patients with tumors such as renal carcinoma, non-Hodgkin
 CC lymphoma related to AIDS, malignant melanoma and leukemias such as
 CC chronic myeloid leukemia, hair cells leukemia and multiple myeloma.
 CC Sequences AAY06901-902 represent specifically claimed antiparallel
 CC peptides of the invention
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DXCXD 5
 Db 4 DFCSD 8

RESULT 77
 ADE25463
 ID ADE25463 standard; peptide; 10 AA.
 XX
 AC ADE25463;
 XX
 XX 29-JAN-2004 (first entry)
 XX
 DE GPIIb/IIIa receptor ligand #27.
 XX
 KW Thrombus imaging agent; GPIIb/IIIa receptor; thrombus.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 2 /note= "L-[S-(3-aminopropyl)cysteine"
 FT Modified-site 6
 FT Modified-site 10 /note= "L-[S-(3-aminopropyl)cysteine"
 FT Modified-site 10 /note= "C-terminal amide"
 XX
 PN US5688474-A.
 XX
 PD 30-MAR-1999.
 XX
 XX 07-JUN-1995; 95US-00478725.
 XX
 PR 08-FEB-1991; 91US-00653012.
 PR 27-NOV-1991; 91US-00807062.
 PR 21-MAY-1992; 92US-00886752.
 PR 22-JUN-1994; 94US-00264176.
 PR 11-JUL-1994; 94US-00273274.
 PR 07-JUN-1995; 95US-00480551.
 XX
 PA (DIAT-) DIATIDE INC.
 XX
 PI Dean RT, Lister-James J;
 XX
 XX WPI; 1999-253220/21.
 XX
 PT Reagent for preparing thrombus imaging agent.
 XX
 XX Claim 2; Col 8; 17pp; English.
 XX
 CC The present invention relates to reagents (A) for preparing thrombus
 CC imaging agents comprising specific binding peptides (I) and a technetium-
 CC 99m binding group (II) covalently attached to the specific binding
 CC peptide. (I) is a ligand for the GPIIb/IIIa receptor and can be a cyclic
 CC or linear peptide not containing the Arg-Gly-Asp (RGD) sequence. (I) are
 CC specific for thrombi, and are small and therefore are rapidly cleared
 CC from blood and background tissue. (A) are used to produce scintigraphic
 CC imaging agents for detection of thrombi in vivo. The present sequence is
 CC one such GPIIb/IIIa receptor ligand.

XX SQ Sequence 10 AA;
 Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DXCXD 5
 | : | : |
 Db 4 DVCQD 8

RESULT 78
 ADE25506
 ID ADE25506 standard; peptide; 10 AA.
 XX AC ADE25506;
 XX DT 29-JAN-2004 (first entry)
 XX DE Tc-99m labelled peptide #34.
 XX KW Thrombus imaging agent; GPIIb/IIIa receptor; thrombus.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "[BAT]-G, where BAT is
 FT HSC(CH3)2CH2NHCH2CH2N(CH2CH2CH2CH2CO-)CH2C(CH3)2SH"
 FT Modified-site 2
 FT /note= "L-[S-(3-aminopropyl)cysteine]"
 FT Modified-site 6
 FT /note= "L-[S-(3-aminopropyl)cysteine]"
 FT Modified-site 10
 FT /note= "C-terminal amide"

XX PN US5888474-A.
 XX PD 30-MAR-1999.
 XX PF 07-JUN-1995; 95US-00478725.
 XX PR 08-FEB-1991; 91US-00653012.
 XX PR 27-NOV-1991; 91US-00807062.
 XX PR 21-MAY-1992; 92US-00886752.
 XX PR 22-JUN-1994; 94US-00264176.
 XX PR 11-JUL-1994; 94US-00273274.
 XX PR 07-JUN-1995; 95US-00480551.
 XX PA (DIAT-) DIATIDE INC.
 XX PI Dean RT, Lister-James J;
 XX WPI; 1999-253220/21.
 XX Reagent for preparing thrombus imaging agent.
 XX Example 2; Col 13; 17pp; English.

XX The present invention relates to reagents (A) for preparing thrombus
 CC imaging agents comprising specific binding peptides (I) and a technetium-
 CC 99m binding group (II) covalently attached to the specific binding
 CC peptide. (I) is a ligand for the GPIIb/IIIa receptor and can be a cyclic
 CC or linear peptide not containing the Arg-Gly-Asp (RGD) sequence. (I) are
 CC specific for thrombi, and are small and therefore are rapidly cleared
 CC from blood and background tissue. (A) are used to produce scintigraphic
 CC imaging agents for detection of thrombi in vivo. The present sequence is
 CC one such Tc-99m labelled peptide.

XX SQ Sequence 10 AA;
 Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 10 AA;
 Query Match 100.0%; Score 23; DB 3; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DXCXD 5
 | : | : |
 Db 4 DVCQD 8

RESULT 79
 AAY58693
 ID AAY58693 standard; peptide; 10 AA.
 XX AC AAY58693;
 XX DT 25-APR-2000 (first entry)
 XX DE Antiangiogenic peptide derived from saposin B.
 XX KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
 XX KW Antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX OS Homo sapiens.
 XX PN WO200002902-A1.
 XX PD 20-JAN-2000.
 XX PF 12-JUL-1999; 99WO-US015772.
 XX PR 13-JUL-1998; 98US-0092647P.
 XX PA (GILL/) GILL P S.
 XX PI Gill PS;
 XX WPI; 2000-171128/15.
 XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
 XX tumor growth.
 XX Disclosure; Page 19; 78pp; English.

XX The present sequence is that of a novel peptide, derived from human
 CC saposin B, that has antiangiogenic activity. The invention is based on
 CC the discovery that saposin B (see AAY58716), previously known to be
 CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
 CC and antitumour activity, and also has antiproliferative and antimigratory
 CC activity against endothelial cells. This activity is conserved in cryptic
 CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
 CC synthetically prepared and used in vitro or in vivo for the treatment of
 CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
 CC (claimed). The polypeptides can also be used in conjunction with
 CC cytotoxic moieties to selectively kill certain cell types, e.g. for
 CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
 CC malformation, nonunion fracture, arthritis and other connective tissue
 CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
 CC corneal graft neovascularization, pyogenic granuloma, retrolental
 CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
 CC vascular adhesions and hypertrophic scars

XX SQ Sequence 10 AA;
 Query Match 100.0%; Score 23; DB 3; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DXCXD 5
 | : | : |
 Db 1 DVCQD 5

RESULT 80
 AAY54930

ID AAY54930 standard; peptide; 10 AA.
 AC AAY54930;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Peptide ligand for fibrin polymerisation site.
 XX
 KW Thrombus imaging; fibrin polymerisation site; technetium-99m; Tc-99m;
 KW GPIIb/IIIa receptor; cyclic peptide ligand.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 2
 FT /note= "S-(3-aminopropyl)cysteine"
 FT Modified-site 6
 FT /note= "S-(3-aminopropyl)cysteine"
 FT Misc-difference 10
 FT /note= "amidated"
 XX
 FT US968476-A.
 PN
 XX 19-OCT-1999.
 XX
 XX 07-JUN-1995; 95US-00484773.
 XX
 PR 21-MAY-1992; 92US-00886052.
 PR 11-JUL-1994; 94US-00273274.
 XX
 PA (DIAT-) DIATIDE INC.
 XX
 PI Dean RT, Lister-James J;
 XX
 DR WPI; 2000-021733/02.
 XX
 XX A complex used for thrombus imaging comprises technetium-99m complexed
 PT with a peptide ligand for GPIIb/IIIa receptor.
 XX
 PS Claim 9; Col 32; 18pp; English.
 XX
 CC This sequence represents a peptide ligand for the fibrin polymerisation
 CC site. The invention relates to a complex (A) for thrombus imaging
 CC comprises technetium-99m (Tc-99m) complexed with a reagent comprising a
 CC peptide (P) with 4 to 100 amino acids sequence and a Tc-99m binding
 CC moiety covalently bound to (P). (P) is selected from a linear peptide
 CC ligand for a GPIIb/IIIa receptor not comprising the amino acid sequence
 CC (arginine-glycine-aspartate), a peptide ligand for a polymerisation site
 CC of fibrin, and a cyclic peptide ligand for the GPIIb/IIIa receptor. The
 CC thrombus imaging reagents provided by the present invention can be used
 CC for visualising thrombi in a mammalian body when Tc-99m is labelled
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 23; DB 3; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DXCXD 5
 DB 4 DVCGD 8
 RESULT 81
 AAG84179
 ID AAG84179 standard; peptide; 10 AA.
 XX
 AC AAG84179;
 XX
 DT 11-SEP-2001 (first entry)
 XX
 DE Arabidopsis thaliana peptide ligand #819.
 XX

KW Plant; peptide pesticide; peptide herbicide; agricultural research.
 XX Arabidopsis thaliana.
 OS WO200142279-A2.
 PN 14-JUN-2001.
 XX
 XX 13-DEC-2000; 2000WO-GB004781.
 XX
 PR 13-DEC-1999; 99GB-00029469.
 XX
 XX (PROT-) PROTEOM LTD.
 PA
 XX Roberts GW, Heal JR;
 PI WPI; 2001-381629/40.
 XX
 XX A set of peptide ligands for agricultural research and development of
 PT therapeutic agents comprise specific complementary peptides to proteins
 PT encoded by genes of plant genomes.
 XX
 PS Example 4; Page 145; 201pp; English.
 XX
 CC The present invention relates to a set of peptide ligands consisting of
 CC specific complementary peptides to proteins encoded by genes of plant
 CC genomes. The present sequence is one such peptide from Arabidopsis
 CC thaliana. The peptides of the present invention are useful in an assay to
 CC identify a peptide, especially a peptide pesticide or herbicide. The
 CC peptides are also useful for tools for agricultural research and
 CC development
 XX
 XX Sequence 10 AA;
 Query Match 100.0%; Score 23; DB 4; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DXCXD 5
 DB 5 DYCSD 9
 RESULT 82
 ADC21150
 ID ADC21150 standard; peptide; 10 AA.
 XX
 AC ADC21150;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Hair growth promoting peptide #74.
 XX
 KW epimorphin coiled coil domain; pep 7; hair growth; vulnery; cytostatic;
 KW antiarteriosclerotic; antianginal; endothelial cell growth;
 KW cardiovascular regeneration; liver regeneration; pancreatic endothelium;
 KW cardiovascular endothelial cell; peridontic disease; fracture;
 KW bone tumour; burn; wound; hair loss;
 KW chronic obstructive arteriosclerosis; Ruerger's disease;
 KW severe angina pectoris; bone deficiency; lung branching morphogenesis;
 KW crypt-villus morphogenesis; gallbladder epithelium;
 KW mammary luminal morphogenesis; pulmonary fibrosis.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS Mus sp.
 XX
 XX US2003086893-A1.
 PN
 XX 08-MAY-2003.
 XX
 XX 23-MAY-2002; 2002US-00155922.
 XX

PR 05-JUN-2000; 2000JP-00166903.
PR 04-JUN-2001; 2001WO-JP004691.
PR 13-NOV-2001; 2001JP-00347338.
PR 13-NOV-2001; 2001JP-00347340.
PR 05-DEC-2001; 2001JP-00371175.
PR 05-DEC-2001; 2001JP-00371366.
XX (HIRA/) HIRAI Y.
PA (OKAY/) OKA Y.
PA (TAKE/) TAKEBE K.
PA (TSUD/) TSUDA H.
PA (TOCH/) TOCHIGI K.
PA (SHIN/) SHINAGAWA T.
PA (MURA/) MURAKAMI K.
PA (KOSH/) KOSHIDA S.
XX
PI Hirai Y, Oka Y, Takebe K, Tauda H, Tochigi K, Shinagawa T;
PI Murakami K, Koshida S;
XX
DR WPI; 2003-786930/74.
XX
PT Novel isolated oligopeptide having hair growth promoting activity, useful
PT for treating burns, wounds.
XX
PS Claim 70; SEQ ID NO 76; 64pp; English.
XX
CC The invention relates to an isolated oligopeptide having hair growth
CC promoting activity. The peptides are mutants or derivatives of the pep7
CC peptide from mouse and/or human epimorphin coiled coil domain. A general
CC formula for the peptides is given in the specification. Also included are
CC an oligopeptide polymer which is obtained by cross-linking the peptides
CC (if that the polymer is not a homopolymer of human epimorphin coiled coil
CC domain or the murine epimorphin coiled coil domain), a monoclonal
CC antibody or its fragments which specifically recognises an antigen of
CC about 220 kDa present in epithelial new follicles, a monoclonal antibody
CC or its fragments produced by the hybridoma deposited with the Patent and
CC Bio-Resource Center of National Institute of Advanced Industrial Science
CC and technology and having an Accession number of FERM P-19578, an antigen
CC or its fragment recognised by the antibody; a hybridoma producing the
CC antibody, and a host cell comprising a nucleic acid encoding the
CC oligopeptides. Compositions comprising the peptides are useful for
CC promoting hair growth in a mammal. The peptides are useful for evaluating
CC hair growth promoting activity involves incubating skin tissue derived
CC from a mammal in the presence of a substance to be tested under suitable
CC conditions and for a time effective to promote hair growth, recovering
CC the skin tissue from above step, reacting the skin tissue with the
CC antibody and detecting the monoclonal antibody or their fragment that
CC reacted with skin tissue. The peptides are useful for treating and/or
CC amelioration of symptoms of diseases or disorders of abnormal
CC morphogenesis of pancreatic endothelium, cardiovascular endothelial cell,
CC periodontics, fracture, bone tumour, burns or wounds, preventing hair
CC loss, chronic obstructive arteriosclerosis, Buerger's disease, severe
CC angina pectoris, bone deficiency, lung branching morphogenesis, crypt-
CC villus morphogenesis, gallbladder epithelium, mammary luminal
CC morphogenesis and also useful for regeneration of liver, pulmonary
CC fibrosis. The present sequence hair growth promoting peptide of the
CC invention.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 23; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
DB 3 DQCCD 7
RESULT 83
ADE67428
ID ADE67428 standard; peptide; 10 AA.
XX

AC ADE67428;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 1433.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX
DR WPI; 2003-441560/41.
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 156; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 23; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
DB 6 DCCAD 10
RESULT 84
ADE69211
ID ADE69211 standard; peptide; 10 AA.
XX
AC ADE69211;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 3216.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.

XX 07-NOV-2002; 2002WO-US036002.
 XX
 XX 07-NOV-2001; 2001US-00005480.
 PR 31-JAN-2002; 2002US-00062109.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 PI Morrison RK, Challita-Eid PM;
 XX WPI; 2003-441560/41.
 XX
 XX A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX
 PS Claim 13; Page 169; 135pp; English.
 XX
 CC This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
 CC be useful for gene therapy or the development of a vaccine. The
 CC composition and methods of the invention are useful in diagnosing,
 CC preventing and treating cancer. The present sequence is the amino acid
 CC sequence of a peptide which is derived from the sequence of the human
 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.
 XX
 SQ Sequence 10 AA;
 XX
 Query Match 100.0%; Score 23; DB 7; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DXCXD 5
 DB 5 DCCAD 9
 XX
 RESULT 85
 ADE70059
 ID ADE70059 standard; peptide; 10 AA.
 XX
 AC ADE70059;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human 161P2F10B protein-related peptide 4064.
 XX
 DE 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
 KW
 KW Homo sapiens.
 OS
 XX
 PN WO2003040340-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 07-NOV-2002; 2002WO-US036002.
 XX
 PR 07-NOV-2001; 2001US-00005480.
 PR 31-JAN-2002; 2002US-00062109.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 PI Morrison RK, Challita-Eid PM;
 XX WPI; 2003-441560/41.
 XX
 XX A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX
 PS Claim 13; Page 169; 135pp; English.
 XX
 CC This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
 CC be useful for gene therapy or the development of a vaccine. The
 CC composition and methods of the invention are useful in diagnosing,
 CC preventing and treating cancer. The present sequence is the amino acid
 CC sequence of a peptide which is derived from the sequence of the human
 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.
 XX
 SQ Sequence 10 AA;
 XX
 Query Match 100.0%; Score 23; DB 7; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DXCXD 5
 DB 5 DCCAD 9
 XX
 RESULT 86
 ADE66456
 ID ADE66456 standard; peptide; 10 AA.
 XX
 AC ADE66456;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human 161P2F10B protein-related peptide 463.
 XX
 DE 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
 KW
 KW Homo sapiens.
 OS
 XX
 PN WO2003040340-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 07-NOV-2002; 2002WO-US036002.
 XX
 PR 07-NOV-2001; 2001US-00005480.
 PR 31-JAN-2002; 2002US-00062109.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 PI Morrison RK, Challita-Eid PM;
 XX WPI; 2003-441560/41.
 XX
 XX A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX
 PS Claim 13; Page 148; 135pp; English.
 XX
 CC This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
 CC be useful for gene therapy or the development of a vaccine. The

PT A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX
 PS Claim 13; Page 175; 135pp; English.
 XX
 CC This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
 CC be useful for gene therapy or the development of a vaccine. The
 CC composition and methods of the invention are useful in diagnosing,
 CC preventing and treating cancer. The present sequence is the amino acid
 CC sequence of a peptide which is derived from the sequence of the human
 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.
 XX
 SQ Sequence 10 AA;
 XX
 Query Match 100.0%; Score 23; DB 7; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DXCXD 5
 DB 5 DCCAD 9
 XX
 RESULT 86
 ADE66456
 ID ADE66456 standard; peptide; 10 AA.
 XX
 AC ADE66456;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human 161P2F10B protein-related peptide 463.
 XX
 DE 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
 KW
 KW Homo sapiens.
 OS
 XX
 PN WO2003040340-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 07-NOV-2002; 2002WO-US036002.
 XX
 PR 07-NOV-2001; 2001US-00005480.
 PR 31-JAN-2002; 2002US-00062109.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 PI Morrison RK, Challita-Eid PM;
 XX WPI; 2003-441560/41.
 XX
 XX A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX
 PS Claim 13; Page 148; 135pp; English.
 XX
 CC This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
 CC be useful for gene therapy or the development of a vaccine. The

CC composition and methods of the invention are useful in diagnosing,
 CC preventing and treating cancer. The present sequence is the amino acid
 CC sequence of a peptide which is derived from the sequence of the human
 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 23; DB 7; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|

Db 6 DCCAD 10

RESULT 87

ADE69729
 ID ADE69729 standard; peptide; 10 AA.
 XX AC ADE69729;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human 161P2F10B protein-related peptide 3734.
 XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
 XX OS Homo sapiens.
 XX PN WO2003040340-A2.
 XX PD 15-MAY-2003.
 XX PF 07-NOV-2002; 2002WO-US036002.
 XX PR 07-NOV-2001; 2001US-00005480.
 XX PR 31-JAN-2002; 2002US-00062109.
 XX PA (AGEN-) AGENSYS INC.
 XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 XX PI Morrison RK, Challita-Eid PM;
 XX DR WPI; 2003-441560/41.
 XX PT A composition for diagnosing, preventing and treating cancer (e.g.
 XX PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 XX PT and polypeptides.
 XX PS Claim 13; Page 172; 135pp; English.
 XX CC This invention relates to a novel composition which comprises a substance
 XX CC that modulates the status of a novel human protein (161P2F10B) and its
 XX CC variants having a sequence of 875 amino acids provided in the
 XX CC specification. The protein of the invention is over-expressed in certain
 XX CC cancers. The compounds of the invention may have cytostatic activity and
 XX CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
 XX CC be useful for gene therapy or the development of a vaccine. The
 XX CC composition and methods of the invention are useful in diagnosing,
 XX CC preventing and treating cancer. The present sequence is the amino acid
 XX CC sequence of a peptide which is derived from the sequence of the human
 XX CC 161P2F10B protein and which may be used in the development of the
 XX CC compounds of the invention.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 23; DB 7; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|

Db 6 DCCAD 10

RESULT 88

ADE69861
 ID ADE69861 standard; peptide; 10 AA.
 XX AC ADE69861;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human 161P2F10B protein-related peptide 3866.
 XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
 XX OS Homo sapiens.
 XX PN WO2003040340-A2.
 XX PD 15-MAY-2003.
 XX PF 07-NOV-2002; 2002WO-US036002.
 XX PR 07-NOV-2001; 2001US-00005480.
 XX PR 31-JAN-2002; 2002US-00062109.
 XX PA (AGEN-) AGENSYS INC.
 XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 XX PI Morrison RK, Challita-Eid PM;
 XX DR WPI; 2003-441560/41.
 XX PT A composition for diagnosing, preventing and treating cancer (e.g.
 XX PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 XX PT and polypeptides.
 XX PS Claim 13; Page 173; 135pp; English.
 XX CC This invention relates to a novel composition which comprises a substance
 XX CC that modulates the status of a novel human protein (161P2F10B) and its
 XX CC variants having a sequence of 875 amino acids provided in the
 XX CC specification. The protein of the invention is over-expressed in certain
 XX CC cancers. The compounds of the invention may have cytostatic activity and
 XX CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
 XX CC be useful for gene therapy or the development of a vaccine. The
 XX CC composition and methods of the invention are useful in diagnosing,
 XX CC preventing and treating cancer. The present sequence is the amino acid
 XX CC sequence of a peptide which is derived from the sequence of the human
 XX CC 161P2F10B protein and which may be used in the development of the
 XX CC compounds of the invention.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 23; DB 7; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|

Db 5 DCCAD 9

RESULT 89

ADE66702
 ID ADE66702 standard; peptide; 10 AA.
 XX AC ADE66702;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human 161P2F10B protein-related peptide 709.

Db 5 DCCAD 9
 |:|

RESULT 88

ADE69861
 ID ADE69861 standard; peptide; 10 AA.
 XX AC ADE69861;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human 161P2F10B protein-related peptide 3866.
 XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
 XX OS Homo sapiens.
 XX PN WO2003040340-A2.
 XX PD 15-MAY-2003.
 XX PF 07-NOV-2002; 2002WO-US036002.
 XX PR 07-NOV-2001; 2001US-00005480.
 XX PR 31-JAN-2002; 2002US-00062109.
 XX PA (AGEN-) AGENSYS INC.
 XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 XX PI Morrison RK, Challita-Eid PM;
 XX DR WPI; 2003-441560/41.
 XX PT A composition for diagnosing, preventing and treating cancer (e.g.
 XX PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 XX PT and polypeptides.
 XX PS Claim 13; Page 173; 135pp; English.
 XX CC This invention relates to a novel composition which comprises a substance
 XX CC that modulates the status of a novel human protein (161P2F10B) and its
 XX CC variants having a sequence of 875 amino acids provided in the
 XX CC specification. The protein of the invention is over-expressed in certain
 XX CC cancers. The compounds of the invention may have cytostatic activity and
 XX CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
 XX CC be useful for gene therapy or the development of a vaccine. The
 XX CC composition and methods of the invention are useful in diagnosing,
 XX CC preventing and treating cancer. The present sequence is the amino acid
 XX CC sequence of a peptide which is derived from the sequence of the human
 XX CC 161P2F10B protein and which may be used in the development of the
 XX CC compounds of the invention.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 23; DB 7; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|

Db 5 DCCAD 9

RESULT 89

ADE66702
 ID ADE66702 standard; peptide; 10 AA.
 XX AC ADE66702;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human 161P2F10B protein-related peptide 709.

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XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX Homo sapiens.
XX WO2003040340-A2.
XX 15-MAY-2003.
XX 07-NOV-2002; 2002WO-US036002.
XX 07-NOV-2001; 2001US-00005480.
XX 31-JAN-2002; 2002US-00062109.
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
XX Morrison RK, Challita-Eid PM;
XX WPI; 2003-441560/41.
XX A composition for diagnosing, preventing and treating cancer (e.g.
XX prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
XX and polypeptides.
XX Claim 13; Page 150; 135pp; English.
XX This invention relates to a novel composition which comprises a substance
XX that modulates the status of a novel human protein (161P2F10B) and its
XX variants having a sequence of 875 amino acids provided in the
XX specification. The protein of the invention is over-expressed in certain
XX cancers. The compounds of the invention may have cytostatic activity and
XX the sequence of the 161P2F10B protein, and the gene which encodes it, may
XX be useful for gene therapy or the development of a vaccine. The
XX composition and methods of the invention are useful in diagnosing,
XX preventing and treating cancer. The present sequence is the amino acid
XX sequence of a peptide which is derived from the sequence of the human
XX 161P2F10B protein and which may be used in the development of the
XX compounds of the invention.
XX Sequence 10 AA;
XX Query Match 100.0%; Score 23; DB 7; Length 10;
XX Best Local Similarity 60.0%; Pred. No. 1.5e+03;
XX Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 DXCXD 5
XX |:|:|
XX 4 DCCAD 8
XX
XX RESULT 90
XX ADE67186
XX ID ADE67186 standard; peptide; 10 AA.
XX AC ADE67186;
XX XX 29-JAN-2004 (first entry)
XX XX Human 161P2F10B protein-related peptide 1191.
XX DE 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX KW Homo sapiens.
XX OS
XX XX WO2003040340-A2.
XX PN 15-MAY-2003.
XX PD
XX PF 07-NOV-2002; 2002WO-US036002.
XX XX 07-NOV-2001; 2001US-00005480.
XX PR 31-JAN-2002; 2002US-00062109.
XX PS
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
XX Morrison RK, Challita-Eid PM;
XX WPI; 2003-441560/41.
XX A composition for diagnosing, preventing and treating cancer (e.g.
XX prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
XX and polypeptides.
XX Claim 13; Page 150; 135pp; English.
XX This invention relates to a novel composition which comprises a substance
XX that modulates the status of a novel human protein (161P2F10B) and its
XX variants having a sequence of 875 amino acids provided in the
XX specification. The protein of the invention is over-expressed in certain
XX cancers. The compounds of the invention may have cytostatic activity and
XX the sequence of the 161P2F10B protein, and the gene which encodes it, may
XX be useful for gene therapy or the development of a vaccine. The
XX composition and methods of the invention are useful in diagnosing,
XX preventing and treating cancer. The present sequence is the amino acid
XX sequence of a peptide which is derived from the sequence of the human
XX 161P2F10B protein and which may be used in the development of the
XX compounds of the invention.
XX Sequence 10 AA;
XX Query Match 100.0%; Score 23; DB 7; Length 10;
XX Best Local Similarity 60.0%; Pred. No. 1.5e+03;
XX Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 DXCXD 5
XX |:|:|
XX 4 DCCAD 8
XX
XX RESULT 90
XX ADE67186
XX ID ADE67186 standard; peptide; 10 AA.
XX AC ADE67186;
XX XX 29-JAN-2004 (first entry)
XX XX Human 161P2F10B protein-related peptide 1191.
XX DE 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX KW Homo sapiens.
XX OS
XX XX WO2003040340-A2.
XX PN 15-MAY-2003.
XX PD
XX PF 07-NOV-2002; 2002WO-US036002.
XX XX 07-NOV-2001; 2001US-00005480.
XX PR 31-JAN-2002; 2002US-00062109.
XX PS
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XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
XX Morrison RK, Challita-Eid PM;
XX WPI; 2003-441560/41.
XX A composition for diagnosing, preventing and treating cancer (e.g.
XX prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
XX and polypeptides.
XX Claim 13; Page 154; 135pp; English.
XX This invention relates to a novel composition which comprises a substance
XX that modulates the status of a novel human protein (161P2F10B) and its
XX variants having a sequence of 875 amino acids provided in the
XX specification. The protein of the invention is over-expressed in certain
XX cancers. The compounds of the invention may have cytostatic activity and
XX the sequence of the 161P2F10B protein, and the gene which encodes it, may
XX be useful for gene therapy or the development of a vaccine. The
XX composition and methods of the invention are useful in diagnosing,
XX preventing and treating cancer. The present sequence is the amino acid
XX sequence of a peptide which is derived from the sequence of the human
XX 161P2F10B protein and which may be used in the development of the
XX compounds of the invention.
XX Sequence 10 AA;
XX Query Match 100.0%; Score 23; DB 7; Length 10;
XX Best Local Similarity 60.0%; Pred. No. 1.5e+03;
XX Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 DXCXD 5
XX |:|:|
XX 3 DCCAD 7
XX
XX RESULT 91
XX ADE66945
XX ID ADE66945 standard; peptide; 10 AA.
XX AC ADE66945;
XX XX 29-JAN-2004 (first entry)
XX XX Human 161P2F10B protein-related peptide 950.
XX DE 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX KW Homo sapiens.
XX OS
XX XX WO2003040340-A2.
XX PN 15-MAY-2003.
XX PD
XX PF 07-NOV-2002; 2002WO-US036002.
XX XX 07-NOV-2001; 2001US-00005480.
XX PR 31-JAN-2002; 2002US-00062109.
XX PS
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
XX Morrison RK, Challita-Eid PM;
XX WPI; 2003-441560/41.
XX A composition for diagnosing, preventing and treating cancer (e.g.
XX prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
XX and polypeptides.
XX Claim 13; Page 152; 135pp; English.
XX PS
```


XX CC This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
 CC be useful for gene therapy or the development of a vaccine. The
 CC composition and methods of the invention are useful in diagnosing,
 CC preventing and treating cancer. The present sequence is the amino acid
 CC sequence of a peptide which is derived from the sequence of the human
 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.

XX SQ Sequence 10 AA;
 Query Match 100.0%; Score 23; DB 7; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1' DXCXD 5
 | : |
 Db 5 DCCAD 9

RESULT 92
 ADE67426
 ID ADE67426 standard; peptide; 10 AA.
 AC ADE67426;
 XX
 XX 29-JAN-2004 (first entry)
 XX Human 161P2F10B protein-related peptide 1431.
 DE 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
 KW Homo sapiens.
 OS
 XX WO2003040340-A2.
 PN 15-MAY-2003.
 PD 07-NOV-2002; 2002WO-US036002.
 PF 07-NOV-2001; 2001US-00005480.
 PR 31-JAN-2002; 2002US-00062109.
 XX (AGEN-) AGENSYS INC.
 PA Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 PI Morrison RK, Challita-Eid PM;
 XX WPI; 2003-441560/41.
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 XX A composition for diagnosing, preventing and treating cancer (e.g.
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 CC specification. The protein of the invention is over-expressed in certain
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 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.

XX SQ Sequence 10 AA;
 Query Match 100.0%; Score 23; DB 7; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DXCXD 5
 | : |
 Db 5 DCCAD 9

RESULT 93
 ADE67676
 ID ADE67676 standard; peptide; 10 AA.
 AC ADE67676;
 XX
 XX 29-JAN-2004 (first entry)
 XX Human 161P2F10B protein-related peptide 1681.
 DE 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
 KW Homo sapiens.
 OS
 XX WO2003040340-A2.
 PN 15-MAY-2003.
 PD 07-NOV-2002; 2002WO-US036002.
 PF 07-NOV-2001; 2001US-00005480.
 PR 31-JAN-2002; 2002US-00062109.
 XX (AGEN-) AGENSYS INC.
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 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
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 CC that modulates the status of a novel human protein (161P2F10B) and its
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 CC specification. The protein of the invention is over-expressed in certain
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 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.

XX SQ Sequence 10 AA;
 Query Match 100.0%; Score 23; DB 7; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DXCXD 5
 | : |
 Db 3 DCCAD 7

RESULT 94

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ADE69470
ID ADE69470 standard; peptide; 10 AA.
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DT 29-JAN-2004 (first entry)
DE Human 161P2F10B protein-related peptide 3475.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
XX
PS 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
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DR WPI; 2003-441560/41.
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PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
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PS Claim 13; Page 171; 135pp; English.
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CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
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CC composition and methods of the invention are useful in diagnosing,
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CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 10 AA;
XX
Query Match 100.0%; Score 23; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DXCXD 5
Db 6 DCCAD 10
RESULT 95
ADE69531
ID ADE69531 standard; peptide; 10 AA.
XX
AC ADE69531;
XX
DT 29-JAN-2004 (first entry)
DE Human 161P2F10B protein-related peptide 3536.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX
DR WPI; 2003-441560/41.
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PS Claim 13; Page 171; 135pp; English.
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CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
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CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 10 AA;
XX
Query Match 100.0%; Score 23; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DXCXD 5
Db 6 DCCAD 10
RESULT 95
ADE69531
ID ADE69531 standard; peptide; 10 AA.
XX
AC ADE69531;
XX
DT 29-JAN-2004 (first entry)
DE Human 161P2F10B protein-related peptide 3536.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
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PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
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DR WPI; 2003-441560/41.
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CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
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CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 10 AA;
XX
Query Match 100.0%; Score 23; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DXCXD 5
Db 4 DCCAD 8
RESULT 96
ADE70006
ID ADE70006 standard; peptide; 10 AA.
XX
AC ADE70006;
XX
DT 29-JAN-2004 (first entry)
DE Human 161P2F10B protein-related peptide 4011.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
XX
PS 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
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XX
DR WPI; 2003-441560/41.
XX
CC A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 171; 135pp; English.
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CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
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CC composition and methods of the invention are useful in diagnosing,
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CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 10 AA;
XX
Query Match 100.0%; Score 23; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DXCXD 5
Db 4 DCCAD 8

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XX WPI; 2003-441560/41.
XX A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
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CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 23; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
Db 5 DCCWD 9
RESULT 97
ADE66217
ID ADE66217 standard; peptide; 10 AA.
XX
AC ADE66217;
XX 29-JAN-2004 (first entry)
XX Human 161P2F10B protein-related peptide 224.
DE
XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
KW
XX Homo sapiens.
OS
XX WO2003040340-A2.
PN
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
XX (AGEN-) AGENSYS INC.
PA
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
PI
XX WPI; 2003-441560/41.
DR
XX Claim 13; Page 146; 135pp; English.
XX This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
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CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 23; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
Db 5 DCCWD 9
RESULT 98
ADE66948
ID ADE66948 standard; peptide; 10 AA.
XX
AC ADE66948;
XX 29-JAN-2004 (first entry)
XX Human 161P2F10B protein-related peptide 953.
DE
XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
KW
XX Homo sapiens.
OS
XX WO2003040340-A2.
PN
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
XX (AGEN-) AGENSYS INC.
PA
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
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CC sequence of a peptide which is derived from the sequence of the human
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XX Sequence 10 AA;
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Query Match 100.0%; Score 23; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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CC compounds of the invention.
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 23; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
Db 3 DCCAD 7
RESULT 98
ADE66948
ID ADE66948 standard; peptide; 10 AA.
XX
AC ADE66948;
XX 29-JAN-2004 (first entry)
XX Human 161P2F10B protein-related peptide 953.
DE
XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
KW
XX Homo sapiens.
OS
XX WO2003040340-A2.
PN
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XX
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CC compounds of the invention.
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 23; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;

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Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
   |:|:|
Db 3 DCCAD 7

RESULT 99
ADE69435
ID ADE69435 standard; peptide; 10 AA.
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AC ADE69435;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 3440.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
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XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 23; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Db 6 DCCAD 10

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AC ADE67185;
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DT 29-JAN-2004 (first entry)
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KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
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OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
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Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
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Db 5 DCCAD 9

Search completed: May 6, 2004, 10:45:50
Job time : 79 secs
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OM protein - protein search, using sw model

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(without alignments)
11.223 Million cell updates/sec

Title: SEQ2
Perfect score: 30
Sequence: 1 dvcqd 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 264921

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	30	100.0	8	4	US-09-352-548-25
5	30	100.0	9	4	US-09-352-548-24
6	30	100.0	10	4	US-09-352-548-21
7	30	100.0	11	4	US-09-352-548-19
8	30	100.0	11	4	US-09-352-548-33
9	30	100.0	15	2	US-08-584-671-4
10	30	100.0	15	3	US-09-027-376-4
11	30	100.0	15	3	US-09-094-192-4
12	30	100.0	15	4	US-09-352-548-13
13	30	100.0	16	4	US-09-352-548-47
14	30	100.0	16	4	US-09-352-548-48
15	30	100.0	16	4	US-09-352-548-54
16	30	100.0	16	4	US-09-352-548-55
17	30	100.0	16	4	US-09-352-548-56
18	30	100.0	16	4	US-09-352-548-57
19	30	100.0	16	4	US-09-352-548-58
20	30	100.0	16	4	US-09-352-548-59
21	30	100.0	19	2	US-08-584-671-5
22	30	100.0	19	3	US-09-027-376-5
23	30	100.0	19	3	US-09-094-192-5
24	30	100.0	70	4	US-09-352-548-44
25	30	100.0	70	4	US-09-352-548-45
26	30	100.0	70	4	US-09-352-548-46
27	30	100.0	70	4	US-09-352-548-49

28	30	100.0	70	4	US-09-352-548-50
29	30	100.0	70	4	US-09-352-548-51
30	30	100.0	70	4	US-09-352-548-52
31	30	100.0	70	4	US-09-352-548-53
32	30	100.0	79	2	US-08-584-671-14
33	30	100.0	79	2	US-08-584-671-15
34	30	100.0	79	3	US-09-027-376-14
35	30	100.0	79	3	US-09-027-376-16
36	30	100.0	79	3	US-09-094-192-14
37	30	100.0	79	3	US-09-094-192-16
38	30	100.0	80	2	US-08-584-671-15
39	30	100.0	80	3	US-09-027-376-15
40	30	100.0	80	3	US-09-094-192-15
41	30	100.0	81	4	US-09-352-548-2
42	30	100.0	81	4	US-09-686-583B-17
43	29	96.7	5	4	US-09-352-548-36
44	27	90.0	5	4	US-09-352-548-37
45	27	90.0	5	4	US-09-352-548-39
46	27	90.0	83	2	US-08-465-380-52
47	27	90.0	83	2	US-08-486-397-52
48	27	90.0	83	2	US-08-486-399-52
49	27	90.0	83	2	US-08-461-965-52
50	27	90.0	83	2	US-08-634-641-52
51	27	90.0	83	3	US-09-249-471-52
52	27	90.0	83	3	US-09-249-472-52
53	27	90.0	83	3	US-09-249-451-52
54	27	90.0	83	3	US-08-809-455-52
55	27	90.0	83	3	US-09-249-461-52
56	27	90.0	83	3	US-09-249-448-52
57	27	90.0	83	4	US-09-249-473-52
58	26	86.7	5	4	US-09-352-548-35
59	26	86.7	86	2	US-08-465-380-45
60	26	86.7	86	2	US-08-465-380-46
61	26	86.7	86	2	US-08-486-397-45
62	26	86.7	86	2	US-08-486-397-46
63	26	86.7	86	2	US-08-486-399-45
64	26	86.7	86	2	US-08-486-399-46
65	26	86.7	86	2	US-08-461-965-45
66	26	86.7	86	2	US-08-461-965-46
67	26	86.7	86	2	US-08-634-641-45
68	26	86.7	86	3	US-09-249-471-45
69	26	86.7	86	3	US-09-249-472-45
70	26	86.7	86	3	US-09-249-472-46
71	26	86.7	86	3	US-09-249-472-45
72	26	86.7	86	3	US-09-249-472-46
73	26	86.7	86	3	US-09-249-451-45
74	26	86.7	86	3	US-09-249-451-46
75	26	86.7	86	3	US-08-809-455-45

ALIGNMENTS

RESULT 1

US-09-352-548-28
; Sequence 28, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:D2-D6
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-28

Query Match 100.0%; Score 30; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
|
|
|
|
Db 1 DVCQD 5

RESULT 2

US-09-352-548-27
; Sequence 27, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-C7
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-27

Query Match 100.0%; Score 30; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
|
|
|
|
Db 1 DVCQD 5

RESULT 3

US-09-352-548-26
; Sequence 26, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-I8
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-26

Query Match 100.0%; Score 30; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
|
|
|
|
Db 1 DVCQD 5

RESULT 4

US-09-352-548-25
; Sequence 25, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-Q9
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-25

Query Match 100.0%; Score 30; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
|
|
|
|
Db 1 DVCQD 5

RESULT 5

US-09-352-548-24
; Sequence 24, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-M10
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-24

Query Match 100.0%; Score 30; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
|
|
|
|
Db 1 DVCQD 5

RESULT 6

```
US-09-352-548-21
; Sequence 21, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-V11
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-21

Query Match      100.0%; Score 30; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVCQD 5
Db      1 DVCQD 5

RESULT 7
US-09-352-548-19
; Sequence 19, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:G1-V11
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-19

Query Match      100.0%; Score 30; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVCQD 5
Db      2 DVCQD 6

RESULT 8
US-09-352-548-33
; Sequence 33, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:G1-(S7)-V11
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-33

Query Match      100.0%; Score 30; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVCQD 5
Db      2 DVCQD 6
```

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US-09-352-548-33
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:G1-(S7)-V11
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-33

Query Match      100.0%; Score 30; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVCQD 5
Db      2 DVCQD 6

RESULT 9
US-08-584-671-4
; Sequence 4, Application US/08584671
; Patent No. 5910568
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,671
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-08-584-671-4

Query Match      100.0%; Score 30; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVCQD 5
Db      2 DVCQD 6
```

```
Db          |||||
           9 DVCQD 13

RESULT 10
US-09-027-376-4
; Sequence 4, Application US/09027376
; Patent No. 6004586
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027.376
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/584,671
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-09-027-376-4

Query Match          100.0%; Score 30; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 DVCQD 5
           |||||
Db          9 DVCQD 13

RESULT 11
US-09-094-192-4
; Sequence 4, Application US/09094192
; Patent No. 6103483
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM TO EGG SURFACES AND PROC
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
```

```
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,192
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-09-094-192-4

Query Match          100.0%; Score 30; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 DVCQD 5
           |||||
Db          9 DVCQD 13

RESULT 12
US-09-352-548-13
; Sequence 13, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1998-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
US-09-352-548-13

Query Match          100.0%; Score 30; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 DVCQD 5
           |||||
Db          7 DVCQD 11

RESULT 13
US-09-352-548-47
; Sequence 47, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
```


; APPLICANT: Gill, Parkash S.
 ; APPLICANT: Parkash S. Gill, M.D., Inc.
 ; TITLE OF INVENTION: No. 6500431e1 Inhibitors of Angiogenesis and Tumor Growth
 ; FILE REFERENCE: 017986-000410US
 ; CURRENT APPLICATION NUMBER: US/09/352,548
 ; CURRENT FILING DATE: 1999-07-12
 ; EARLIER APPLICATION NUMBER: US 60/092,647
 ; EARLIER FILING DATE: 1998-07-13
 ; NUMBER OF SEQ ID NOS: 59
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 47
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
 ; OTHER INFORMATION: polypeptide
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)..(6)
 ; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-6 may be
 ; OTHER INFORMATION: present or absent
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (12)..(16)
 ; OTHER INFORMATION: Xaa = any amino acid
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (13)..(16)
 ; OTHER INFORMATION: Xaa at positions 13-16 may be present or absent
 ; US-09-352-548-47

Query Match 100.0%; Score 30; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
 Db 7 DVCQD 11

RESULT 14
 US-09-352-548-48
 ; Sequence 48, Application US/09352548
 ; Patent No. 6500431
 ; GENERAL INFORMATION:
 ; APPLICANT: Gill, Parkash S.
 ; APPLICANT: Parkash S. Gill, M.D., Inc.
 ; TITLE OF INVENTION: No. 6500431e1 Inhibitors of Angiogenesis and Tumor Growth
 ; FILE REFERENCE: 017986-000410US
 ; CURRENT APPLICATION NUMBER: US/09/352,548
 ; CURRENT FILING DATE: 1999-07-12
 ; EARLIER APPLICATION NUMBER: US 60/092,647
 ; EARLIER FILING DATE: 1998-07-13
 ; NUMBER OF SEQ ID NOS: 59
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 48
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
 ; OTHER INFORMATION: polypeptide
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)..(6)
 ; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-6 may be
 ; OTHER INFORMATION: present or absent
 ; US-09-352-548-48

Query Match 100.0%; Score 30; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
 Db 7 DVCQD 11

RESULT 15
 US-09-352-548-54
 ; Sequence 54, Application US/09352548
 ; Patent No. 6500431
 ; GENERAL INFORMATION:
 ; APPLICANT: Gill, Parkash S.
 ; APPLICANT: Parkash S. Gill, M.D., Inc.
 ; TITLE OF INVENTION: No. 6500431e1 Inhibitors of Angiogenesis and Tumor Growth
 ; FILE REFERENCE: 017986-000410US
 ; CURRENT APPLICATION NUMBER: US/09/352,548
 ; CURRENT FILING DATE: 1999-07-12
 ; EARLIER APPLICATION NUMBER: US 60/092,647
 ; EARLIER FILING DATE: 1998-07-13
 ; NUMBER OF SEQ ID NOS: 59
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 54
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
 ; OTHER INFORMATION: polypeptide
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)..(4)
 ; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
 ; OTHER INFORMATION: present or absent
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (5)
 ; OTHER INFORMATION: Xaa = any amino acid
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (6)
 ; OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (12)
 ; OTHER INFORMATION: Xaa = any amino acid
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (13)..(16)
 ; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 13-16 may
 ; OTHER INFORMATION: be present or absent
 ; US-09-352-548-54

Query Match 100.0%; Score 30; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
 Db 7 DVCQD 11

RESULT 16
 US-09-352-548-55
 ; Sequence 55, Application US/09352548
 ; Patent No. 6500431
 ; GENERAL INFORMATION:
 ; APPLICANT: Gill, Parkash S.
 ; APPLICANT: Parkash S. Gill, M.D., Inc.
 ; TITLE OF INVENTION: No. 6500431e1 Inhibitors of Angiogenesis and Tumor Growth
 ; FILE REFERENCE: 017986-000410US
 ; CURRENT APPLICATION NUMBER: US/09/352,548
 ; CURRENT FILING DATE: 1999-07-12
 ; EARLIER APPLICATION NUMBER: US 60/092,647

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/ EARLIER FILING DATE: 1998-07-13
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 55
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
/ OTHER INFORMATION: polypeptide
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)..(4)
/ OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
/ OTHER INFORMATION: present or absent
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (5)_RES
/ OTHER INFORMATION: Xaa = any. amino acid
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (6)_
/ OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (13)..(16)
/ OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 13-16 may
/ OTHER INFORMATION: be present or absent
US-09-352-548-55

Query Match          100.0%; Score 30; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
Db 7 DVCQD 11

RESULT 17
US-09-352-548-56
/ Sequence 56, Application US/09352548
/ Patent No. 6500431
/ GENERAL INFORMATION:
/ APPLICANT: Gill, Parkash S.
/ TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
/ FILE REFERENCE: 017986-000410US
/ CURRENT APPLICATION NUMBER: US/09/352,548
/ CURRENT FILING DATE: 1999-07-12
/ EARLIER APPLICATION NUMBER: US 60/092,647
/ EARLIER FILING DATE: 1998-07-13
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 56
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
/ OTHER INFORMATION: polypeptide
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)..(4)
/ OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
/ OTHER INFORMATION: present or absent
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (5)_
/ OTHER INFORMATION: Xaa = any amino acid
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (6)_
/ OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)..(4)
/ OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
/ OTHER INFORMATION: present or absent
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (5)_
/ OTHER INFORMATION: Xaa = any amino acid
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (6)_
```

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/ OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (12)
/ OTHER INFORMATION: Xaa = any amino acid
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (14)..(16)
/ OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 14-16 may
/ OTHER INFORMATION: be present or absent
US-09-352-548-56

Query Match          100.0%; Score 30; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
Db 7 DVCQD 11

RESULT 18
US-09-352-548-57
/ Sequence 57, Application US/09352548
/ Patent No. 6500431
/ GENERAL INFORMATION:
/ APPLICANT: Gill, Parkash S.
/ TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
/ FILE REFERENCE: 017986-000410US
/ CURRENT APPLICATION NUMBER: US/09/352,548
/ CURRENT FILING DATE: 1999-07-12
/ EARLIER APPLICATION NUMBER: US 60/092,647
/ EARLIER FILING DATE: 1998-07-13
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 57
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
/ OTHER INFORMATION: polypeptide
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)..(4)
/ OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
/ OTHER INFORMATION: present or absent
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (5)_
/ OTHER INFORMATION: Xaa = any amino acid
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (6)_
/ OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (12)..(13)
/ OTHER INFORMATION: Xaa = any amino acid
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (15)..(16)
/ OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 15 and 16
/ OTHER INFORMATION: may be present or absent
US-09-352-548-57

Query Match          100.0%; Score 30; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
Db 7 DVCQD 11
```

Db 7 DVCQD 11

RESULT 19

US-09-352-548-58
; Sequence 58, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431lel Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 58

LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
OTHER INFORMATION: polypeptide
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)-(4)
OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
OTHER INFORMATION: present or absent
FEATURE:
NAME/KEY: MOD RES
LOCATION: (5)
OTHER INFORMATION: Xaa = any amino acid
FEATURE:
NAME/KEY: MOD RES
LOCATION: (6)
OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
FEATURE:
NAME/KEY: MOD RES
LOCATION: (12)-(14)
OTHER INFORMATION: Xaa = any amino acid
FEATURE:
NAME/KEY: MOD RES
LOCATION: (16)
OTHER INFORMATION: Xaa = any amino acid, Xaa at position 16 may be
OTHER INFORMATION: present or absent

US-09-352-548-58

Query Match

Best Local Similarity 100.0%; Score 30; DB 4; Length 16;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5

Db 7 DVCQD 11

RESULT 20

US-09-352-548-59
; Sequence 59, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431lel Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 59

LENGTH: 16

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic

OTHER INFORMATION: polypeptide

FEATURE:

NAME/KEY: MOD RES

LOCATION: (1)-(4)

OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be

OTHER INFORMATION: present or absent

FEATURE:

NAME/KEY: MOD RES

LOCATION: (5)

OTHER INFORMATION: Xaa = any amino acid

FEATURE:

NAME/KEY: MOD RES

LOCATION: (6)

OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr

FEATURE:

NAME/KEY: MOD RES

LOCATION: (12)-(15)

OTHER INFORMATION: Xaa = any amino acid

US-09-352-548-59

Query Match

Best Local Similarity 100.0%; Score 30; DB 4; Length 16;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5

Db 7 DVCQD 11

RESULT 21

US-08-584-671-5
; Sequence 5, Application US/08584671
; Patent No. 5910568
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,

TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM

TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE

TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA

ADDRESSEE: STATE UNIVERSITY

STREET: 113 TECHNOLOGY CENTER

CITY: UNIVERSITY PARK

STATE: PENNSYLVANIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 16802-7000

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: NEC 286

OPERATING SYSTEM: DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/584,671

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MONAHAN, THOMAS J

REGISTRATION NUMBER: 29835

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 814-865-6277

TELEFAX: 814-865-3591

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 19

```
;
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-08-584-671-5

Query Match 100.0%; Score 30; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
Db 8 DVCQD 12

RESULT 22
US-09-027-376-5
; Sequence 5, Application US/09027376
; Patent No. 6004586
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,376
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/584,671
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-09-027-376-5

Query Match 100.0%; Score 30; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
Db 8 DVCQD 12

RESULT 23
US-09-094-192-5
; Sequence 5, Application US/09094192
; Patent No. 6103483
```

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;
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM TO EGG SURFACES AND PROCI
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,192
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-09-094-192-5

Query Match 100.0%; Score 30; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
Db 8 DVCQD 12

RESULT 24
US-09-352-548-44
; Sequence 44, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(6)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-6 may be
; OTHER INFORMATION: present or absent
; FEATURE:
```

```
; NAME/KEY: MOD_RES
; LOCATION: (12)..(70)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 12-70 may
; OTHER INFORMATION: be present or absent
US-09-352-548-44

Query Match      100.0%; Score 30; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVCQD 5
        |||||
Db       7 DVCQD 11

RESULT 25
US-09-352-548-45
; Sequence 45, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(5)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(4)
; OTHER INFORMATION: Xaa at positions 1-4 may be present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)..(70)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 12-70 may
; OTHER INFORMATION: be present or absent
US-09-352-548-45

Query Match      100.0%; Score 30; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVCQD 5
        |||||
Db       7 DVCQD 11

RESULT 26
US-09-352-548-46
; Sequence 46, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
```

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; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
; NAME/KEY: MOD_RES
; LOCATION: (12)..(70)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 12-70 may
; OTHER INFORMATION: be present or absent
US-09-352-548-46

Query Match      100.0%; Score 30; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVCQD 5
        |||||
Db       7 DVCQD 11

RESULT 27
US-09-352-548-49
; Sequence 49, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
; NAME/KEY: MOD_RES
; LOCATION: (2)..(5)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)..(70)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 12-70 may
; OTHER INFORMATION: be present or absent
US-09-352-548-49

Query Match      100.0%; Score 30; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVCQD 5
        |||||
Db       7 DVCQD 11
```

```

Db      7 DVCQD 11

RESULT 28
US-09-352-548-50
; Sequence 50, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; FEATURE: polypeptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(2)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1 and 2 may
; OTHER INFORMATION: be present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(5)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)..(70)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 12-70 may
; OTHER INFORMATION: be present or absent
US-09-352-548-51
Query Match      100.0%; Score 30; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVCQD 5
Db      7 DVCQD 11

RESULT 30
US-09-352-548-52
; Sequence 52, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; FEATURE: polypeptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(3)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-3 may be
; OTHER INFORMATION: present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)..(70)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 12-70 may
; OTHER INFORMATION: be present or absent
US-09-352-548-52

Db      7 DVCQD 11

RESULT 29
US-09-352-548-51
; Sequence 51, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence

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Query Match      100.0%; Score 30; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
Db 7 DVCQD 11

RESULT 31
US-09-352-548-53
; Sequence 53, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; NAME/KEY: MOD RES
; LOCATION: (1)..(4)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
; OTHER INFORMATION: present or absent
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (12)..(70)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 12-70 may
; OTHER INFORMATION: be present or absent
US-09-352-548-53

Query Match      100.0%; Score 30; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
Db 7 DVCQD 11

RESULT 32
US-08-584-671-14
; Sequence 14, Application US/08584671
; Patent No. 5910568
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK

QY 1 DVCQD 5
Db 7 DVCQD 11

RESULT 33
US-08-584-671-16
; Sequence 16, Application US/08584671
; Patent No. 5910568
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
```

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STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,671
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONAHAN, THOMAS J
REGISTRATION NUMBER: 29835
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 814-865-6277
TELEFAX: 814-865-3591
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 79
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
US-08-584-671-14

Query Match      100.0%; Score 30; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
Db 67 DVCQD 71

RESULT 33
US-08-584-671-16
; Sequence 16, Application US/08584671
; Patent No. 5910568
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,671
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONAHAN, THOMAS J
REGISTRATION NUMBER: 29835
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 814-865-6277
TELEFAX: 814-865-3591
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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; LENGTH: 79
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-08-584-671-16

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 67 DVCQD 71

RESULT 34
US-09-027-376-14
; Sequence 14, Application US/09027376
; Patent No. 6004586
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,376
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/584,671
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-09-027-376-14

Query Match
Best Local Similarity 100.0%; Score 30; DB 3; Length 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 67 DVCQD 71

RESULT 35
US-09-027-376-16
; Sequence 16, Application US/09027376
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; Patent No. 6004586
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,376
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/584,671
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-09-027-376-16

Query Match
Best Local Similarity 100.0%; Score 30; DB 3; Length 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 67 DVCQD 71

RESULT 36
US-09-094-192-14
; Sequence 14, Application US/09094192
; Patent No. 6103483
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM TO EGG SURFACES AND PROC
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
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;; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,192
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-3591
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-09-094-192-14

Query Match 100.0%; Score 30; DB 3; Length 79;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5

DB 67 DVCQD 71

RESULT 37
US-09-094-192-16
; Sequence 16, Application US/09094192
; Patent No. 6103483
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM TO EGG SURFACES AND PROC
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,192
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-3591
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-09-094-192-16

Query Match 100.0%; Score 30; DB 3; Length 79;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5

DB 67 DVCQD 71

RESULT 38
US-08-584-671-15
; Sequence 15, Application US/08584671
; Patent No. 5910568
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,671
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-08-584-671-15

Query Match 100.0%; Score 30; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5

DB 68 DVCQD 72

RESULT 39
US-09-027-376-15
; Sequence 15, Application US/09027376
; Patent No. 6004586
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA

COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.
FILING DATE: 1999-07-12
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,671
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MONAHAN, THOMAS J
REGISTRATION NUMBER: 29835
REFERENCE/DOCKET NUMBER:
TELEPHONE: 814-865-6277
TELEFAX: 814-865-3591
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 80
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
US-09-027-376-15

Query Match 100.0%; Score 30; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 68 DVCQD 72

RESULT 40
US-09-094-192-15
; Sequence 15, Application US/09094192
; Patent No. 6103483
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM TO EGG SURFACES AND PRO
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,192
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80

TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
US-09-094-192-15

Query Match 100.0%; Score 30; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 68 DVCQD 72

RESULT 41
US-09-352-548-2
; Sequence 2, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431e1 Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Saposin B
US-09-352-548-2

Query Match 100.0%; Score 30; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 2 DVCQD 6

RESULT 42
US-09-686-583B-17
; Sequence 17, Application US/09686583B
; Patent No. 6576750
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: FLEA PERITROPHIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; FILE REFERENCE: FC-6-C2
; CURRENT APPLICATION NUMBER: US/09/686,583B
; CURRENT FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 09/543,668
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,704
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Ctenocephalides felis
US-09-686-583B-17

Query Match 100.0%; Score 30; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
| | | |
Db 23 DVCQD 27

Search completed: May 6, 2004, 10:44:19
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: May 6, 2004, 10:42:41 ; Search time 39 Seconds
(without alignments)
40.451 Million cell updates/sec

Title: SEQ1
Perfect score: 23
Sequence: 1 dxcxd 5

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 262

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 1000 summaries

Database : SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	23	100.0	24	Q13661 homo sapien
2	23	100.0	24	Q13660 homo sapien
3	23	100.0	26	Q30578 bacillus su
4	23	100.0	31	Q9BXM4 homo sapien
5	23	100.0	33	Q8KBZ0 chlorobium
6	23	100.0	35	P95513 pasteurella
7	23	100.0	36	Q9PDN7 xylella fas
8	23	100.0	37	Q8ULK4 pyrococcus
9	23	100.0	39	Q9TBJ6 bos taurus
10	23	100.0	40	Q65775 chlamydomon
11	23	100.0	41	Q810D5 mus musculu
12	23	100.0	42	Q9GQ92 centruiroide
13	23	100.0	42	Q86QV6 centruiroide
14	23	100.0	42	Q86QV3 centruiroide
15	23	100.0	42	Q86QV2 centruiroide
16	23	100.0	42	Q86QV0 centruiroide

17	23	100.0	42	5	Q86QU6	Q86qu6 centruiroide
18	23	100.0	42	5	Q86QU1	Q86qu1 centruiroide
19	23	100.0	42	16	Q9PG31	Q9pg31 xylella fas
20	23	100.0	43	5	Q86QV9	Q86qv9 centruiroide
21	23	100.0	43	5	Q86QV8	Q86qv8 centruiroide
22	23	100.0	43	5	Q86QV7	Q86qv7 centruiroide
23	23	100.0	43	5	Q86QV5	Q86qv5 centruiroide
24	23	100.0	43	5	Q86QV4	Q86qv4 centruiroide
25	23	100.0	43	5	Q86QU9	Q86qu9 centruiroide
26	23	100.0	43	5	Q86QU8	Q86qu8 centruiroide
27	23	100.0	43	5	Q86QU7	Q86qu7 centruiroide
28	23	100.0	43	5	Q86QU5	Q86qu5 centruiroide
29	23	100.0	43	5	Q86QU4	Q86qu4 centruiroide
30	23	100.0	43	5	Q86QU3	Q86qu3 centruiroide
31	23	100.0	43	5	Q86QU0	Q86qu0 centruiroide
32	23	100.0	43	5	Q86QT9	Q86qt9 centruiroide
33	23	100.0	43	5	Q86QT8	Q86qt8 centruiroide
34	23	100.0	43	16	Q51033	Q51033 borrelia bu
35	23	100.0	44	8	Q96814	Q96814 skeletonema
36	23	100.0	44	16	Q9PB90	Q9pb90 xylella fas
37	23	100.0	46	4	Q9P027	Q9p027 homo sapien
38	23	100.0	47	5	Q86QV1	Q86qv1 centruiroide
39	23	100.0	47	5	Q86QU2	Q86qu2 centruiroide
40	23	100.0	47	16	Q83DL3	Q83dl3 coxiella bu
41	23	100.0	47	16	Q7VKA9	Q7vka9 haemophilus
42	23	100.0	48	16	Q87ZL0	Q87zl0 pseudomonas
43	23	100.0	50	16	Q8P322	Q8p322 xanthomonas
44	23	100.0	50	16	Q87HS5	Q87hs5 vibrio para
45	23	100.0	51	4	Q9HBW4	Q9hbw4 homo sapien
46	23	100.0	51	4	Q95127	Q95127 homo sapien
47	23	100.0	51	5	Q8WVR3	Q8wvr3 trypanosoma
48	23	100.0	51	11	Q89063	Q89063 mus musculu
49	23	100.0	51	16	Q8CKL0	Q8ckl0 yersinia pe
50	23	100.0	52	4	Q9UHS7	Q9uhs7 homo sapien
51	23	100.0	53	9	Q853J6	Q853j6 mycobacteri
52	23	100.0	53	10	Q8RYU2	Q8ryu2 oryza sativ
53	23	100.0	53	11	Q8R194	Q8r194 mus musculu
54	23	100.0	53	17	Q8PU57	Q8pu57 methanosarc
55	23	100.0	54	4	Q9H2D8	Q9h2d8 homo sapien
56	23	100.0	54	11	Q8C7R8	Q8c7r8 mus musculu
57	23	100.0	54	16	Q9Z7G0	Q9z7g0 chlamydia p
58	23	100.0	54	17	Q9HQ14	Q9hq14 halobacteri
59	23	100.0	55	16	Q9BJC8	Q9bjc8 rhizobium l
60	23	100.0	55	16	Q8ZNX9	Q8znx9 salmonella
61	23	100.0	55	16	Q8XSR6	Q8xsr6 ralstonia s
62	23	100.0	57	2	Q87086	Q87086 streptomyc
63	23	100.0	57	6	Q95MD7	Q95md7 bos taurus
64	23	100.0	57	10	Q8W066	Q8w066 oryza sativ
65	23	100.0	57	10	Q80060	Q80060 zea mays m
66	23	100.0	58	16	Q9K0Y7	Q9k0y7 neisseria m
67	23	100.0	58	17	Q8TIF8	Q8tif8 methanosarc
68	23	100.0	58	17	Q8PYU1	Q8pyu1 methanosarc
69	23	100.0	59	12	Q8B442	Q8b442 human cytom
70	23	100.0	59	16	Q7UFE3	Q7ufe3 rhodospirill
71	23	100.0	59	17	Q8TTH2	Q8tth2 methanosarc
72	23	100.0	59	17	Q8PMD7	Q8pmd7 methanosarc
73	23	100.0	60	16	Q9JSZ2	Q9jsz2 neisseria m
74	23	100.0	61	16	Q8XN68	Q8xn68 clostridium
75	23	100.0	61	16	Q87SC2	Q87sc2 vibrio para
76	23	100.0	62	5	Q86QT3	Q86qt3 centruiroide
77	23	100.0	62	5	Q7YVA8	Q7yva8 trypanosoma
78	23	100.0	62	12	Q36357	Q36357 alcelaphine
79	23	100.0	62	12	Q7T831	Q7t831 avian infec
80	23	100.0	62	17	Q9HQH6	Q9hqh6 halobacteri
81	23	100.0	63	5	Q95PA2	Q95pa2 bradyesia by
82	23	100.0	63	12	Q719R1	Q719r1 adoxophyes
83	23	100.0	64	4	Q96RF1	Q96rf1 homo sapien
84	23	100.0	64	10	Q9SPF8	Q9spf8 vitis labru
85	23	100.0	65	13	Q9PRY3	Q9pry3 dendroaspis
86	23	100.0	65	16	P72838	P72838 synechocyst
87	23	100.0	65	16	Q8X3J3	Q8x3j3 escherichia
88	23	100.0	65	16	Q7VL66	Q7vl66 haemophilus
89	23	100.0	65	17	Q8TNN8	Q8tnn8 methanosarc

90	23	100.0	9	Q8SBL8	Q8b18 bacterioph	163	23	100.0	81	11	P97778	P97778 rattus norv
91	23	100.0	66	Q9PYQ3	Q9pyq3 xestia c-ni	164	23	100.0	81	11	Q8R4W5	Q8r4w5 mus musculu
92	23	100.0	67	Q9SS57	Q9ss57 drosophila	165	23	100.0	81	12	Q8JTQ1	Q8jtk1 lumpy skin
93	23	100.0	67	Q9HI31	Q9hi31 halobacteri	166	23	100.0	81	16	Q8NNG1	Q8nng1 corynebacte
94	23	100.0	68	Q8VBV2	Q8vbv2 rattus norv	167	23	100.0	81	16	Q8G7S6	Q8g7s6 bifidobacte
95	23	100.0	68	Q8U5J9	Q8u5j9 agrobacteri	168	23	100.0	81	16	Q8EFW3	Q8efw3 shewanella
96	23	100.0	68	Q8G9X8	Q8g9x8 bradyrhizob	169	23	100.0	81	17	Q8RTS0	Q8rts0 methanosarc
97	23	100.0	68	Q7UP61	Q7up61 rhodopirell	170	23	100.0	82	4	Q9P1K9	Q9p1k9 homo sapien
98	23	100.0	69	Q8WWM0	Q8wwm0 homo sapien	171	23	100.0	82	5	Q7YWN0	Q7ywn0 caenorhabdi
99	23	100.0	69	Q8K4N2	Q8k4n2 mus musculu	172	23	100.0	82	6	Q8SQC5	Q8sqc5 macaca mula
100	23	100.0	70	Q8UPT5	Q8ut5 nereis vire	173	23	100.0	82	10	Q8H3L7	Q8h3l7 oryza sativ
101	23	100.0	70	Q9QNG5	Q9qng5 variola min	174	23	100.0	83	13	Q7ZTT8	Q7ztt8 brachydanio
102	23	100.0	70	Q9K9J0	Q9k9j0 bacillus ha	175	23	100.0	83	4	Q8H2E0	Q8h2e0 homo sapien
103	23	100.0	70	Q8P9W9	Q8p9w9 xanthomonas	176	23	100.0	83	5	Q8I969	Q8i969 drosophila
104	23	100.0	70	Q8EJ14	Q8ej14 shewanella	177	23	100.0	83	5	Q8PFC2	Q8pfc2 xylella fas
105	23	100.0	71	Q8KUX0	Q8kux0 synechococ	178	23	100.0	83	16	Q8D9W4	Q8d9w4 vibrio vuln
106	23	100.0	71	Q8X5W8	Q8x5w8 pantoecia cit	179	23	100.0	84	10	Q9LGN9	Q9lgn9 oryza sativ
107	23	100.0	71	Q8F4M7	Q8f4m7 leptospira	180	23	100.0	84	13	Q9PU22	Q9pu22 trachemys s
108	23	100.0	71	Q8H316	Q8h316 lactobacill	181	23	100.0	84	16	Q7VK05	Q7vk05 helicobacte
109	23	100.0	72	Q8RVZ6	Q8rvz6 trifolium r	182	23	100.0	84	16	Q7UEP4	Q7uep4 rhodopirell
110	23	100.0	72	Q8XU54	Q8xu54 ralestonia s	183	23	100.0	85	4	Q8ND53	Q8nd53 homo sapien
111	23	100.0	74	Q8UMP4	Q8ump4 homo sapien	184	23	100.0	85	10	Q9LFB6	Q9lfb6 arabidopsis
112	23	100.0	74	Q8A2A2	Q8a2a2 oryza sativ	185	23	100.0	85	13	Q8JHD5	Q8jhd5 xenopus lae
113	23	100.0	74	Q8DKU7	Q8dku7 human papil	186	23	100.0	85	16	Q7V751	Q7v751 prochloroco
114	23	100.0	74	Q8DKU4	Q8dku4 human papil	187	23	100.0	86	2	P94195	P94195 agrobacteri
115	23	100.0	74	Q8JVD0	Q8jvd0 macaca fasc	188	23	100.0	86	4	Q8NQN2	Q8nqn2 homo sapien
116	23	100.0	74	Q882T9	Q882t9 rhizobium l	189	23	100.0	86	9	Q8HAGO	Q8hago salmonella
117	23	100.0	74	Q8BEP9	Q8bep9 vibrio vuln	190	23	100.0	86	16	Q8G0B9	Q8g0b9 brucella su
118	23	100.0	74	Q7V7P1	Q7v7p1 prochloroco	191	23	100.0	86	16	Q7WDA0	Q7wda0 bordetella
119	23	100.0	74	Q7U6R0	Q7u6r0 synechococ	192	23	100.0	86	16	Q7W5R4	Q7w5r4 bordetella
120	23	100.0	75	Q45864	Q45864 caenorhabdi	193	23	100.0	86	16	Q7VWA3	Q7vwa3 bordetella
121	23	100.0	75	Q7TTQ1	Q7ttq1 equus cabal	194	23	100.0	87	9	Q9FZU7	Q9fzu7 bacterioph
122	23	100.0	75	Q8R952	Q8r952 thermoanaer	195	23	100.0	87	16	Q9JYB8	Q9jyb8 neisseria m
123	23	100.0	75	Q8P5W3	Q8p5w3 methanosarc	196	23	100.0	87	16	Q9FBZ3	Q9fbz3 streptomyce
124	23	100.0	76	Q8BPB8	Q8bp8 conus arena	197	23	100.0	88	5	Q9VZ42	Q9vz42 drosophila
125	23	100.0	76	Q857B4	Q857b4 mycobacteri	198	23	100.0	88	16	Q8G6B5	Q8g6b5 bifidobacte
126	23	100.0	76	Q82415	Q82415 nicotiana t	199	23	100.0	88	16	Q87QN8	Q87qn8 vibrio para
127	23	100.0	76	Q7XK18	Q7xk18 oryza sativ	200	23	100.0	89	10	Q40036	Q40036 hordeum vul
128	23	100.0	76	Q9PYI0	Q9pyi0 xestia c-ni	201	23	100.0	89	10	Q43665	Q43665 triticum ae
129	23	100.0	76	Q8A530	Q8a530 bacteroides	202	23	100.0	89	10	Q8GWN0	Q8gwn0 arabidopsis
130	23	100.0	76	Q27847	Q27847 methanobact	203	23	100.0	89	16	Q7V0Y2	Q7v0y2 prochloroco
131	23	100.0	77	Q8BP90	Q8bp90 conus arena	204	23	100.0	89	16	Q7UV51	Q7uv51 rhodopirell
132	23	100.0	77	Q8BP91	Q8bp91 conus arena	205	23	100.0	90	5	Q8T784	Q8t784 branchiost
133	23	100.0	77	Q862V4	Q862v4 bos taurus	206	23	100.0	90	10	Q7X1B0	Q7x1b0 oryza sativ
134	23	100.0	77	Q9DSW4	Q9dsw4 ascovirus d	207	23	100.0	90	11	Q8R449	Q8r449 hydromys ch
135	23	100.0	77	Q9KPL0	Q9kpl0 vibrio chol	208	23	100.0	90	13	Q90Y15	Q90y15 fugu rubrip
136	23	100.0	77	Q988S7	Q988s7 rhizobium l	209	23	100.0	90	16	Q7WCZ7	Q7wcz7 bordetella
137	23	100.0	77	Q7U9Y8	Q7u9y8 synechococ	210	23	100.0	90	16	Q7W5G2	Q7w5g2 bordetella
138	23	100.0	78	Q95VT8	Q95vt8 homarus ame	211	23	100.0	91	5	Q9VCS1	Q9vcs1 drosophila
139	23	100.0	78	Q95VT5	Q95vt5 homarus ame	212	23	100.0	91	5	Q9N661	Q9n661 mesobuthus
140	23	100.0	78	Q8SB02	Q8sb02 oryza sativ	213	23	100.0	92	2	Q9XAV8	Q9xav8 macaca mula
141	23	100.0	78	Q7XG95	Q7xg95 oryza sativ	214	23	100.0	92	4	Q9HB18	Q9hba18 pseudomonas
142	23	100.0	78	Q8OV88	Q8ov88 mus musculu	215	23	100.0	92	10	Q8W2J7	Q8w2j7 setaria adh
143	23	100.0	78	Q92RTS	Q92rts pyrobaculum	216	23	100.0	92	11	Q9QZU2	Q9qzu2 mus musculu
144	23	100.0	79	Q92RT6	Q92rt6 crocus vern	217	23	100.0	92	11	Q91ZHS	Q91zh5 rattus norv
145	23	100.0	79	Q8V3G9	Q8v3g9 swinepox vi	218	23	100.0	92	16	Q9A4J8	Q9a4j8 caulobacter
146	23	100.0	79	Q8CC93	Q8cc93 mycobacteri	219	23	100.0	92	16	Q8FT14	Q8ft14 corynebacte
147	23	100.0	79	Q8EQH0	Q8eqh0 oceanobacil	220	23	100.0	92	16	Q8BAP9	Q8bap9 pseudomonas
148	23	100.0	79	Q8EN47	Q8ena7 oceanobacil	221	23	100.0	92	16	Q7WC39	Q7wc39 bordetella
149	23	100.0	79	Q7HPN6	Q7hpn6 halobacteri	222	23	100.0	93	16	Q8F9K1	Q8f9k1 leptospira
150	23	100.0	79	Q9HN06	Q9hn06 halobacteri	223	23	100.0	93	16	Q7WMJ2	Q7wmj2 bordetella
151	23	100.0	80	Q32899	Q32899 mycobacteri	224	23	100.0	93	16	Q7VZA4	Q7vza4 bordetella
152	23	100.0	80	Q9H4P9	Q9h4p9 homo sapien	225	23	100.0	94	2	Q8V510	Q8v510 klebsiella
153	23	100.0	80	Q9M226	Q9m226 pan troglod	226	23	100.0	94	2	Q8VUF9	Q8vuf9 azoarcus ev
154	23	100.0	80	Q8SQD3	Q8sqd3 macaca mula	227	23	100.0	94	2	Q8GE48	Q8ge48 hellobacill
155	23	100.0	80	Q9MCF5	Q9mcf5 bacterioph	228	23	100.0	94	11	Q8BTA5	Q8bta5 mus musculu
156	23	100.0	80	Q8L5M1	Q8l5m1 vitis vinif	229	23	100.0	94	16	Q8E2X1	Q8e2x1 streptococ
157	23	100.0	80	Q8L5M1	Q8l5m1 escherichia	230	23	100.0	94	16	Q9A1S6	Q9a1s6 streptococ
158	23	100.0	81	Q8GCH0	Q8gch0 pseudomonas	231	23	100.0	94	16	Q8EZZ0	Q8ezz0 leptospira
159	23	100.0	81	Q8NM07	Q8nm07 ctenocephal	232	23	100.0	94	16	Q88IQ9	Q88iq9 pseudomonas
160	23	100.0	81	Q8M6Q7	Q8m6q7 medicago tr	233	23	100.0	94	16	Q81XH3	Q81xh3 bacillus an
161	23	100.0	81	Q8GW84	Q8gw84 arabidopsis	234	23	100.0	94	16		
162	23	100.0	81	Q9QZU1	Q9qzu1 rattus norv	235	23	100.0	94	16		

236 Q815V8 bacillus ce
 237 Q7YWB2 panulirus a
 238 Q8UYT3 tomato aspe
 239 Q9JUG1 neisseria m
 240 Q8EE89 shewanella
 241 Q8MIT7 macaca mula
 242 Q8HXZ5 macaca mula
 243 Q98NT2 rhizobium l
 244 Q984E7 rhizobium l
 245 Q982P8 rhizobium l
 246 Q8F842 leptospira
 247 Q879Q1 streptococ
 248 Q25549 naegleria f
 249 Q8CF27 mus musculu
 250 Q8UZA9 garlic late
 251 Q8ZUM6 pyrobaculum
 252 Q95VB0 spiroetra
 253 Q17007 caenorhabdi
 254 Q8IAJ9 arabidopsis
 255 Q8YQV1 anabaena sp
 256 Q83DR4 coxiella bu
 257 Q22220 caenorhabdi
 258 Q95MD5 bos taurus
 259 Q856W5 mycobacteri
 260 Q93ZJ3 arabidopsis
 261 Q9CVF7 mus musculu
 262 Q9ZMM9 helicobacte

ALIGNMENTS

RESULT 1
 Q13661
 ID Q13661 PRELIMINARY; PRT; 24 AA.
 AC Q13661;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
 DE Mannose 6-phosphate/insulin-like growth factor-II receptor
 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96083596; PubMed=7493029;
 RA De Souza A.T., Hankins G.R., Washington M.K., Orton T.C., Jirtle R.L.;
 RT "M6P/IGF2R gene is mutated in human hepatocellular carcinomas with
 loss of heterozygosity.";
 RL Nat. Genet. 11:447-449(1995).
 DR EMBL; S80785; AAB35665.1; -;
 DR GO; GO:0005764; C:lysosome; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000479; CIRM.
 DR Pfam; PF00878; CIMR; 1.
 KW Receptor.
 FT NON_TER 1
 SQ SEQUENCE 24 AA; 2829 MW; E6F2901053E17602 CRC64;

Query Match 100.0%; Score 23; DB 4; Length 24;
 Best Local Similarity 60.0%; Pred. No. 8.5e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:|
 Db 16 DLCPD 20

RESULT 2
 Q13660
 ID Q13660 PRELIMINARY; PRT; 24 AA.
 AC Q13660;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Mannose 6-phosphate/insulin-like growth factor-II receptor
 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96083596; PubMed=7493029;
 RA De Souza A.T., Hankins G.R., Washington M.K., Orton T.C., Jirtle R.L.;
 RT "M6P/IGF2R gene is mutated in human hepatocellular carcinomas with
 loss of heterozygosity.";
 RL Nat. Genet. 11:447-449(1995).
 DR EMBL; S80783; AAB35664.1; -;
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER 1
 SQ SEQUENCE 24 AA; 2799 MW; E6F28C7F43E17602 CRC64;

Query Match 100.0%; Score 23; DB 4; Length 24;
 Best Local Similarity 60.0%; Pred. No. 8.5e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:|
 Db 16 DLCPD 20

RESULT 3
 Q30578
 ID Q30578 PRELIMINARY; PRT; 26 AA.
 AC Q30578;
 DT 01-JAN-1998 (TREMELrel. 05, Created)
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
 DE YefA (Fragment).
 GN YEF_A.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=168 trpC2;
 RA Borriss R., Schroeter R.;
 RT "The 55-58 degree segment of the Bacillus subtilis chromosome, a
 region spanning from the purA gene cluster to the cotJ operon.";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF012532; AAB66480.1; -;
 FT NON_TER 1
 SQ SEQUENCE 26 AA; 2743 MW; 8318669E39293D38 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 26;
 Best Local Similarity 60.0%; Pred. No. 9.1e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:|
 Db 12 DNGCD 16

RESULT 4
 Q9BXM4
 ID Q9BXM4 PRELIMINARY; PRT; 31 AA.
 AC Q9BXM4;
 DT 01-JUN-2001 (TREMELrel. 17, Created)
 DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Transcription factor BACH1t (Fragment).
GN BACH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21269257; PubMed=11069897;
RA Kanazaki R., Toki T., Yokoyama M., Yomogida K., Sugiyama K.,
RA Yamamoto M., Igarashi K., Ito E.;
RT "Transcription factor BACH1 is recruited to nucleus by its novel
RT alternative spliced isoform.";
RL J. Biol. Chem. 276:7278-7284(2001).
DR EMBL; AF317902; AAK08197.1; -
FT NON TER
FT NON TER
SQ SEQUENCE 31 AA; 3400 MW; 62516F09E92F861D CRC64;

Query Match 100.0%; Score 23; DB 4; Length 31;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 20 DTCS D 24

RESULT 5
Q8KXZ0
ID Q8KXZ0 PRELIMINARY; PRT; 33 AA.
AC Q8KXZ0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein Ctl1642.
GN Ctl1642.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TLS / ATCC 49652 / DSM 12025;
RC MEDLINE=22103685; PubMed=1203901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
DR EMBL; AE012919; AAM72867.1; -
DR TIGR; Ctl1642; -
SQ SEQUENCE 33 AA; 3578 MW; 1FE88681806666BB CRC64;

Query Match 100.0%; Score 23; DB 16; Length 33;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 21 DSCID 25

RESULT 6
P95513
ID P95513 PRELIMINARY; PRT; 35 AA.
AC P95513;

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DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE Hypothetical protein (Fragment).
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=T3;
RA Burrows L.L., Lam J.S., Lo R.Y.C.;
RT "The kdsA gene of Pasteurella trelhalosi (haemolytica) serotype T3 is
RT functionally and genetically homologous to that of Escherichia coli.";
RL J. Endotoxin Res. 3:353-359(1996).
DR EMBL; U52971; AAB36512.1; -
FT NON TER
FT NON TER
SQ SEQUENCE 35 AA; 4024 MW; B64F1593DB4F8F43 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 35;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 7 DQCPD 11

RESULT 7
Q9PDN7
ID Q9PDN7 PRELIMINARY; PRT; 36 AA.
AC Q9PDN7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Xfl1342.
GN Xfl1342.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=9a5c;
RC MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA da Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";

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RL Nature 406:151-159(2000).
DR EMBL; AE003966; AAF84151.1; -.
DR PIR; C82694; C82694.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 36 AA; 4063 MW; 31FC391CC534BEAB CRC64;

Query Match 100.0%; Score 23; DB 16; Length 36;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 14 DDCLD 18

RESULT 8
Q8U1K4 PRELIMINARY; PRT; 37 AA.
AC Q8U1K4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical protein PF1202.
GN PF1202.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010228; AL81326.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 37 AA; 4351 MW; A060EDD9D29EE5C CRC64;

Query Match 100.0%; Score 23; DB 17; Length 37;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 24 DECKD 28

RESULT 9
Q9TSJ6 PRELIMINARY; PRT; 39 AA.
AC Q9TSJ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Acetylcholinesterase T-subunit (Fragment).
GN ACHE.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98359754; PubMed=9693127;
RA Mendelson I., Kroman C., Ariel N., Shafferman A., Velan B.;
RT "Bovine acetylcholinesterase: cloning, expression and
characterization.";
RL Biochem. J. 334:251-259(1998).
DR EMBL; AF061816; AAC64269.1; -.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4959 MW; 72F3379D0F8B6557 CRC64;

Query Match 100.0%; Score 23; DB 11; Length 41;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 35 DYCKD 39

RESULT 11
Q810D5 PRELIMINARY; PRT; 41 AA.
AC Q810D5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MPer3 protein (Fragment).
GN MPer3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RA Takami T., Okamura H., Takashima N.;
RT "mper3 promoter sequence.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB023026; BAC66464.1; -.
FT NON_TER 41
FT NON_TER 41
SQ SEQUENCE 41 AA; 3980 MW; 920663C58221BA5F CRC64;

Query Match 100.0%; Score 23; DB 11; Length 41;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 35 DYCKD 39
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Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
|:|:|
Db 2 DPCGD 6

RESULT 12
Q9GQ92 PRELIMINARY; PRT; 42 AA.
AC Q9GQ92;
DT 01-WAR-2001 (TREMBlrel. 16, Created)
DT 01-WAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 25, Last annotation update)
DE Ergtoxin (Fragment).
OS Centruroides noxius (Mexican scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthidea; Butthidae; Centruroides.
OX NCBI_TaxID=6878;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2046069; PubMed=11023354;
RA Battiglieri C., Ferrara L., Corona M., Gurrola G.B., Batista C.,
RA Wanke E., Possani L.D.;
RT "Disulfide bridges of ergtoxin, a member of a new sub-family of
RT peptide blockers of the ether-a-go-go-related K+ channel.";
RL FEBS Lett. 479:156-157(2000).
DR EMBL; AF288205; AAG38523.1; -.
DR PDB; 1NE5; 01-APR-03.
FT NON_TER 1
SQ SEQUENCE 42 AA; 4738 MW; B33345144841BD1 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 42;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
|:|:|
Db 3 DSCVD 7

RESULT 13
Q86QV6 PRELIMINARY; PRT; 42 AA.
AC Q86QV6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Ergtoxin-like protein 1 (Fragment).
GN ERG1.
OS Centruroides elegans (Bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthidea; Butthidae; Centruroides.
OX NCBI_TaxID=217897;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Venom gland;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159337; AAO22215.1; -.
FT NON_TER 1
SQ SEQUENCE 42 AA; 4817 MW; F905F5144847AD7F CRC64;

Query Match 100.0%; Score 23; DB 5; Length 42;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
|:|:|
Db 3 DSCVD 7

RESULT 14
Q86QV3 PRELIMINARY; PRT; 42 AA.
AC Q86QV3;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Ergtoxin-like protein 1 (Fragment).
GN ERG1.
OS Centruroides gracilis (Slenderbrown scorpion) (Florida bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthidea; Butthidae; Centruroides.
OX NCBI_TaxID=217898;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Venom gland;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159340; AAO22218.1; -.
FT NON_TER 1
SQ SEQUENCE 42 AA; 4791 MW; F905E5054947AD7F CRC64;

Query Match 100.0%; Score 23; DB 5; Length 42;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
|:|:|
Db 3 DSCVD 7

RESULT 15
Q86QV2 PRELIMINARY; PRT; 42 AA.
AC Q86QV2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Ergtoxin-like protein 2 (Fragment).
GN ERG2.
OS Centruroides gracilis (Slenderbrown scorpion) (Florida bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthidea; Butthidae; Centruroides.
OX NCBI_TaxID=217898;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Venom gland;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159341; AAO22219.1; -.
FT NON_TER 1
SQ SEQUENCE 42 AA; 4716 MW; 2FA0F36A15F10C76 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 42;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
|:|:|
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Db          3 DSCVD 7

RESULT 16
Q86QV0
ID Q86QV0 PRELIMINARY; PRT; 42 AA.
AC Q86QV0;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Ergotoxin-like protein 1 (Fragment).
GN ERGI.
OS Centruroides limpidus limpidus (Mexican scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthidea; Butthidae; Centruroides.
OX NCBI_TaxID=29941;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergotoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159343; AAO22221.1; -.
FT NON TER 1
FT SEQUENCE 42 AA; 4768 MW; 9BE5F514484108F0 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 42;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 3 DSCVD 7

RESULT 17
Q86QV6
ID Q86QV6 PRELIMINARY; PRT; 42 AA.
AC Q86QV6;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Ergotoxin-like protein 1 (Fragment).
GN ERGI.
OS Centruroides sculpturatus (bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthidea; Butthidae; Centruroides.
OX NCBI_TaxID=218467;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergotoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159347; AAO22225.1; -.
FT NON TER 1
FT SEQUENCE 42 AA; 4752 MW; B585F51448411BD1 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 42;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 3 DSCVD 7

RESULT 18
Q86QUL
ID Q86QUL PRELIMINARY; PRT; 42 AA.
AC Q86QUL;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Ergotoxin-like protein 1 (Fragment).
GN ERGI.
OS Centruroides sculpturatus (Bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthidea; Butthidae; Centruroides.
OX NCBI_TaxID=6879;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergotoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159352; AAO22230.1; -.
FT NON TER 1
FT SEQUENCE 42 AA; 4725 MW; B585F51452681BD1 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 42;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 3 DSCVD 7

RESULT 19
Q9PG31
ID Q9PG31 PRELIMINARY; PRT; 42 AA.
AC Q9PG31;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein Xf0471.
GN XF0471.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvares R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Canargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Pacincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hobeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.B., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,

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RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawaaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AF003897; AAF83281.1; -.
DR FIC; AB2802; A82802
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 42 AA; 4690 MW; AAF5B1F2FA8E6DC9 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 42;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 13 DLCCD 17

RESULT 20
Q86QV9
ID Q86QV9 PRELIMINARY; PRT; 43 AA.
AC Q86QV9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ergotoxin-like protein 3 (Fragment).
GN ERG3.
OS Centruroides noxius (Mexican scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butioidae; Butiidae; Centruroides.
OX NCBI_TaxID=6878;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergotoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159334; AAO22212.1; -.
FT NON_TER 1
SQ SEQUENCE 43 AA; 4813 MW; BDA4C2E723CCF0D2 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 3 DSCVD 7

RESULT 21
Q86QV8
ID Q86QV8 PRELIMINARY; PRT; 43 AA.
AC Q86QV8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ergotoxin-like protein 4 (Fragment).
GN ERG4.
OS Centruroides noxius (Mexican scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butioidae; Butiidae; Centruroides.
OX NCBI_TaxID=6878;

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[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergotoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159335; AAO22213.1; -.
FT NON_TER 1
SQ SEQUENCE 43 AA; 4855 MW; BDB07DACD147F197 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 3 DSCVD 7

RESULT 22
Q86QV7
ID Q86QV7 PRELIMINARY; PRT; 43 AA.
AC Q86QV7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ergotoxin-like protein 5 (Fragment).
GN ERG5.
OS Centruroides noxius (Mexican scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butioidae; Butiidae; Centruroides.
OX NCBI_TaxID=6878;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergotoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159336; AAO22214.1; -.
FT NON_TER 1
SQ SEQUENCE 43 AA; 4836 MW; SDF441212448539F CRC64;

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 3 DSCVD 7

RESULT 23
Q86QV5
ID Q86QV5 PRELIMINARY; PRT; 43 AA.
AC Q86QV5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ergotoxin-like protein 2 (Fragment).
GN ERG2.
OS Centruroides elegans (Bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butioidae; Butiidae; Centruroides.
OX NCBI_TaxID=217897;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides."
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159338; AAO22216.1; -.
FT NON TER 1
SQ SEQUENCE 43 AA; 4947 MW; 77C231F5145B5AF1 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db |:|:|
3 DSCVD 7

RESULT 24
Q86QV4 PRELIMINARY; PRT; 43 AA.
AC Q86QV4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ergtoxin-like protein 3 (Fragment).
GN ERG3.
OS Centruroides elegans (Bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthoidea; Butthidae; Centruroides.
OX NCBI_TaxID=217897;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides."
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159339; AAO22217.1; -.
FT NON TER 1
SQ SEQUENCE 43 AA; 4906 MW; BDAB2EEA23CCF0D2 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db |:|:|
3 DSCVD 7

RESULT 25
Q86QU9 PRELIMINARY; PRT; 43 AA.
AC Q86QU9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ergtoxin-like protein 2 (Fragment).
GN ERG2.
OS Centruroides limpidus limpidus (Mexican scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthoidea; Butthidae; Centruroides.
OX NCBI_TaxID=29941;
RN [1]_
RP SEQUENCE FROM N.A.

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RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides."
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159344; AAO22222.1; -.
FT NON TER 1
SQ SEQUENCE 43 AA; 4840 MW; D0651E1523CCE257 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db |:|:|
3 DSCVD 7

RESULT 26
Q86QU8 PRELIMINARY; PRT; 43 AA.
AC Q86QU8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ergtoxin-like protein 3 (Fragment).
GN ERG3.
OS Centruroides limpidus limpidus (Mexican scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthoidea; Butthidae; Centruroides.
OX NCBI_TaxID=29941;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides."
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159345; AAO22223.1; -.
FT NON TER 1
SQ SEQUENCE 43 AA; 4871 MW; DID51E1523C6E2F7 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db |:|:|
3 DSCVD 7

RESULT 27
Q86QU7 PRELIMINARY; PRT; 43 AA.
AC Q86QU7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ergtoxin-like protein 4 (Fragment).
GN ERG4.
OS Centruroides limpidus limpidus (Mexican scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthoidea; Butthidae; Centruroides.
OX NCBI_TaxID=29941;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;

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RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RL blocking peptides from scorpions of the genus Centruroides."
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159346; AAO22224.1; -.
FT NON_TER 1
SQ SEQUENCE 43 AA; 4821 MW; E64B7E1523CCEM4 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
Db 3 DSCVD 7

RESULT 28
Q86QU5
ID Q86QU5 PRELIMINARY; PRT; 43 AA.
AC Q86QU5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ergtoxin-like protein 2 (Fragment).
GN ERG2.
OS Centruroides sculpturatus (bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Centruroides.
OX NCBI_TaxID=218467;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RL blocking peptides from scorpions of the genus Centruroides."
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159348; AAO22226.1; -.
FT NON_TER 1
SQ SEQUENCE 43 AA; 4848 MW; 76905083144D3621 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
Db 3 DSCVD 7

RESULT 29
Q86QU4
ID Q86QU4 PRELIMINARY; PRT; 43 AA.
AC Q86QU4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ergtoxin-like protein 3 (Fragment).
GN ERG3.
OS Centruroides sculpturatus (bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Centruroides.
OX NCBI_TaxID=218467;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;

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RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RL blocking peptides from scorpions of the genus Centruroides."
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159349; AAO22227.1; -.
FT NON_TER 1
SQ SEQUENCE 43 AA; 4827 MW; BDB2808313CD2BA2 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
Db 3 DSCVD 7

RESULT 30
Q86QU3
ID Q86QU3 PRELIMINARY; PRT; 43 AA.
AC Q86QU3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ergtoxin-like protein 4 (Fragment).
GN ERG4.
OS Centruroides sculpturatus (bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Centruroides.
OX NCBI_TaxID=218467;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RL blocking peptides from scorpions of the genus Centruroides."
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AY159350; AAO22228.1; -.
FT NON_TER 1
SQ SEQUENCE 43 AA; 4841 MW; BDB2808313CCF0D2 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
Db 3 DSCVD 7

RESULT 31
Q86QU0
ID Q86QU0 PRELIMINARY; PRT; 43 AA.
AC Q86QU0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ergtoxin-like protein 2 (Fragment).
OS Centruroides sculpturatus (bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Centruroides.
OX NCBI_TaxID=6879;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,

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RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RL blocking peptides from scorpions of the genus Centruroides.";
DR FEBS Lett. 532:121-126(2002).
RL EMBL; AY159353; AAO22231.1; -.
FT NON_TER 1
SQ SEQUENCE 43 AA; 4855 MW; AA3BD8CE23CF0D2 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 3 DSCVD 7

RESULT 32
Q86QT9 PRELIMINARY; PRT; 43 AA.
AC Q86QT9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ergtoxin-like protein 3 (Fragment).
GN ERG3.
OS Centruroides sculpturatus (Bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Centruroides.
OX NCBI_TaxID=6879;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RL blocking peptides from scorpions of the genus Centruroides.";
DR FEBS Lett. 532:121-126(2002).
RL EMBL; AY159354; AAO22232.1; -.
FT NON_TER 1
SQ SEQUENCE 43 AA; 4948 MW; F07B831923CCE244 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 3 DSCVD 7

RESULT 33
Q86QT8 PRELIMINARY; PRT; 43 AA.
AC Q86QT8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ergtoxin-like protein 4 (Fragment).
GN ERG4.
OS Centruroides sculpturatus (Bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Centruroides.
OX NCBI_TaxID=6879;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
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RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RL blocking peptides from scorpions of the genus Centruroides.";
DR FEBS Lett. 532:121-126(2002).
RL EMBL; AY159355; AAO22233.1; -.
FT NON_TER 1
SQ SEQUENCE 43 AA; 4947 MW; F06F3C523CCE244 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 3 DSCVD 7

RESULT 34
O51033 PRELIMINARY; PRT; 43 AA.
ID O51033
AC O51033;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein BBF28.
GN BBF28.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid lp28-1.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=1139;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lachigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Hanson M.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Utterback T., Wattney L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586(1997).
DR EMBL; AE000794; AAC66389.1; -.
DR PIR; A70231; A70231.
DR TIGR; BBF28; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 43 AA; 4811 MW; 27E629767280F538 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 20 DMCRD 24

RESULT 35
O96814 PRELIMINARY; PRT; 44 AA.
ID O96814
AC O96814;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PSII D2 reaction-centre protein (fragment).
GN PSBD.
OS Skeletonema costatum (Marine centric diatom).
OG Chloroplast.
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
OC Thalassiosirophycidae; Thalassiosirales; Skeletonemataceae;
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OC Skeletonema.
OX NCBI_TaxID=2843;
RN [1]
RP STRAIN=NIES 323;
RC STRAIN=NIES 323;
RA Tada N., Otsuka S., Oyaizu H., Matsumoto S.;
RT "Plastid DNA sequences of Skeletonema costatum NIES 323."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132266; CAA10635.1; -
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 44 AA; 5035 MW; 65D5E6BC481FC49 CRC64;

Query Match 100.0%; Score 23; DB 8; Length 44;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
DB 15 DLCD 19

RESULT 36
Q9PB90 PRELIMINARY; PRT; 44 AA.
AC Q9PB90;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein XF2254.
GN XF2254.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5c;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.C., Camargo L.E.A., Carraro D.M., Carver H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neco C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Pacincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A.G., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Paixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesequero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa."
RL Nature 406:151-159 (2000).
DR EMBL; AE004038; AAF85053.1; -
DR FIR; D82579; D82579.
DR GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001969; Asprotease_AS.

DR PROSITE; PS00141; ASP_PROTEASE; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 44 AA; 4646 MW; 94C8A6938789B2E CRC64;

Query Match 100.0%; Score 23; DB 16; Length 44;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
DB 9 DLCD 13

RESULT 37
Q9P0Z7 PRELIMINARY; PRT; 46 AA.
AC Q9P0Z7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Latent transforming growth factor beta binding protein 3
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Saharinen J., Penttinen C., Keski-Oja J.;
RT "Cloning of human LTBP-3."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF135961; AAF62353.2; -
DR HSSP; P35955; 1EMN.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR00152; ASX_hydroxyl_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 1.
DR SMART; SM00179; EGF_Ca; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01186; EGF_2; 1.
KW EGF-like domain.
FT NON TER
FT NON TER
FT NON TER
SQ SEQUENCE 46 AA; 4971 MW; 211C501D8B844A8C CRC64;

Query Match 100.0%; Score 23; DB 4; Length 46;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
DB 2 DECQD 6

RESULT 38
Q86QV1 PRELIMINARY; PRT; 47 AA.
AC Q86QV1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ergotxin-like protein 3 (Fragment).
GN ERG3.
OS Centruroides gracilis (Slenderbrown scorpion) (Florida bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Euthoida; Buthidae; Centruroides.
OX NCBI_TaxID=217898;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,

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RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergotxin-like genes and ERG K $\alpha$ -channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AV159342; AAO22220.1; -.
FT NON_TER 1
SQ SEQUENCE 47 AA; 5116 MW; AA76672DB459108A CRC64;

Query Match 100.0%; Score 23; DB 5; Length 47;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
DB 3 DSCVD 7

RESULT 39
Q86QU2
ID Q86QU2 PRELIMINARY; PRT; 47 AA.
AC Q86QU2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Ergotxin-like protein 5 (fragment).
GN ERGS.
OS Centruroides sculpturatus (bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Centruroides.
OX NCBI_TaxID=218467;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergotxin-like genes and ERG K $\alpha$ -channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
DR EMBL; AV159351; AAO22229.1; -.
FT NON_TER 1
SQ SEQUENCE 47 AA; 5271 MW; 97F44AF20B6CA086 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 47;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
DB 3 DSCVD 7

RESULT 40
Q83DL3
ID Q83DL3 PRELIMINARY; PRT; 47 AA.
AC Q83DL3;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Ergotxin-like protein.
GN CBU0711.
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coxiellaceae; Coxiella.
OX NCBI_TaxID=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nine Mile phase I / RSA 493;
RX MEDLINE=22608657; PubMed=12704232;
RA Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
RA Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J.,

RA DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
RA Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
RT "Complete genome sequence of the Q-fever pathogen, Coxiella
RT burnetii.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
DR EMBL; AE016962; AAO90254.1; -.
DR TIGR; CBU0711; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 47 AA; 5448 MW; 943CB474CAFF062 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 47;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
DB 7 DYCVD 11

RESULT 41
Q7VKA9
ID Q7VKA9 PRELIMINARY; PRT; 47 AA.
AC Q7VKA9;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
GN HD2014.
OS Haemophilus ducreyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=730;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=35000HP / ATCC 700724;
RA Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
RT "The complete genome sequence of Haemophilus ducreyi.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017156; AAP96723.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 47 AA; 5396 MW; A9066DCD0D839864 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 47;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
DB 29 DQCVD 33

RESULT 42
Q87ZLO
ID Q87ZLO PRELIMINARY; PRT; 48 AA.
AC Q87ZLO;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein.
GN PSPT03414.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
RA Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,

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RA White O., Fraser C., Collmer A.;
RT "Complete sequence of pseudomonas syringae.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016968; AAC56892.1; -
DR TIGR; PSPT03414; -
KW Hypochemical protein; Complete proteome.
SQ SEQUENCE 48 AA; 5403 MW; 1D3EBE506CF188FC CRC64;

Query Match 100.0%; Score 23; DB 16; Length 48;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 32 DTCAD 36

RESULT 43
Q8P3Z2 PRELIMINARY; PRT; 50 AA.
AC Q8P3Z2;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Entericidin A
GN ECNA OR XCC3925.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Canargo L.E.A.,
RA Canarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.B., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinoza L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE012513; AAM43147.1; -
DR InterPro; IPR000437; Prok_lipoprot_S.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Complete proteome.
SQ SEQUENCE 50 AA; 5173 MW; 002B2FF8F8DFC4B CRC64;

Query Match 100.0%; Score 23; DB 16; Length 50;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 43 DKCSD 47

RESULT 44
Q87HS5 PRELIMINARY; PRT; 50 AA.
AC Q87HS5;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

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DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN VFA0881.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najiima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; AP005087; BAC62224.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 50 AA; 5945 MW; 0082F9429956CAE CRC64;

Query Match 100.0%; Score 23; DB 16; Length 50;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 37 DECDD 41

RESULT 45
Q9HBW4 PRELIMINARY; PRT; 51 AA.
AC Q9HBW4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE GRAF (Fragment).
GN GRAF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bojesen S.E., Borkhardt A., Fuchs U., Lampert F.;
RT "5' Flanking Region of the Human GRAF Gene.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF196313; AAG30729.2; -
FT NON_TER 51
SQ SEQUENCE 51 AA; 5749 MW; 5A10BDA1B7433E69 CRC64;

Query Match 100.0%; Score 23; DB 4; Length 51;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 10 DCCLD 14

RESULT 46
O95127 PRELIMINARY; PRT; 51 AA.
AC O95127;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Laminin beta-4 chain (Fragment).
GN LAMB4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Olson P.F., Koch M., Champliand M.F., Rowland K., Jin W.,
RA Burgess R.E.;
RT "Cloning and characterization of the human laminin beta-4 chain.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029325; AAC95124.1; -.
DR HSSP; P02468; 1KLO.
FT NON_TER 1
SQ SEQUENCE 51 AA; 5630 MW; B50866B0C31795D0 CRC64;

Query Match 100.0%; Score 23; DB 4; Length 51;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 12 DRCAD 16

RESULT 47
QBVR3
ID Q8MVR3 PRELIMINARY; PRT; 51 AA.
AC Q8MVR3;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Anasigote surface protein (Fragment).
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y;
RA Olivas-Rubio M., Rosales-Encina J.L.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF480942; AA01117.1; -.
FT NON_TER 1
SQ SEQUENCE 51 AA; 5147 MW; 07451B15AEA63590 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 51;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 36 DACRD 40

RESULT 48
OB9063
ID OB9063 PRELIMINARY; PRT; 51 AA.
AC OB9063;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hexokinase type I (EC 2.7.1.1) (Fragment).
GN HK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Spleen;
RX MEDLINE=99012997; PubMed=9798653;
RA Chu C.C., Paul W.E.;
RT "Expressed genes in interleukin-4 treated B cells identified by cDNA
representational difference analysis.";
RL Mol. Immunol. 35:487-502(1998).
DR EMBL; U89409; AAC36516.1; -.

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DR HSSP; P05708; 1BG3.
DR MGD; MGI:96103; Hk1.
DR GO; GO:000524; P:ATP binding; IEA.
DR GO; GO:0004396; P:hexokinase activity; IEA.
DR GO; GO:0016301; P:kinase activity; IEA.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002086; Aldehyde dehydr.
DR InterPro; IPR001312; Hexokinase.
DR Pfam; PF03727; hexokinase2; 1.
DR ProDom; PD001109; Hexokinase; 1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
KW Kinase; Transferase.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 6151 MW; 2F802C9ED8B7913D CRC64;

Query Match 100.0%; Score 23; DB 11; Length 51;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 21 DGCLD 25

RESULT 49
QBCKLO
ID QBCKLO PRELIMINARY; PRT; 51 AA.
AC QBCKLO;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical.
GN Y3358.
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Versinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AE013937; AA086908.1; -.
KW Hypothetical protein.
SQ SEQUENCE 51 AA; 5780 MW; B5A1DF27FCFFBDFC CRC64;

Query Match 100.0%; Score 23; DB 16; Length 51;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 45 DKCED 49

RESULT 50
Q9UHS7
ID Q9UHS7 PRELIMINARY; PRT; 52 AA.
AC Q9UHS7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PRO1992.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
RA He F.;
RT "Functional prediction of the coding sequences of 33 new genes deduced
RT by analysis of cDNA clones from human fetal liver.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF118086; AAF22030.1; -
SQ SEQUENCE 52 AA; 6038 MW; E53FA0ED27A8504C CRC64;

Query Match 100.0%; Score 23; DB 4; Length 52;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 42 DLCPD 46

RESULT 51
Q853J6 PRELIMINARY; PRT; 53 AA.
ID Q853J6
AC Q853J6
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Gp81.
OS Mycobacteriophage Bx1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=205877;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22592660; PubMed=12705866;
RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
RA Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
RA Hatfull G.F.;
RT "Origins of highly mosaic mycobacteriophage genomes.";
RL Cell 113:171-182(2002).
DR EMBL; AY129337; AANI6741.1; -
SQ SEQUENCE 53 AA; 5990 MW; 9F017997D0603D70 CRC64;

Query Match 100.0%; Score 23; DB 9; Length 53;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 32 DACLD 36

RESULT 52
Q8RYU2 PRELIMINARY; PRT; 53 AA.
ID Q8RYU2
AC Q8RYU2
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE B1156H12.4 protein.
GN B1156H12.4.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC
RT clone:B1156H12.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004225; BAB90671.1; -
DR Gramene; Q8RYU2; -
SQ SEQUENCE 53 AA; 5691 MW; AC911587F53C3A7F CRC64;

Query Match 100.0%; Score 23; DB 10; Length 53;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 43 DICDD 47

RESULT 53
Q8R194 PRELIMINARY; PRT; 53 AA.
ID Q8R194
AC Q8R194
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025010; AAH25010.1; -
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 53 AA; 5654 MW; 3CF6B0P82CDF02C CRC64;

Query Match 100.0%; Score 23; DB 11; Length 53;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 7 DCCQD 11

RESULT 54
Q8PU57 PRELIMINARY; PRT; 53 AA.
ID Q8PU57
AC Q8PU57
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative ferredoxin.
GN MM2492.
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartach T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wiszer A., Baumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
RA Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
RT transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).

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DR EMBL; AE013493; AAM3188.1; -.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; fer4; 2.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 53 AA; 5568 MW; 007C79EC7454FCF8 CRC64;

Query Match 100.0%; Score 23; DB 17; Length 53;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 32 DACVD 36

RESULT 55
Q9H2D8 PRELIMINARY; PRT; 54 AA.
AC Q9H2D8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE Hypothetical protein Cpn0745.
GN CPN0745 OR CPJ0745 OR CPJ127 OR CPB0773.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=TW-183;
RA Geng M.M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RT other Chlamydia strains based on whole genome sequence analysis.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE001656; AAD18884.1; -.
DR EMBL; AE002268; AAF38893.1; -.
DR EMBL; AP002547; BAA98952.1; -.
DR EMBL; AE017159; AAP98702.1; -.
DR PIR; F86583; F86583.
DR PIR; G72040; G72040.
DR TIGR; CP1127; -.
KW Hypothetical protein; Complete proteome.

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SQ SEQUENCE 54 AA; 6216 MW; F14E63F22AA779B9 CRC64;
Query Match 100.0%; Score 23; DB 16; Length 54;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 2 DSCFD 6

RESULT 58
Q98JC8
ID Q98JC8 PRELIMINARY; PRT; 54 AA.
AC Q98JC8
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Vng1376h.
GN VNG1376H.
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1] _
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Balliga N.S., Thorsson V., Shrogha J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauer B., Keller K., Cruz R., Danson M.J., Hough D.W.A.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isebaertger T.A., Peck R.F., Pohlshroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.W., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR PIR; C84292; C84292.
DR InterPro; IPR007087; Znf_C2H2.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
KW Complete proteome.
SQ SEQUENCE 54 AA; 6036 MW; 53CCA1B1534E81AE CRC64;

Query Match 100.0%; Score 23; DB 17; Length 54;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 6 DGCID 10

RESULT 59
Q98JC8
ID Q98JC8 PRELIMINARY; PRT; 55 AA.
AC Q98JC8
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical protein msr2002.
GN MSR2002.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1] _
RP SEQUENCE FROM N.A.
RX STRAIN=MAF303099; PubMed=11214968;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
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RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL; AP002998; BAB49238.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 55 AA; 6551 MW; A2E1BA22114268F CRC64;
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Query Match 100.0%; Score 23; DB 16; Length 55;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DXCXD 5
Db 23 DLCD 27
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RESULT 60

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Q8ZNX9
ID Q8ZNX9 PRELIMINARY; PRT; 55 AA.
AC Q8ZNX9
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Lytic enzyme.
GN STMI868A.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1] _
RP SEQUENCE FROM N.A.
RX STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
DR EMBL; AE008783; AAL20783.1; -.
KW Complete proteome.
SQ SEQUENCE 55 AA; 6076 MW; 2F9311CFA493BD0 CRC64;
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Query Match 100.0%; Score 23; DB 16; Length 55;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DXCXD 5
Db 28 DECLD 32
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RESULT 61

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Q8XSR6
ID Q8XSR6 PRELIMINARY; PRT; 55 AA.
AC Q8XSR6
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Probable lipoprotein.
GN RSP0401 OR RSP0829.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1] _
RP SEQUENCE FROM N.A.
RX STRAIN=GM11000;
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RX MEDLINE=21681879; PubMed=11823852;
RA Saldoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502 (2002).
DR EMBL; AL646078; CAD17552.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR000437; Prok_lipoprot_S.
DR InterPro; IPR000600; ROK.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
DR PROSITE; PS01125; ROK; 1.
KW Plasmid; Complete proteome.
SQ SEQUENCE 55 AA; 5415 MW; CCF80FE2F8030456 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 55;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 48 DACAD 52

RESULT 62
O87086 PRELIMINARY; PRT; 57 AA.
AC O87086
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ferredoxin (Fragment).
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HH1;
RX MEDLINE=93320944; PubMed=8458843;
RA Ueda K., Miyake K., Horinouchi S., Beppu T.;
RT "A gene cluster involved in aerial mycelium formation in Streptomyces griseus encodes proteins similar to the response regulators of Two-component regulatory systems and membrane translocators.";
RL J. Bacteriol. 175:2006-2016 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HH1;
RX MEDLINE=98422460; PubMed=9748440;
RA Ueda K., Hahne C.-W., Tosaki T., Shinkawa H., Beppu T., Horinouchi S.;
RT "Characterization of an A-factor-responsive repressor for amFR essential for onset of aerial mycelium formation in Streptomyces griseus.";
RL J. Bacteriol. 180:5085-5093 (1998).
DR EMBL; AB006206; BAA33533.3; -.
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6375 MW; FDFE72FBCD76C170 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 57;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 38 DECVD 42

RESULT 63
Q95MD7 PRELIMINARY; PRT; 57 AA.
ID Q95MD7

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AC Q95MD7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase-related protein 1 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Schmutz S.M., Berryere T.G., Schimpf R.J.;
RT "Sequence analysis and mapping of TYRPI in cattle.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF398512; AAK94986.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
FT NON_TER 1 1
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6435 MW; F4C2C7E34FAADFBA CRC64;

Query Match 100.0%; Score 23; DB 6; Length 57;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 12 DICTD 16

RESULT 64
Q8W066 PRELIMINARY; PRT; 57 AA.
ID Q8W066
AC Q8W066
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P0014E08.2 protein (OSJNB0063G05.18 protein).
GN P0014E08.2 OR OSJNB0063G05.18.
OS Oryza sativa (Rice), and
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530, 39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC clone: P0014E08.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC clone: OSJNB0063G05.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004194; BAB84491.1; -.
DR EMBL; AP003760; BAB90509.1; -.
DR Gramene; Q8W066; -.
SQ SEQUENCE 57 AA; 6195 MW; D6A1C334912230CE CRC64;

Query Match 100.0%; Score 23; DB 10; Length 57;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5

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Db      17 DSCRD 21
|:|:|
|:|:|

RESULT 65
Q08060
ID Q08060 PRELIMINARY; PRT; 57 AA.
AC Q08060;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative glyceraldehyde-3-phosphate dehydrogenase (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Leaves and sheaths of upper twelve nodes;
RX MEDLINE=94105294; PubMed=8278499;
RA Keith C.S., Hoang D.O., Barrett B.M., Feigelman B., Nelson M.C.,
RA Thai H., Baysdorfer C.;
RT "Partial sequence analysis of 130 randomly selected maize cDNA
RT clones.";
RL Plant Physiol. 101:329-332(1993).
DR EMBL; M95076; AA072117.1; -.
DR PIR; T03654; T03654.
DR HSSP; P00354; 3GPD.
DR InterPro; IPR003823; Unk_CP12.
DR Pfam; PF02672; CP12; 1.
FT NON TER 1
SQ SEQUENCE 57 AA; 6287 MW; 118C888E3ECA1C18 CRC64;

Query Match 100.0%; Score 23; DB 10; Length 57;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
|:|:|
DB 41 DFCKD 45

RESULT 66
Q9K0Y7
ID Q9K0Y7 PRELIMINARY; PRT; 58 AA.
AC Q9K0Y7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein NMB0417.
GN NMB0417.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Citrone H., Clark E.B.,
RA Cotton M.D., Uterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Masignani V., Pizzo M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815(2000).
DR EMBL; AE002397; AAF40855.1; -.
DR PIR; E81202; E81202.

DR TIGR; NMB0417; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 58 AA; 6398 MW; 27B295981AF8879 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 58;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
|:|:|
DB 33 DLCLD 37

RESULT 67
Q8TIF8
ID Q8TIF8 PRELIMINARY; PRT; 58 AA.
AC Q8TIF8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ferredoxin.
GN MA4194.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talanas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Graham D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE011131; AA07540.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001080; 3Fe4S_ferredoxin.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; fer4; 2.
DR PRINTS; PR00352; 3FE4SFRDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW Complete proteome.
SQ SEQUENCE 58 AA; 5812 MW; 3792A76E103A8ED7 CRC64;

Query Match 100.0%; Score 23; DB 17; Length 58;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
|:|:|
DB 38 DECLD 42

RESULT 68
Q8PYU1
ID Q8PYU1 PRELIMINARY; PRT; 58 AA.
AC Q8PYU1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ferredoxin.
GN MM0760.

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OS Methanosarcina maezi (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wierzer A., Baeumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
RA Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina maezi: evidence for lateral gene
RT transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AE013301; AAM30456.1; -.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001080; 3Fe4S_ferredoxin.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; fer4; 2.
DR PRINTS; PR00352; 3FE4SFRDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW Complete proteome.
SQ SEQUENCE 58 AA; 5809 MW; 897B8FDDAAE1F906 CRC64;

Query Match 100.0%; Score 23; DB 17; Length 58;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 38 DECLD 42

RESULT 69
Q8B442 PRELIMINARY; PRT; 59 AA.
AC Q8B442;
DT 01-WAR-2003 (TReMBLrel. 23, Created)
DT 01-WAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-WAR-2003 (TReMBLrel. 23, Last annotation update)
DE Truncated UL128.
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3157;
RA Akter P., Cunningham C., McSharry B.P., Dolan A., Addison C.,
RA Dargan D.J., Hassan-Walker A.F., Emery V.C., Griffiths P.D.,
RA Wilkinson G.W., Davison A.J.;
RA "Two novel spliced genes in human cytomegalovirus.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY169795; AAO11755.1; -.
SQ SEQUENCE 59 AA; 6993 MW; D63768A1B4348439 CRC64;

Query Match 100.0%; Score 23; DB 12; Length 59;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 41 DRCYD 45

RESULT 70
Q7UFE3 PRELIMINARY; PRT; 59 AA.
ID Q7UFE3
AC Q7UFE3;
DT 01-OCT-2003 (TReMBLrel. 25, Created)

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DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN RB10167.
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294151; CAD78739.1; -.
KW EMBL; Complete proteome.
SQ SEQUENCE 59 AA; 6356 MW; C56F884663D661CA CRC64;

Query Match 100.0%; Score 23; DB 16; Length 59;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 42 DRCSD 46

RESULT 71
Q8TTH2 PRELIMINARY; PRT; 59 AA.
AC Q8TTH2;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Ferredoxin.
GN MA0463.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nuebaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Krzycki J.A.,
RA Hedderich R., Ingram-Smith C., Kuettnner H.C., Guss A.M.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RA "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE010706; AAM03909.1; -.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001080; 3Fe4S_ferredoxin.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR00813; 7Fe_ferredoxin.
DR Pfam; PF00037; fer4; 2.
DR PRINTS; PR00352; 3FE4SFRDOXIN.
DR PRINTS; PR00353; 4FE4SFRDOXIN.
DR PRINTS; PR00354; 7FE4SFRDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.

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KW Complete proteome.
SQ SEQUENCE 59 AA; 6096 MW; 89BDD8927B00CFEA CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 17; Length 59;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 39 DECDV 43

RESULT 72
Q8PND7 PRELIMINARY; PRT; 59 AA.
ID Q8PND7
AC Q8PND7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Ferredoxin.
GN NM1652.
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gel / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wierze A., Baeumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Friez H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
RT transfer between Bacteria and Archaea."
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AF013400; AM31348.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR000813; 7Fe_ferredoxin.
DR Pfam; PF00037; fer4; 2.
DR PRINTS; PR00354; 7FE8SFRDXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW Complete proteome.
SQ SEQUENCE 59 AA; 6168 MW; 0F63B489FC46997D CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 17; Length 59;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 39 DECDV 43

RESULT 73
Q9JSZ2 PRELIMINARY; PRT; 60 AA.
AC Q9JSZ2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Putative periplasmic protein.
GN NMA2067.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / Serogroup A / Serotype 4A;

KW Complete proteome.
SQ SEQUENCE 59 AA; 6096 MW; 89BDD8927B00CFEA CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 17; Length 59;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 39 DECDV 43

RESULT 72
Q8PND7 PRELIMINARY; PRT; 59 AA.
ID Q8PND7
AC Q8PND7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Ferredoxin.
GN NM1652.
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gel / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wierze A., Baeumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Friez H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
RT transfer between Bacteria and Archaea."
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AF013400; AM31348.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR000813; 7Fe_ferredoxin.
DR Pfam; PF00037; fer4; 2.
DR PRINTS; PR00354; 7FE8SFRDXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW Complete proteome.
SQ SEQUENCE 59 AA; 6168 MW; 0F63B489FC46997D CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 17; Length 59;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 39 DECDV 43

RESULT 73
Q9JSZ2 PRELIMINARY; PRT; 60 AA.
AC Q9JSZ2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Putative periplasmic protein.
GN NMA2067.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / Serogroup A / Serotype 4A;

KW Complete proteome.
SQ SEQUENCE 60 AA; 6547 MW; 27B0216187B2EE34 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 16; Length 60;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 35 DLCLD 39

RESULT 74
Q8XN68 PRELIMINARY; PRT; 61 AA.
ID Q8XN68
AC Q8XN68;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Hypothetical protein CPE0470.
GN CPE0470.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003186; BAB80176.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 61 AA; 6856 MW; ED20E3770F0AD6F1 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 16; Length 61;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 45 DCCDD 49

RESULT 75
Q87SC2 PRELIMINARY; PRT; 61 AA.
ID Q87SC2
AC Q87SC2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Hypothetical protein.
GN VP0502.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=KIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
DR EMBL; AP005074; BAC58765.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 61 AA; 7389 MW; 9D179435E86F95C5 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 61;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 49 DVCND 53

RESULT 76
Q86QT3 PRELIMINARY; PRT; 62 AA.
AC Q86QT3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ergotoxin-like protein 1.
GN ERG1.
OS Centruroides noxius (Mexican scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Centruroides.
OX NCBI_TaxID=6878;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergotoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126 (2002).
DR EMBL; AV164271; AAO22234.1; -.
SQ SEQUENCE 62 AA; 6970 MW; 53F88F4B9F187E37 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 62;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 23 DSCVD 27

RESULT 77
Q7YV8 PRELIMINARY; PRT; 62 AA.
AC Q7YV8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN TB927.2.3240.
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUT10.1;
RT "The genomic sequence and characterization of a novel AIBV.";
RA El-Sayed N.M.A., Ghedin E., Song J., MacLeod A., Bringaud F.,

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RA Larkin C., Wanless D., Peterson J., Hou L., Taylor S., Tweedie A.,
RA Biteau N., Khalak H.G., Lin X., Mason T., Hannick L., Cater E.,
RA Blandin G., Bartholomeu D., Simpson A.J., Kaul S., Zhao H., Pai G.,
RA Van Aken S., Utterback T., Haas B., Koo H.L., Umayam L., Suh B.,
RA Gerrard C., Leech V., Qi R., Zhou S., Schwartz D., Feldblyum T.,
RA Salzberg S., Tait A., Turner M.R., Ullu E., White O., Melville S.,
RA Adams M.D., Fraser C.M., Donelson J.E.;
RT "The sequence and analysis of Trypanosoma brucei chromosome II.";
RL Nucleic Acids Res. 0:0-0 (2003).
DR EMBL; AE017168; AAQ15781.1; -.
KW Hypothetical protein.
SQ SEQUENCE 62 AA; 7012 MW; EE686BDD6171427E CRC64;

Query Match 100.0%; Score 23; DB 5; Length 62;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 20 DQCVD 24

RESULT 78
Q36357 PRELIMINARY; PRT; 62 AA.
AC Q36357;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Putative immediate early ORF57 protein (Fragment).
OS Alcelaphine herpesvirus 1 (wildbeest herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=35252;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404659; PubMed=9261371;
RA Esser A., Pflanz R., Fleckenstein B.;
RT "Primary structure of the alcelaphine herpesvirus 1 genome.";
RL J. Virol. 71:6517-6525 (1997).
DR EMBL; AF005362; AAC58050.1; -.
FT NON_TER 62
SQ SEQUENCE 62 AA; 6848 MW; 51A2963E7E08AAA4 CRC64;

Query Match 100.0%; Score 23; DB 12; Length 62;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 44 DDCMD 48

RESULT 79
Q7T831 PRELIMINARY; PRT; 62 AA.
AC Q7T831;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 3b protein.
OS Avian infectious bronchitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11120;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BJ;
RA Jin W.W., Chen C., Zhang Y., Zhao Y.Q., Chen F.Y., Feng J.D.,
RA Yang H.C., Yu J.L., Wu Q.M., Wang M., Li N., Gong Y.S., Sun Q.X.,
RA Chen Z.L.;
RT "The genomic sequence and characterization of a novel AIBV.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBSJ databases.

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DR EMBL; AY319651; AAP92677.1; -.
SQ SEQUENCE 62 AA; 7188 MW; 8A6EB91085BBE2E5 CRC64;

Query Match 100.0%; Score 23; DB 12; Length 62;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 54 DDCSD 58
[1] [1]

RESULT 80
Q9HQH6 PRELIMINARY; PRT; 62 AA.
AC Q9HQH6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE S0S ribosomal protein L24E (LSU ribosomal protein L24E).
GN RPL24E OR VNG1159G.
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081), and
OS Halobacterium cutirubrum.
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091, 2242;
[1] [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Halobacterium sp. (strain NRC-1);
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J.A., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Madocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=H. cutirubrum;
RA Ishibashi M., Hiratauka K., Yonezawa Y., Tokunaga H., Tokunaga M.;
RT "NDK from Halobacterium cutirubrum.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE005044; AAG19539.1; -.
DR EMBL; AB036344; BAB17307.1; -.
DR PIR; G84271; G84271.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000988; Ribosomal_L24E.
DR Pfam; PF01246; Ribosomal_L24E; 1.
DR PROSITE; PS01073; RIBOSOMAL_L24E; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 62 AA; 6993 MW; EE6FE3E4C23984C7 CRC64;

Query Match 100.0%; Score 23; DB 17; Length 62;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 8 DYCD 12
[1] [1]

RESULT 81
Q95PA2 PRELIMINARY; PRT; 63 AA.
AC Q95PA2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PC4-1 protein (Fragment).
GN PC4-1.
OS Bradysea hygida.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Sciaroidea; Sciaridae;
OC Bradysea.
OX NCBI_TaxID=35572;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95393845; PubMed=7664619;
RA Monesi N., Fernandez M.A., Fontes A.M., Basso L.R. Jr., Nakanishi Y.,
RA Baron B., Buttin G., Faco-Larson M.L.;
RT "Molecular characterization of an 18 kb segment of DNA puff C4 of
RT Bradysea hygida (Diptera, sciaridae).";
RL Chromosoma 103:715-724(1995).
DR EMBL; U13892; AAA83555.2; -.
FT NON TER 63
SQ SEQUENCE 63 AA; 7147 MW; C7E64D47D3179F49 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 63;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 41 DDCDD 45
[1] [1]

RESULT 82
Q7T9R1 PRELIMINARY; PRT; 63 AA.
AC Q7T9R1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ORF 104.
OS Adoxophyes orana granulovirus (AoGV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=170617;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22728233; PubMed=12842624;
RA Wormleaton S., Kuzio J., Winstanley D.;
RT "The complete sequence of the Adoxophyes orana granulovirus genome.";
RL Virology 311:350-365(2003).
DR EMBL; AF547984; AAP85741.1; -.
SQ SEQUENCE 63 AA; 6911 MW; EDE1E7684AC2EC48 CRC64;

Query Match 100.0%; Score 23; DB 12; Length 63;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 6 DSCLD 10
[1] [1]

RESULT 83
Q96RF1 PRELIMINARY; PRT; 64 AA.
AC Q96RF1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HEJ1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RA Rhodes C.H., Call K.M., Little R., Braunschweiger K., Park J.P.;
RT "NOR3: a novel olfactomedin/noselin/pancortin homolog identified near
RL an appendymoma-associated translocation breakpoint.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF395440; AAK73122.1; -
SQ SEQUENCE 64 AA; 7298 MW; 3CAE1FF088C658B6 CRC64;

Query Match 100.0%; Score 23; DB 4; Length 64;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 38 DRCED 42

RESULT 84
Q9SPF8 PRELIMINARY; PRT; 64 AA.
AC Q9SPF8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Elongation factor eEF1 gamma chain (Fragment).
GN EEF1-GAMMA.
OS Vitis labrusca x Vitis vinifera.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Vitaceae; Vitis.
OX NCBI_TaxID=105599;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Kyoho;
RA Pyee J.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF176496; AD54312.1; -
DR GO; GO:0005853; C:eukaryotic translation elongation factor 1 . . . ; IEA.
DR GO; GO:0003746; P:translation elongation factor activity; IEA.
DR GO; GO:0006414; P:translational elongation; IEA.
DR InterPro; IPR001662; EF1.G.
DR ProDom; PD006217; EF1.G; 1.
FT NON_TER 1
SQ SEQUENCE 64 AA; 7673 MW; 0FA06547FA4CEBBA CRC64;

Query Match 100.0%; Score 23; DB 10; Length 64;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 14 DECXD 18

RESULT 85
Q9PRY3 PRELIMINARY; PRT; 65 AA.
AC Q9PRY3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MT2-MUSCARINIC toxin/acetylcholine receptor binding protein.
OS Dendroaspis angusticeps (Eastern green mamba).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Dendroaspis.
OX NCBI_TaxID=8618;
RN [1]
RP SEQUENCE.
RX MEDLINE=94205875; PubMed=8154745;
RA Karlsson E., Jolkonen M., Satyapan N., Adem A., Kumlin E.,
RA Hellman U., Wernstedt C.;
RL Ann. N.Y. Acad. Sci. 710:153-161(1994).
DR HSP; P01382; INTN.

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DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR003572; Cytotoxin.
DR InterPro; IPR003571; Snake_toxin.
DR Pfam; PF00087; toxin; 1.
DR PRINTS; PR00282; CYTOTOXIN.
DR ProDom; PD000206; Snake toxin; 1.
DR PROSITE; PS00272; SNAKE_TOXIN; 1.
SQ SEQUENCE 65 AA; 7084 MW; 3C76802D5B32E978 CRC64;

Query Match 100.0%; Score 23; DB 13; Length 65;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 61 DKCND 65

RESULT 86
P72838 PRELIMINARY; PRT; 65 AA.
ID P72838;
AC P72838;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein ssr2153.
GN SSR2153.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hikosawa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Taniguchi A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90901; BAA16853.1; -.
DR PIR; S74702; S74702.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 65 AA; 7131 MW; 248DDCFE5C0E3B85 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 65;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 61 DDCRD 65

RESULT 87
Q8X3J3 PRELIMINARY; PRT; 65 AA.
ID Q8X3J3;
AC Q8X3J3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein z4950.
GN Z4950.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Genome 409:529-533 (2001).
DR EMBL; AE005579; AAG58677.1; -.
DR PIR; A86027; A86027.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 65 AA; 6887 MW; 774D9830B5225A9CB CRC64;

Query Match 100.0%; Score 23; DB 16; Length 65;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 37 DCPD 41

RESULT 88
Q7VL66 PRELIMINARY; PRT; 65 AA.
AC Q7VL66;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DE Hypothetical protein.
GN HD1615
OS Haemophilus ducreyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=730;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=35000HP / ATCC 700724;
RA Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
RT "The complete genome sequence of Haemophilus ducreyi.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017155; AAP96393.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 65 AA; 7365 MW; 44F75287FA4D3EEE CRC64;

Query Match 100.0%; Score 23; DB 16; Length 65;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 45 DYCLD 49

RESULT 89
Q8TNN8 PRELIMINARY; PRT; 65 AA.
AC Q8TNN8;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DE Ferredoxin.
GN MA2245.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;

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RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeAtellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Haddarich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542 (2002).
DR EMBL; AE010911; AAM05640.1; -.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; fer4; 2.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
KW Complete proteome.
SQ SEQUENCE 65 AA; 6808 MW; E379D19912C469DB CRC64;

Query Match 100.0%; Score 23; DB 17; Length 65;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 38 DKCND 42

RESULT 90
Q8SBL8 PRELIMINARY; PRT; 66 AA.
AC Q8SBL8;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DE Gp36 protein.
OS Bacteriophage phi3626.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=190478;
RN [1]
RP SEQUENCE FROM N.A.
RA Zimmer M., Scherer S., Loesner M.J.;
RT "Bacteriophage phi3626 complete genome.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY082070; AAL96806.1; -.
SQ SEQUENCE 66 AA; 7937 MW; DC017790FF0158A3 CRC64;

Query Match 100.0%; Score 23; DB 9; Length 66;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 18 DICKD 22

RESULT 91
Q9PYQ3 PRELIMINARY; PRT; 66 AA.
AC Q9PYQ3;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TremBLrel. 22, Last annotation update)
DE ORF143.
OS Xestia c-nigrum granulosis virus (XnGV) (Xestia c-nigrum
OS Granulovirus).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=51677;

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RN  SEQUENCE FROM N.A.
RP  MEDLINE=99434230; PubMed=10502508;
RA  Hayakawa T., Ko R., Okano K., Seong S.I., Goto C., Maeda S.;
RT  "Sequence analysis of the Xestia c-nigrum granulovirus genome.";
RL  Virology 262:277-297(1999);
DR  EMBL; AF162221; AAF05257.1;
SQ  SEQUENCE 66 AA; 7457 MW;  DD814F5A3F0ABE10 CRC64;

Query Match      100.0%; Score 23; DB 12; Length 66;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 DXCXD 5
DB  6 DNCMD 10

RESULT 92
Q95557 PRELIMINARY; PRT; 67 AA.
AC Q95557;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE GM08588P.
GN BCDNA:GM08588.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN  SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnikier S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY060947; AAL28495.1;
DR FlyBase; FBgn0047260; BCDNA:GM08588.
DR InterPro; IPR006629; LITAF.
DR SMART; SM00714; LITAF; 1.
SQ SEQUENCE 67 AA; 7533 MW;  58654467C32A8805 CRC64;

Query Match      100.0%; Score 23; DB 5; Length 67;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 DXCXD 5
DB  46 DDCMD 50

RESULT 93
Q9H131 PRELIMINARY; PRT; 67 AA.
AC Q9H131;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vng6391h (Vng1651h) (Vng0210h) (Vng0994h) (Vng1007h) (Vng6093h)
DE (Vng6098h) (Vng6141h) (Vng6146h).
GN VNG6391H OR VNG1651H OR VNG0210H OR VNG0994H OR VNG1007H OR VNG6093H
GN OR VNG6098H OR VNG6141H OR VNG6146H.
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OG Plasmid pNRC200.
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
[1]
RN  SEQUENCE FROM N.A.

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RX  MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welter R., Goo Y.A.,
RA Leitchauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Studich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebnhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005167; AAG21004.1;
DR EMBL; AE005074; AAG19906.1;
DR EMBL; AE004986; AAG18818.1;
DR EMBL; AE005035; AAG19411.1;
DR EMBL; AE005036; AAG19423.1;
DR EMBL; AE005146; AAG20778.1;
DR EMBL; AE005146; AAG20782.1;
DR EMBL; AE005150; AAG20814.1;
DR EMBL; AE005150; AAG20819.1;
DR PIR; G84255; G84255.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid; Complete proteome.
SQ SEQUENCE 67 AA; 7660 MW;  7292F0B54D2D3E5F CRC64;

Query Match      100.0%; Score 23; DB 17; Length 67;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 DXCXD 5
DB  23 DECSD 27

RESULT 94
Q8VBV2 PRELIMINARY; PRT; 68 AA.
AC Q8VBV2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Anti-microbial-like protein BIN-1B.
GN BIN-1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN  SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Caput epididymis;
RA Li P., Shang Q., Zhang Y.D., Zhang Y.L.;
RT "Genomic DNA cloning of a rat epididymis-specific gene (Bin-1b).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN  SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Caput epididymis;
RA Li P., He B., Zhang Y.D., Zhang Y.L.;
RT "Cloning and characterization of a rat epididymis caput region-
RT specific cDNA (Bin-1b).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF217089; AAL55637.1;
DR EMBL; AF217088; AAL55636.1;
SQ SEQUENCE 68 AA; 7799 MW;  86BBCC7A5D2PA53E CRC64;

Query Match      100.0%; Score 23; DB 11; Length 68;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 DXCXD 5
DB  50 DICSD 54

```

RESULT 95

Q8U5J9 PRELIMINARY; PRT; 68 AA.
 AC Q8U5J9;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE AGR_C_892p.
 GN AGR_C_892.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursun J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58."
 RL Science 294:2323-2328(2001).
 DR EMBL; AF007986; AAK86318.1; -.
 DR PIR; E97420; E97420.
 SQ SEQUENCE 68 AA; 7282 MW; CEABF57B7BA6C5D7 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 68;
 Best Local Similarity 60.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
 |::|
 Db 3 DPCGD 7

RESULT 96

Q89GX8 PRELIMINARY; PRT; 68 AA.
 AC Q89GX8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Bst6217 protein.
 GN BSR6217.
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=USDA 110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Sasaki T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Idegawa K., Iriuchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada I., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110."
 RL DNA Res. 9:189-197(2002).
 DR EMBL; AP005957; BAC51482.1; -.
 KW Complete proteome.
 SQ SEQUENCE 68 AA; 7440 MW; CAB6CEB6491B7BA CRC64;

Query Match 100.0%; Score 23; DB 16; Length 68;
 Best Local Similarity 60.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
 |::|
 Db 6 DPCYD 10

RESULT 97

Q7UP61 PRELIMINARY; PRT; 68 AA.
 AC Q7UP61;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN RB7136.
 OS Rhodopirellula baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schliesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 RT strain 1."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 DR EMBL; BX294145; CAD75201.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 68 AA; 7499 MW; C09D89504F60940C CRC64;

Query Match 100.0%; Score 23; DB 16; Length 68;
 Best Local Similarity 60.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
 |::|
 Db 9 DSCSD 13

RESULT 98

Q8WWM0 PRELIMINARY; PRT; 69 AA.
 AC Q8WWM0;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE XAGE-4 protein (Fragment).
 GN XAGE-4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zandman A.J.W., van Kraats A.A., Weidle U.H., Ruiter D.J.,
 RA Van Muijen G.N.P.;
 RT "Expression profile and alignment of the XAGE family of cancer/testis
 RT associated genes."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ318895; CAC83092.1; -.
 DR InterPro; IPR008625; GAGE.
 DR Pfam; PF05831; GAGE; 1.
 FT NON_TER 1
 FT NON_TER 69
 SQ SEQUENCE 69 AA; 7621 MW; 698F06B9B400E650 CRC64;

Query Match 100.0%; Score 23; DB 4; Length 69;
 Best Local Similarity 60.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
 |::|
 Db 49 DECSD 53


```
RESULT 99
Q8K4N2
ID Q8K4N2 PRELIMINARY; PRT; 69 AA.
AC Q8K4N2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE EP2e (ANTI-microbial-like protein BIN-1B homolog).
GN 9230111C08RIK OR MEP2E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epididymis;
RX MEDLINE=22181517; PubMed=12193721;
RA Yamaguchi Y., Nagase T., Makita R., Fukuhara S., Tomita T.,
RA Tominaga T., Kurihara H., Ouchi Y.;
RT "Identification of Multiple Novel Epididymis-Specific beta-Defensin
RT Isoforms in Humans and Mice.";
RL J. Immunol. 169:2516-2523(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Epididymis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AB089183; BAC10633.1; --
DR EMBL; AK020333; BAC25623.1; --
DR MGD; MGI:1925378; 9230111C08RIK.
SQ SEQUENCE 69 AA; 7901 MW; 635BBS249FF84F49 CRC64;

Query Match 100.0%; Score 23; DB 11; Length 69;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 50 DICSD 54

RESULT 100
Q9U9T5
ID Q9U9T5 PRELIMINARY; PRT; 70 AA.
AC Q9U9T5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Lox4 homeobox protein (Fragment).
DE Lox4.
GN LOX4.
OS Nereis virens (Sandworm).
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;
OC Phyllodoceida; Nereididae; Nereis.
OX NCBI_TaxID=6353;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99318125; PubMed=10391241;
RA de Rosa R., Grenier J.K., Andreeva T., Cook C.E., Adoutte A., Akam M.,
RA Carroll S.B., Balavoine G.;
RT "Hox genes in brachiopods and priapulids and protostome evolution.";
RL Nature 399:772-776(1999).
DR EMBL; AF151670; AAD46173.1; --
DR GO; GO:0005634; C:nucleus; IEA.
DR DR GO; GO:0003700; F:transcription factor activity; IEA.
DR DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
```

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KW DNA-binding; Homeobox; Nuclear protein.
FT NON TER 1
SQ SEQUENCE 70 AA; 8384 MW; 08096EF49A1CC3D2 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 70;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 43 DECSD 47

Search completed: May 6, 2004, 10:46:49
Job time : 47 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2004, 10:41:40 ; Search time 11 seconds
(without alignments)
23.668 Million cell updates/sec

Title: SEQ1

Perfect score: 23

Sequence: 1 dxcxd 5

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 76

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 1000 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	23	100.0	15	1	ITRB_ALBUJU
2	23	100.0	24	1	SCX5_BUTOC
3	23	100.0	36	1	SCX8_BUTOC
4	23	100.0	36	1	TXD3_PARLU
5	23	100.0	37	1	ME20_EUPRA
6	23	100.0	38	1	IDSB_PROJU
7	23	100.0	42	1	ILLB_LEUGL
8	23	100.0	42	1	SEK1_CENEL
9	23	100.0	42	1	SEK1_CENEL
10	23	100.0	42	1	SEK1_CENGR
11	23	100.0	42	1	SEK1_CENLL
12	23	100.0	42	1	SEK1_CENSC
13	23	100.0	42	1	SEK2_CENGR
14	23	100.0	43	1	SEK2_CENEL
15	23	100.0	43	1	SEK2_CENEX
16	23	100.0	43	1	SEK2_CENLL
17	23	100.0	43	1	SEK2_CENSC
18	23	100.0	43	1	SEK3_CENEL
19	23	100.0	43	1	SEK3_CENEX
20	23	100.0	43	1	SEK3_CENLL
21	23	100.0	43	1	SEK3_CENNO
22	23	100.0	43	1	SEK3_CENSC
23	23	100.0	43	1	SEK4_CENEX
24	23	100.0	43	1	SEK4_CENLL
25	23	100.0	43	1	SEK4_CENNO
26	23	100.0	43	1	SEK4_CENSC
27	23	100.0	43	1	SEK5_CENNO
28	23	100.0	47	1	SEK3_CENGR
29	23	100.0	47	1	SEK5_CENSC
30	23	100.0	47	1	TX45_PHONI
31	23	100.0	54	1	FER_MEGEL
32	23	100.0	54	1	FER_PEPAS
33	23	100.0	55	1	FER1_RHOUR

34	23	100.0	55	1	FER_CLOAC	P00198 clostridium
35	23	100.0	55	1	FER_CLOBU	P00196 clostridium
36	23	100.0	55	1	FER_CLOPA	P00195 clostridium
37	23	100.0	55	1	FER_CLOPE	P22846 clostridium
38	23	100.0	55	1	FER_CLOSP	P00197 clostridium
39	23	100.0	55	1	FER_CLOTS	P00200 clostridium
40	23	100.0	57	1	YA95_PASMU	Q9C1V6 pasteurella
41	23	100.0	62	1	SEK1_CENNO	Q86qt3 centruiroide
42	23	100.0	63	1	SCXV_CENSC	P46066 centruiroide
43	23	100.0	64	1	IBB1_COILA	P07679 coix lachry
44	23	100.0	65	1	SIX1_BUTOC	P55902 buthus occi
45	23	100.0	74	1	Y777_TREPA	O83756 treponema p
46	23	100.0	76	1	ISE1_HUMAN	O43715 homo sapien
47	23	100.0	76	1	ISE1_MOUSE	Q9D822 mus musculu
48	23	100.0	77	1	COMA_CONNA	Q9TW19 conus magus
49	23	100.0	77	1	FER_BACSC	Q45560 bacillus sc
50	23	100.0	78	1	FER_ALIAC	P03941 alicyclobac
51	23	100.0	80	1	SAP_PIG	P81405 sus scrofa
52	23	100.0	81	1	NUML_HUMAN	O00483 homo sapien
53	23	100.0	81	1	PORD_METTH	P56815 methanobact
54	23	100.0	85	1	ITI5_ARATH	O22867 arabidopsis
55	23	100.0	86	1	TXM2_DENAN	P18328 dendroaspis
56	23	100.0	87	1	NUOS_HUMAN	Q9NRX3 homo sapien
57	23	100.0	87	1	Y898_MYCTU	Q10566 mycobacteri
58	23	100.0	88	1	Y06G_BPT4	P13314 bacterioph
59	23	100.0	89	1	ITI2_ARATH	Q42328 arabidopsis
60	23	100.0	89	1	ITI6_ARATH	O22869 arabidopsis
61	23	100.0	90	1	ITI4_ARATH	O22866 arabidopsis
62	23	100.0	90	1	YORK_TTVL	P19295 thermoprote
63	23	100.0	91	1	GATC_HALNL	Q9HR44 halobacteri
64	23	100.0	92	1	SY22_MOUSE	O88430 mus musculu
65	23	100.0	93	1	FER1_AFIPE	Q44037 afipia feli
66	23	100.0	94	1	S110_RAT	P05943 rattus norv
67	23	100.0	95	1	S110_PIG	P04163 sus scrofa
68	23	100.0	96	1	S110_CHICK	P27003 gallus gall
69	23	100.0	96	1	S110_MOUSE	P08206 homo sapien
70	23	100.0	96	1	S110_HUMAN	P08207 mus musculu
71	23	100.0	97	1	EOTA_HUMAN	P51671 homo sapien
72	23	100.0	97	1	XPA_CRIGR	Q64029 cricetus
73	23	100.0	98	1	BXE1_BOMMO	P21808 bombyx mori
74	23	100.0	99	1	ITI2_SIGNAL	P26780 sinapis alb
75	23	100.0	99	1	RS10_HALMA	P23357 haloarcula
76	23	100.0	99	1	SY08_BOVIN	Q09141 bos taurus

ALIGNMENTS

RESULT 1

ID	ITRB_ALBUJU	STANDARD;	PRT;	15 AA.
AC	P24927;			
DT	01-MAR-1992 (Rel. 21, Created)			
DT	01-MAR-1992 (Rel. 21, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Trypsin inhibitor B chain (Fragment)			
OS	Albizzia julibrissin (Silk tree)			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid 1; Fabales; Fabaceae; Mimosoideae; Ingeae; Albizia.			
OX	NCBI_TaxID=3813;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Seed;			
RX	MEDLINE=80115605; PubMed=528539;			
RA	Odani S., Ono T., Ikenaka T.;			
RT	"Proteinase inhibitors from a mimosoideae legume, Albizzia			
RT	julibrissin. Homologues of soybean trypsin inhibitor (Kunitz).";			
RL	J. Biochem. 86:1795-1805(1979).			
CC	-!- FUNCTION: Inhibits trypsin and alpha-chymotrypsin.			
CC	-!- SUBUNIT: Heterodimer of an "A" and a "B" chain linked by a			
CC	disulfide bond.			
CC	-!- SIMILARITY: Belongs to the leguminous Kunitz-type inhibitor			

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CC family.
KW Serine protease inhibitor.
FT NON TER 15
SQ SEQUENCE 15 AA; 1705 MW; 53165F7B9C45B4D0 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
   |::|
Db 3 DHCKD 7

RESULT 2
SCX5_BUTOC
ID SCX5_BUTOC STANDARD; PRT; 24 AA.
AC P04097;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotoxin V (Fragment).
OS Buthus occitanus tunetanus (Common European scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Buthus.
OX NCBI_TaxID=6871;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=84224814; PubMed=6729843;
RA Martin M.-F., Rochat H.;
RT "Purification of thirteen toxins active on mice from the venom of the
RL North African scorpion Buthus occitanus tunetanus.";
RL Toxicon 22:279-291(1984).
CC -!- FUNCTION: Binds to sodium channels and inhibits the inactivation
CC of the activated channels, thereby blocking neuronal transmission.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
QY 1 DXCXD 5
   |::|
Db 3 DHCKD 7

RESULT 2
SCX8_BUTOC
ID SCX8_BUTOC STANDARD; PRT; 36 AA.
AC P04098;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotoxin VIII (Fragment).
OS Buthus occitanus tunetanus (Common European scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Buthus.
OX NCBI_TaxID=6871;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=84224814; PubMed=6729843;
RA Martin M.-F., Rochat H.;
RT "Purification of thirteen toxins active on mice from the venom of the
RL North African scorpion Buthus occitanus tunetanus.";
RL Toxicon 22:279-291(1984).
CC -!- FUNCTION: Binds to sodium channels and inhibits the inactivation
CC of the activated channels, thereby blocking neuronal transmission.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
QY 1 DXCXD 5
   |::|
Db 3 DHCKD 7

Query Match 100.0%; Score 23; DB 1; Length 24;
Best Local Similarity 60.0%; Pred. No. 82;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
   |::|
Db 20 DYCND 24

RESULT 3
SCX8_BUTOC
ID SCX8_BUTOC STANDARD; PRT; 36 AA.
AC P04098;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotoxin VIII (Fragment).
OS Buthus occitanus tunetanus (Common European scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Buthus.
OX NCBI_TaxID=6871;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=84224814; PubMed=6729843;
RA Martin M.-F., Rochat H.;
RT "Purification of thirteen toxins active on mice from the venom of the
RL North African scorpion Buthus occitanus tunetanus.";
RL Toxicon 22:279-291(1984).
CC -!- FUNCTION: Binds to sodium channels and inhibits the inactivation
CC of the activated channels, thereby blocking neuronal transmission.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
QY 1 DXCXD 5
   |::|
Db 20 DYCND 24

Query Match 100.0%; Score 23; DB 1; Length 24;
Best Local Similarity 60.0%; Pred. No. 82;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
   |::|
Db 20 DYCND 24

RESULT 3
SCX8_BUTOC
ID SCX8_BUTOC STANDARD; PRT; 36 AA.
AC P04098;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotoxin VIII (Fragment).
OS Buthus occitanus tunetanus (Common European scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Buthus.
OX NCBI_TaxID=6871;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=84224814; PubMed=6729843;
RA Martin M.-F., Rochat H.;
RT "Purification of thirteen toxins active on mice from the venom of the
RL North African scorpion Buthus occitanus tunetanus.";
RL Toxicon 22:279-291(1984).
CC -!- FUNCTION: Binds to sodium channels and inhibits the inactivation
CC of the activated channels, thereby blocking neuronal transmission.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
QY 1 DXCXD 5
   |::|
Db 20 DYCND 24

Query Match 100.0%; Score 23; DB 1; Length 36;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
   |::|
Db 20 DYCND 24

RESULT 4
TXD3_PARLU
ID TXD3_PARLU STANDARD; PRT; 36 AA.
AC P83258;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Delta-palutoxin IT3 (Delta-palut3).
OS Paracelotes luctuosus (Spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Amaurobiidae; Paracelotes.
OX NCBI_TaxID=185217;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=20428467; PubMed=10971590;
RA Corzo G., Escoubas P., Stankiewicz M., Pelhate M., Kristensen C.P.,
RA Nakajima T.;
RT "Isolation, synthesis and pharmacological characterization of
RT delta-palutoxins IT, novel insecticidal toxins from the spider
RL Paracelotes luctuosus (Amaurobiidae).";
RL Eur. J. Biochem. 267:5783-5795(2000).
CC -!- FUNCTION: Potent activity against S.litura larvae.
CC -!- FUNCTION: Binds to sodium channels and inhibits the inactivation
CC of the activated channels. This toxin is active only on insects
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=3926.2; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the mu-agatoxin family.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0019871; F:sodium channel inhibitor activity; IDA.
DR GO; GO:0015070; F:toxin activity; IDA.
KW Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor.
FT DISULFID 3 19 BY SIMILARITY.
FT DISULFID 10 24 BY SIMILARITY.
FT DISULFID 18 34 BY SIMILARITY.
FT DISULFID 26 32 BY SIMILARITY.
SQ SEQUENCE 36 AA; 3934 MW; 9CDFAD043AI9804 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 36;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
   |::|
Db 20 DYCND 24

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QY 1 DXCXD 5
Db 8 DWACD 12

RESULT 5
ME20_EUPRA
ID ME20_EUPRA STANDARD; PRT; 37 AA.
AC P26888;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mating pheromone Er-20 (Euplome R20) (Fragment).
GN MAT20.
OS Euplotes raikovi.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euplotida; Euplotidae; Euplotes.
OX NCBI_TaxID=5938;
RN [1]
RP SEQUENCE.
RC STRAIN=GA-4;
RX MEDLINE=92196059; PubMed=1549567;
RA Raffioni S., Miceli C., Vallesi A., Chowdhury S.K., Chait B.T.,
RA Luporini P., Bradshaw R.A.;
RT "Primary structure of Euplotes raikovi pheromones: comparison of five
RT sequences of pheromones from cells with variable mating
RT interactions."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2071-2075(1992).
CC -!- FUNCTION: Mating ciliate pheromones (or gamones) are diffusible
CC extra-cellular communication signals that distinguish different
CC intraspecific classes of cells commonly referred to as "mating
CC types". They prepare the latter for conjugation by changing their
CC cell surface properties.
CC -!- SUBUNIT: Homodimer (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; C41933; C41933.
DR HSSP; P26887; 1ERY.
KW Pheromone.
FT DISULFID 3 18 BY SIMILARITY.
FT DISULFID 10 32 BY SIMILARITY.
FT DISULFID 15 24 BY SIMILARITY.
FT NON_TER 37 37
SQ SEQUENCE 37 AA; 4002 MW; D8C85FD78F704CF CRC64;

Query Match 100.0%; Score 23; DB 1; Length 37;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 1 DICDD 5

RESULT 6
ID5B_PROJU
ID ID5B_PROJU STANDARD; PRT; 38 AA.
AC P32734;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE Kunitz-type trypsin inhibitor beta chain.
OS Prosopis juliflora (Mesquite) (Algorrobo).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Mimosoideae; Mimoseae; Prosopis.
OX NCBI_TaxID=13230;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RX MEDLINE=92118295; PubMed=1367792;
RA Negreiros A.N., Carvalho M.M., Xavier Filho J., Blanco-Labra A.,
RA Shewry P.R., Richardson M.;
RT "The complete amino acid sequence of the major Kunitz trypsin

```

```

RT inhibitor from the seeds of Prosopis juliflora."
RL Phytochemistry 30:2829-2833(1991).
CC -!- FUNCTION: Inhibition of trypsin.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain linked by a
CC disulfide bond.
CC -!- SIMILARITY: Belongs to the leguminous Kunitz-type inhibitor
CC family.
DR PIR; A45588; A45588.
DR InterPro; IPR002160; Kunitz legume.
DR Pfam; PF00197; Kunitz legume; 1.
KW Serine protease inhibitor.
FT DISULFID 4 4 INTERCHAIN (WITH ALPHA CHAIN)
FT (BY SIMILARITY).
SQ SEQUENCE 38 AA; 4313 MW; 99CE89720E39F84B CRC64;

Query Match 100.0%; Score 23; DB 1; Length 38;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 2 DRCKD 6

RESULT 7
ILLB_LEUGL
ID ILLB_LEUGL STANDARD; PRT; 42 AA.
AC P83037;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Kunitz-type trypsin inhibitor LITI, beta chain.
OS Leucaena glauca (White popinac) (Leucaena leucocephala).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Mimosoideae; Mimoseae; Leucaena.
OX NCBI_TaxID=3866;
RN [1]
RP SEQUENCE, FUNCTION, SUBUNIT, TISSUE SPECIFICITY, VARIANT, AND
RP MASS SPECTROMETRY.
RC TISSUE=Cotyledon;
RX MEDLINE=20175262; PubMed=10708849;
RA Oliva M.L.V., Souza-Pinto J.C., Batista I.F.C., Araujo M.S.,
RA Silveira V.F., Auerwald E.A., Mentele R., Eckerskorn C.,
RA Sampaio M.U., Sampaio C.A.M.;
RT "Leucaena leucocephala serine proteinase inhibitor: primary structure
RT and action on blood coagulation, kinin release and rat paw edema."
RL Biochim. Biophys. Acta 1477:64-74(2000).
CC -!- FUNCTION: Inhibits trypsin, plasmin, human plasma kallikrein,
CC chymotrypsin and factor XIIa activity.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain linked by a
CC disulfide bond.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Abundant in dry seeds.
CC -!- MASS SPECTROMETRY: MW=4764; METHOD=Electrospray.
CC -!- MASS SPECTROMETRY: MW=4765; METHOD=Electrospray.
CC -!- MISCELLANEOUS: There are two isoforms with slightly different
CC molecular masses: 4764 and 4765 Da. These isoforms differ in their
CC N- and C-terminal amino acids.
CC -!- SIMILARITY: Belongs to the leguminous Kunitz-type inhibitor
CC family.
DR PDB; 1LT2; 05-JUN-02.
DR InterPro; IPR002160; Kunitz legume.
DR Pfam; PF00197; Kunitz legume; 1.
KW Serine protease inhibitor; 3D-structure.
FT DISULFID 6 6 INTERCHAIN (WITH ALPHA CHAIN) (BY
FT SIMILARITY).
FT VARIANT 1 1 MISSING (IN 4764 Da POLYPEPTIDE).
FT VARIANT 42 42 D -> DD (IN 4764 Da POLYPEPTIDE).
SQ SEQUENCE 42 AA; 4659 MW; AFE515DF7B93626F CRC64;

Query Match 100.0%; Score 23; DB 1; Length 42;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;

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DR EMBL; AY159340; AAO22218.1; --
 KW Toxin; Ionic channel inhibitor; Neurotoxin;
 FT DISULFID 5 23 BY SIMILARITY.
 FT DISULFID 11 34 BY SIMILARITY.
 FT DISULFID 20 39 BY SIMILARITY.
 FT DISULFID 24 41 BY SIMILARITY.
 SQ SEQUENCE 42 AA; 4791 MW; F905E5054947AD7F CRC64;

Query Match 100.0%; Score 23; DB 1; Length 42;
 Best Local Similarity 60.0%; Pred. No. 1.5e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
 Db 3 DSCVD 7

RESULT 11

SEK1_CENLL STANDARD; PRT; 42 AA.
 AC Q86OV0;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ergtoxin-like protein 1 (ErgTx1) (CllBrg1) (CllBrgTx1) (Gamma-KTx
 DE 1.5).
 GN ERG1.

OS Centruroides limpidus limpidus (Mexican scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butioidae; Butiidae; Centruroides.

ON NCBI_TaxID=29941;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Venom gland;
 RX MEDLINE=22347251; PubMed=12459475;
 RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
 RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
 RA Wanke E., Possani L.D.;
 RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
 RT blocking peptides from scorpions of the genus Centruroides.";
 RL FEBS Lett. 532:121-126(2002).
 CC -!- FUNCTION: Blocks ERG-potassium channels (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the ergtoxin family.

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DR EMBL; AY159343; AAO22221.1; --
 KW Toxin; Ionic channel inhibitor; Neurotoxin;
 FT DISULFID 5 23 BY SIMILARITY.
 FT DISULFID 11 34 BY SIMILARITY.
 FT DISULFID 20 39 BY SIMILARITY.
 FT DISULFID 24 41 BY SIMILARITY.
 SQ SEQUENCE 42 AA; 4768 MW; 9BE5F514484108F0 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 42;
 Best Local Similarity 60.0%; Pred. No. 1.5e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
 Db 3 DSCVD 7

RESULT 12

SEK1_CENSC STANDARD; PRT; 42 AA.
 AC Q86OV6;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ergtoxin-like protein 1 (ErgTx1) (CsErg1) (CsErgTx1) (Gamma-KTx 1.4).
 GN ERG1.

OS Centruroides sculpturatus (Bark scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butioidae; Butiidae; Centruroides.
 ON NCBI_TaxID=218467;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Venom gland;
 RX MEDLINE=22347251; PubMed=12459475;
 RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
 RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
 RA Wanke E., Possani L.D.;
 RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
 RT blocking peptides from scorpions of the genus Centruroides.";
 RL FEBS Lett. 532:121-126(2002).
 CC -!- FUNCTION: Blocks ERG-potassium channels (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the ergtoxin family.

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DR EMBL; AY159347; AAO22225.1; --
 KW Toxin; Ionic channel inhibitor; Neurotoxin;
 FT DISULFID 5 23 BY SIMILARITY.
 FT DISULFID 11 34 BY SIMILARITY.
 FT DISULFID 20 39 BY SIMILARITY.
 FT DISULFID 24 41 BY SIMILARITY.
 SQ SEQUENCE 42 AA; 4752 MW; B585F51448411BD1 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 42;
 Best Local Similarity 60.0%; Pred. No. 1.5e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
 Db 3 DSCVD 7

RESULT 13

SEK2_CENGR STANDARD; PRT; 42 AA.
 AC Q86OV2;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ergtoxin-like protein 2 (ErgTx2) (CgErg2) (CgErgTx2) (Gamma-KTx 3.4).
 GN ERG2.

OS Centruroides gracilis (Slenderbrown scorpion) (Florida bark scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butioidae; Butiidae; Centruroides.
 ON NCBI_TaxID=217898;

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RN RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RL blocking peptides from scorpions of the genus Centruroides."
RL FEBS Lett. 532:121-126(2002).
CC -!- FUNCTION: Blocks ERG-potassium channels (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the ergtoxin family.
CC
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CC
CC EMBL; AY159341; AAC22219.1; -
KW Toxin; Ionic channel inhibitor; Neurotoxin;
KW Potassium channel inhibitor.
FT DISULFID 5 23
FT DISULFID 11 34 BY SIMILARITY.
FT DISULFID 20 39 BY SIMILARITY.
FT DISULFID 24 41 BY SIMILARITY.
SQ SEQUENCE 42 AA; 4716 MW; 2FA0F36A15F10C76 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 42;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 3 DSCVD 7

RESULT 14
SEK2_CENEL STANDARD; PRT; 43 AA.
AC Q86QV5;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ergtoxin-like protein 2 (ErgTx2) (CeErg2) (Gamma-KTx 3.2).
GN ERG2.
OS Centruroides elegans (Bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butiidae; Centruroides.
OX NCBI_TaxID=217897;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RL blocking peptides from scorpions of the genus Centruroides."
RL FEBS Lett. 532:121-126(2002).
CC -!- FUNCTION: Blocks ERG-potassium channels (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the ergtoxin family.
CC
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CC
CC EMBL; AY159338; AAC22216.1; -
KW Toxin; Ionic channel inhibitor; Neurotoxin;
KW Potassium channel inhibitor.
FT DISULFID 5 23 BY SIMILARITY.
FT DISULFID 11 34 BY SIMILARITY.
FT DISULFID 20 39 BY SIMILARITY.
FT DISULFID 24 41 BY SIMILARITY.
SQ SEQUENCE 43 AA; 4947 MW; 77C231F5145B5AF1 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 3 DSCVD 7

RESULT 15
SEK2_CENEL STANDARD; PRT; 43 AA.
AC Q86QV5;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ergtoxin-like protein 2 (ErgTx2) (CexErg2) (Gamma-KTx
DE 4.3).
OS Centruroides exilicauda (Bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butiidae; Centruroides.
OX NCBI_TaxID=6879;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RL blocking peptides from scorpions of the genus Centruroides."
RL FEBS Lett. 532:121-126(2002).
CC -!- FUNCTION: Blocks ERG-potassium channels (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the ergtoxin family.
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CC
CC EMBL; AY159353; AAC22231.1; -
KW Toxin; Ionic channel inhibitor; Neurotoxin;
KW Potassium channel inhibitor.
FT DISULFID 5 23 BY SIMILARITY.
FT DISULFID 11 34 BY SIMILARITY.
FT DISULFID 20 39 BY SIMILARITY.
FT DISULFID 24 41 BY SIMILARITY.
SQ SEQUENCE 43 AA; 4855 MW; AA3BD8CE23CCF0D2 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 3 DSCVD 7
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CC -----
DR EMBL; AY159339; AAC22217.1; -.
KW Toxin; Ionic channel inhibitor; Neurotoxin;
KW Potassium channel inhibitor.
FT DISULFID 5 23 BY SIMILARITY.
FT DISULFID 11 34 BY SIMILARITY.
FT DISULFID 20 39 BY SIMILARITY.
FT DISULFID 24 41 BY SIMILARITY.
SQ SEQUENCE 43 AA; 4906 MW; BDAB2EEA23CCF0D2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 43;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db |:|:|
3 DSCVD 7

RESULT 19
SEK3_CENEX STANDARD; PRT; 43 AA.
AC Q86Q79;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Ergtoxin-like protein 3 (ErgTx3) (CexErg3) (Gamma-KTx
DE 4.4).
GN ERG3.
OS Centruroides exilicauda (Bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Centruroides.
OX NCBI_TaxID=6879;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassullini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
CC -!- FUNCTION: Blocks ERG-potassium channels (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the ergtoxin family.
CC -----
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CC -----
DR EMBL; AY159345; AAC22232.1; -.
KW Toxin; Ionic channel inhibitor; Neurotoxin;
KW Potassium channel inhibitor.
FT DISULFID 5 23 BY SIMILARITY.
FT DISULFID 11 34 BY SIMILARITY.
FT DISULFID 20 39 BY SIMILARITY.
FT DISULFID 24 41 BY SIMILARITY.
SQ SEQUENCE 43 AA; 4871 MW; DID51E1523C6E2F7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 43;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db |:|:|
3 DSCVD 7

RESULT 21
SEK3_CENNO STANDARD; PRT; 43 AA.
AC Q86QV9;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Ergtoxin-like protein 3 (ErgTx3) (CnErg3) (CnErgTx3) (Gamma-KTx 4.13).
GN ERG3.
OS Centruroides noxius (Mexican scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Centruroides.
OX NCBI_TaxID=6878;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;

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RESULT 24
SEK4_CENLL STANDARD; PRT; 43 AA.
AC Q86Q07;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ergotoxin-like protein 4 (ErgTx4) (CllErg4) (CllErgTx4) (Gamma-KTx
DE 4.7).
GN ERG4.
OS Centruroides limpidus limpidus (Mexican scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthoidea; Butthidae; Centruroides.
OX NCBI_TaxID=29941;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Casulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergotoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
CC -!- FUNCTION: Blocks ERG-potassium channels (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the ergotoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AY159346; AAC22224.1; --
CC Toxin; Ionic channel inhibitor; Neurotoxin;
CC Potassium channel inhibitor.
CC DISULFID 5 23 BY SIMILARITY.
CC DISULFID 11 34 BY SIMILARITY.
CC DISULFID 20 39 BY SIMILARITY.
CC DISULFID 24 41 BY SIMILARITY.
CC SEQUENCE 43 AA; 4821 MW; E64B7E1523CCEA4 CRC64;
CC
CC Query Match 100.0%; Score 23; DB 1; Length 43;
CC Best Local Similarity 60.0%; Pred. NO. 1.5e+02;
CC Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CC
CC Qy 1 DXCXD 5
CC |::|
CC Db 3 DSCVD 7
CC
CC RESULT 25
SEK4_CENNO STANDARD; PRT; 43 AA.
AC Q86Q08;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ergotoxin-like protein 4 (ErgTx4) (CnErg4) (CnErgTx4) (Gamma-KTx 4.11).
GN ERG4.
OS Centruroides noxius (Mexican scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthoidea; Butthidae; Centruroides.
OX NCBI_TaxID=6878;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Casulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergotoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
CC -!- FUNCTION: Blocks ERG-potassium channels (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the ergotoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AY159346; AAC22224.1; --
CC Toxin; Ionic channel inhibitor; Neurotoxin;
CC Potassium channel inhibitor.
CC DISULFID 5 23 BY SIMILARITY.
CC DISULFID 11 34 BY SIMILARITY.
CC DISULFID 20 39 BY SIMILARITY.
CC DISULFID 24 41 BY SIMILARITY.
CC SEQUENCE 43 AA; 4821 MW; E64B7E1523CCEA4 CRC64;
CC
CC Query Match 100.0%; Score 23; DB 1; Length 43;
CC Best Local Similarity 60.0%; Pred. NO. 1.5e+02;
CC Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CC
CC Qy 1 DXCXD 5
CC |::|
CC Db 3 DSCVD 7
CC
CC RESULT 26
SEK4_CENSC STANDARD; PRT; 43 AA.
AC Q86Q03;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ergotoxin-like protein 4 (ErgTx4) (CsErg4) (CsErgTx4) (Gamma-KTx 4.10).
GN ERG4.
OS Centruroides sculpturatus (Bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthoidea; Butthidae; Centruroides.
OX NCBI_TaxID=218467;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Casulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergotoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
CC -!- FUNCTION: Blocks ERG-potassium channels (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the ergotoxin family.
CC
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CC
CC EMBL; AV159335; AAC22213.1; --
CC Toxin; Ionic channel inhibitor; Neurotoxin;
CC Potassium channel inhibitor.
CC DISULFID 5 23 BY SIMILARITY.
CC DISULFID 11 34 BY SIMILARITY.
CC DISULFID 20 39 BY SIMILARITY.
CC DISULFID 24 41 BY SIMILARITY.
CC SEQUENCE 43 AA; 4855 MW; BDB07DACD147F197 CRC64;
CC
CC Query Match 100.0%; Score 23; DB 1; Length 43;
CC Best Local Similarity 60.0%; Pred. NO. 1.5e+02;
CC Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CC
CC Qy 1 DXCXD 5
CC |::|
CC Db 3 DSCVD 7
CC

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DR EMBL; AY159350; AA022228.1; --
KW Toxin; Ionic channel inhibitor; Neurotoxin;
FT Potassium channel inhibitor.
FT DISULFID 5 23 BY SIMILARITY.
FT DISULFID 11 34 BY SIMILARITY.
FT DISULFID 20 39 BY SIMILARITY.
FT DISULFID 24 41 BY SIMILARITY.
SQ SEQUENCE 43 AA; 4841 MW; BDB2808313CCF0D2 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 3 DSCVD 7

RESULT 27
SEK5_CENNO STANDARD; PRT; 43 AA.
AC Q86QV7;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ergtoxin-like protein 5 (ErgTx5) (CnErg5) (Gamma-KTx 4.2).
GN ERG5.
OS Centruroides noxius (Mexican scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butioidae; Butiidae; Centruroides.
OX NCBI_TaxID=6878;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
CC -!- FUNCTION: Blocks ERG-potassium channels (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the ergtoxin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AY159342; AA022220.1; --
DR Toxin; Ionic channel inhibitor; Neurotoxin;
KW Potassium channel inhibitor.
FT DISULFID 5 23 BY SIMILARITY.
FT DISULFID 11 34 BY SIMILARITY.
FT DISULFID 20 39 BY SIMILARITY.
FT DISULFID 24 41 BY SIMILARITY.
SQ SEQUENCE 47 AA; 5116 MW; AA76672DB459108A CRC64;

Query Match 100.0%; Score 23; DB 1; Length 47;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 3 DSCVD 7

RESULT 29
SEK5_CENSC STANDARD; PRT; 47 AA.
AC Q86QV2;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ergtoxin-like protein 5 (ErgTx5) (CsErgTx5) (Gamma-KTx 5.1).
GN ERG5.
OS Centruroides sculpturatus (Bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butioidae; Butiidae; Centruroides.
OX NCBI_TaxID=218467;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22347251; PubMed=12459475;
RA Corona M., Gurrola G.B., Merino E., Cassulini R.R., Valdez-Cruz N.A.,
RA Garcia B., Ramirez-Dominguez M.E., Coronas F.I., Zamudio F.Z.,
RA Wanke E., Possani L.D.;
RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.";
RL FEBS Lett. 532:121-126(2002).
CC -!- FUNCTION: Blocks ERG-potassium channels (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the ergtoxin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY159336; AA022214.1; --
KW Toxin; Ionic channel inhibitor; Neurotoxin;
KW Potassium channel inhibitor.
FT DISULFID 5 23 BY SIMILARITY.
FT DISULFID 11 34 BY SIMILARITY.
FT DISULFID 20 39 BY SIMILARITY.
FT DISULFID 24 41 BY SIMILARITY.
SQ SEQUENCE 43 AA; 4836 MW; 5DF441212448539F CRC64;

Query Match 100.0%; Score 23; DB 1; Length 43;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 3 DSCVD 7

RESULT 28

```

RT "A large number of novel Ergtoxin-like genes and ERG K+-channels
RT blocking peptides from scorpions of the genus Centruroides.",
RL FBBS Lett. 532:121-126(2002).
CC -!- FUNCTION: Blocks ERG-potassium channels (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the ergtoxin family.
CC -----
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CC -----
DR EMBL; AY159351; AAC22229.1; -;
KW Toxin; Ionic channel inhibitor; Neurotoxin;
KW Potassium channel inhibitor.
FT DISULFID 5 23 BY SIMILARITY.
FT DISULFID 11 34 BY SIMILARITY.
FT DISULFID 20 39 BY SIMILARITY.
FT DISULFID 24 41 BY SIMILARITY.
SQ SEQUENCE 47 AA; 5271 MW; 97F44AF20B6CA086 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 47;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 3 DSCVD 7

RESULT 30
TX45_PHONI
ID TX45_PHONI STANDARD; PRT; 47 AA.
AC P59367;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Insecticidal neurotoxin Tx4 (5-5).
OS Phoneutria nigriventer (Brazilian armed spider).
OC Araneomorphae; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX NCBI_TaxID=6918;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, AND BIOASSAY.
RX MEDLINE=20436233; PubMed=10978749;
RA de Figueiredo S.G., de Lima M.E., Nascimento Cordeiro M., Diniz C.R.,
RA Patten D., Halliwell R.F., Gilroy J., Richardson M.;
RA "Purification and amino acid sequence of a highly insecticidal toxin
RA from the venom of the Brazilian spider Phoneutria nigriventer which
RA inhibits NMDA-evoked currents in rat hippocampal neurones.";
RL Toxicol. 39:309-317(2001).
CC -!- FUNCTION: This neurotoxin reversibly inhibits the N-methyl-D-
CC aspartate (NMDA)-subtype of ionotropic glutamate receptor, and has
CC little or no effect on kainate-, alpha-amino-3-hydroxy-5-methyl-4-
CC isoxazole-propionic acid (AMPA)- or gamma-aminobutyric acid
CC (GABA)-activated currents. It is highly toxic to house fly (*Musca*
CC domestica), cockroach (*Periplaneta americana*), and cricket (*Acheta*
CC domesticus). It has no effect when intracerebroventricularly
CC injected into mice.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- PTM: Contains five disulfide bonds (Probable).
CC -!- MASS SPECTROMETRY: MW=5170; METHOD=Electrospray.
CC -!- MISCELLANEOUS: LD(50) is 9.3 mg/house fly.
CC -!- SIMILARITY: Belongs to the spider toxin Tx2 family.
KW Toxin; Neurotoxin.
SQ SEQUENCE 47 AA; 5185 MW; 5943DD92667B3E2E CRC64;

Query Match 100.0%; Score 23; DB 1; Length 47;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 13 DCCGD 17

RESULT 31
FER_MEGEL
ID FER_MEGEL STANDARD; PRT; 54 AA.
AC P00201;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ferredoxin.
OS Megaspheara eladenii.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Acidaminococcaceae;
OC Megaspheara.
OX NCBI_TaxID=907;
RN [1]
RP SEQUENCE.
RA Azari P., Glantz M., Tsunoda J., Yasunobu K.T.;
RA Unpublished results, cited by:
RL Yasunobu K.T., Tanaka M.;
RL Syst. Zool. 22:570-589(1973).
CC -!- FUNCTION: Ferredoxins are iron-sulfur proteins that transfer
CC electrons in a wide variety of metabolic reactions.
CC -!- COFACTOR: Binds 2 4Fe-4S clusters.
CC -!- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
DR HSP; A00203; FEME.
DR HSP; O45560; 1BWE.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR000813; 7Fe_ferredoxin.
DR Pfam; PF00037; fer4; 2.
DR PRINTS; PR00354; 7FE8SFRDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
FT METAL 8 8 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 11 11 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 14 14 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 18 18 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 36 36 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 39 39 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 42 42 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 46 46 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 54 AA; 5430 MW; 90C6BC38EAE3A577 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 54;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 34 DSCID 38

RESULT 32
FER_PEPAS
ID FER_PEPAS STANDARD; PRT; 54 AA.
AC P00193;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ferredoxin.
OS Peptostreptococcus asaccharolyticus (Peptococcus asaccharolyticus).
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Peptoniphilus.
OX NCBI_TaxID=1258;
RN [1]
RP SEQUENCE.
RX MEDLINE=69054261; PubMed=5723466;

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RA Tsunoda J.N., Yasunobu K.T., Whiteley H.R.;
RT "Non-heme iron proteins. IX. The amino acid sequence of ferredoxin
RT from Micrococcus aerogenes.";
RL J. Biol. Chem. 243:6262-6272(1968).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=73187389; PubMed=4708097;
RA Adman E.T., Sieker L.C., Jensen L.H.;
RT "Structure of a bacterial ferredoxin.";
RL J. Biol. Chem. 248:3987-3996(1973).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76213238; PubMed=932007;
RA Adman E.T., Sieker L.C., Jensen L.H.;
RT "Structure of Peptococcus aerogenes ferredoxin. Refinement at 2-A
RT resolution.";
RL J. Biol. Chem. 251:3801-3806(1976).
CC -|- FUNCTION: Ferredoxins are iron-sulfur proteins that transfer
CC electrons in a wide variety of metabolic reactions.
CC -|- COFACTOR: Binds 2 4Fe-4S clusters.
CC -|- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
DR PIR: A00196; FEPE.
DR PDB: 1DUR; 20-DEC-00.
DR InterPro: IPR001450; 4Fe4S_ferredoxin.
DR Pfam: PF00037; fer4; 2.
DR PROSITE: PS00198; 4FE4S_FERREDOXIN; 2.
DR Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
FT METAL 8 8 IRON-SULFUR 1 (4FE-4S).
FT METAL 11 11 IRON-SULFUR 1 (4FE-4S).
FT METAL 14 14 IRON-SULFUR 1 (4FE-4S).
FT METAL 18 18 IRON-SULFUR 2 (4FE-4S).
FT METAL 35 35 IRON-SULFUR 2 (4FE-4S).
FT METAL 38 38 IRON-SULFUR 2 (4FE-4S).
FT METAL 41 41 IRON-SULFUR 2 (4FE-4S).
FT METAL 45 45 IRON-SULFUR 1 (4FE-4S).
FT STRAND 3 4
FT TURN 6 7
FT TURN 13 14
FT HELIX 15 17
FT TURN 19 20
FT TURN 23 23
FT STRAND 30 30
FT TURN 32 34
FT HELIX 40 44
FT STRAND 50 51
SQ SEQUENCE 54 AA; 5452 MW; C7DCEFA08223CB5D CRC64;

Query Match 100.0%; Score 23; DB 1; Length 54;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 33 DSCID 37

RESULT 33
PERI_RHURU
ID FERI_RHURU STANDARD; PRT; 55 AA.
AC P00194;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ferredoxin I (Fdi).
OS Rhodospirillum rubrum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Rhodospirillum.
OX NCBI_TaxID=1085;
RN [1]
RP SEQUENCE.
RX MEDLINE=83290779; PubMed=6411697;
RA Matsubara H., Inoue K., Hase T., Hiura H., Kakuno T., Yamashita J.,
RA Horio T.;

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RT "Structure of the extracellular ferredoxin from Rhodospirillum
RT rubrum: close similarity to clostridial ferredoxins.";
RL J. Biochem. 93:1385-1390(1983).
CC -|- FUNCTION: Ferredoxins are iron-sulfur proteins that transfer
CC electrons in a wide variety of metabolic reactions.
CC -|- COFACTOR: Binds 2 4Fe-4S clusters.
CC -|- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
DR PIR: A00197; FEQFR.
DR InterPro: IPR001450; 4Fe4S_ferredoxin.
DR Pfam: PF00037; fer4; 2.
DR PRINTS: PR00354; 7FE8SPRDOXIN.
DR PROSITE: PS00198; 4FE4S_FERREDOXIN; 2.
DR Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
FT METAL 8 8 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 11 11 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 14 14 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 18 18 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 37 37 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 40 40 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 43 43 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 47 47 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 55 AA; 5567 MW; 9467DC27F25170C8 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 55;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 35 DTCID 39

RESULT 34
FER_CLOAC
ID FER_CLOAC STANDARD; PRT; 55 AA.
AC P00198;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ferredoxin.
OS Clostridium acidu-urici.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1556;
RN [1]
RP SEQUENCE.
RX MEDLINE=69253175; PubMed=5799135;
RA Rall S.C., Bolinger R.B., Cole R.D.;
RT "The amino acid sequence of ferredoxin from Clostridium acidu-urici.";
RL Biochemistry 8:2486-2496(1969).
RN [2]
RP REVISIONS TO 15; 21; 25 AND 28.
RC STRAIN=ATCC 7906;
RX MEDLINE=93384542; PubMed=8373379;
RA Meyer J., Moulis J., Scherrer N., Gagnon J., Ulrich J.;
RT "Sequences of clostridial ferredoxins: determination of the
RT Clostridium sticklandii sequence and correction of the Clostridium
RT acidu-urici sequence.";
RL Biochem. J. 294:622-623(1993).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.84 ANGSTROMS).
RX MEDLINE=95055710; PubMed=7966291;
RA Duee E.D., Fanchon E., Vicat J., Sieker L.C., Meyer J., Moulis J.M.;
RT "Refined crystal structure of the 2[4Fe-4S] ferredoxin from
RT Clostridium acidu-urici at 1.84-A resolution.";
RL J. Mol. Biol. 243:683-695(1994).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (0.94 ANGSTROMS).
RX MEDLINE=98070231; PubMed=9405040;
RA Dauter Z., Wilson K.S., Sieker L.C., Meyer J., Moulis J.M.;
RT "Atomic resolution (0.94 A) structure of Clostridium acidu-urici

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RT ferredoxin. Detailed geometry of [4Fe-4S] clusters in a protein.";
RL Biochemistry 36:16065-16073(1997).
CC -!- FUNCTION: Ferredoxins are iron-sulfur proteins that transfer
CC electrons in a wide variety of metabolic reactions.
CC -!- COFACTOR: Binds 2 4Fe-4S clusters.
CC -!- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
DR PIR; S36790; FECLCU.
DR PDB; 1FDN; 31-AUG-94.
DR PDB; 2FDN; 08-APR-98.
DR PDB; 1FCA; 10-JUL-95.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR000813; 7Fe_ferredoxin.
DR Pfam; PF00037; fer4; 2.
DR PRINTS; PR00354; 7FE8SFRDXXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW Electron transport; Iron-sulfur; Repeat; 4Fe-4S; 3D-structure.
FT METAL 8 8 IRON-SULFUR 1 (4FE-4S).
FT METAL 11 11 IRON-SULFUR 1 (4FE-4S).
FT METAL 14 14 IRON-SULFUR 1 (4FE-4S).
FT METAL 18 18 IRON-SULFUR 2 (4FE-4S).
FT METAL 37 37 IRON-SULFUR 2 (4FE-4S).
FT METAL 40 40 IRON-SULFUR 2 (4FE-4S).
FT METAL 43 43 IRON-SULFUR 2 (4FE-4S).
FT METAL 47 47 IRON-SULFUR 2 (4FE-4S).
FT STRAND 2 4 IRON-SULFUR 1 (4FE-4S).
FT TURN 6 7
FT TURN 13 14
FT HELIX 15 17
FT TURN 19 20
FT STRAND 23 24
FT STRAND 31 32
FT TURN 34 36
FT HELIX 42 45
FT TURN 46 46
FT TURN 48 49
FT STRAND 52 55
SQ SEQUENCE 55 AA; 5539 MW; D038C1364A1B97E6 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 55;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DXCX 5
DB 35 DTCID 39

RESULT 35
FER_CLOBU
AC P00196; STANDARD; PRT; 55 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ferredoxin.
OS Clostridium butyricum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1492;
RN [1]_SEQUENCE.
RX MEDLINE=67125829; PubMed=5227671;
RA Benson A.M., Mower H.F., Yasunobu K.T.;
RT "The amino acid sequence of Clostridium butyricum ferredoxin.";
RL Proc. Natl. Acad. Sci. U.S.A. 55:1532-1535(1966).
CC -!- FUNCTION: Ferredoxins are iron-sulfur proteins that transfer
CC electrons in a wide variety of metabolic reactions.
CC -!- COFACTOR: Binds 2 4Fe-4S clusters.
CC -!- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
DR HSSP; P00195; FECLCB.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR000813; 7Fe_ferredoxin.

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DR Pfam; PF00037; fer4; 2.
DR PRINTS; PR00354; 7FE8SFRDXXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
FT METAL 8 8 IRON-SULFUR 1 (4FE-4S).
FT METAL 11 11 IRON-SULFUR 1 (4FE-4S).
FT METAL 14 14 IRON-SULFUR 1 (4FE-4S).
FT METAL 18 18 IRON-SULFUR 2 (4FE-4S).
FT METAL 37 37 IRON-SULFUR 2 (4FE-4S).
FT METAL 40 40 IRON-SULFUR 2 (4FE-4S).
FT METAL 43 43 IRON-SULFUR 2 (4FE-4S).
FT METAL 47 47 IRON-SULFUR 1 (4FE-4S).
SQ SEQUENCE 55 AA; 5498 MW; 3853176BFA97A49A CRC64;

Query Match 100.0%; Score 23; DB 1; Length 55;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DXCX 5
DB 35 DTCID 39

RESULT 36
FER_CLOPA
AC P00195; STANDARD; PRT; 55 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ferredoxin.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]_SEQUENCE FROM N.A.
RX MEDLINE=85166189; PubMed=3856844;
RA Graves M.C., Mullenbach G.T., Rabinowitz J.C.;
RT "Cloning and nucleotide sequence determination of the Clostridium
RT pasteurianum ferredoxin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:1653-1657(1985).
RN [2]_SEQUENCE.
RX MEDLINE=67120720; PubMed=5335811;
RA Tanaka M., Nakashima T., Benson A.M., Mower H.F., Yasunobu K.T.;
RT "The amino acid sequence of Clostridium pasteurianum ferredoxin.";
RL Biochemistry 5:1666-1680(1966).
RN [3]_STRUCTURE BY NMR.
RX MEDLINE=96048047; PubMed=7556151;
RA Bertini I., Donaire A., Feinberg B.A., Luchinat C., Piccioli M.,
RA Yuan H.;
RT "Solution structure of the oxidized 2[4Fe-4S] ferredoxin from
RT Clostridium pasteurianum.";
RL Eur. J. Biochem. 232:192-205(1995).
CC -!- FUNCTION: Ferredoxins are iron-sulfur proteins that transfer
CC electrons in a wide variety of metabolic reactions.
CC -!- COFACTOR: Binds 2 4Fe-4S clusters.
CC -!- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
CC -----
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CC -----
DR EMBL; M1214; AA083524.1; -
DR PIR; A94028; FECLCP.
DR PDB; 1CLF; 29-JAN-96.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.

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DR InterPro; IPR000813; 7Fe_ferredoxin.
DR Pfam; PF00037; fer4; 2.
DR PRINTS; PR00354; 7FE8SFRDOXIN.
DR PROSITE; PS00198; 4FE4S FERREDOXIN; 2.
KW Electron transport; Iron-sulfur; Repeat; 4Fe-4S; 3D-structure.
FT INIT MET 0 0
FT METAL 8 8 IRON-SULFUR 1 (4FE-4S).
FT METAL 11 11 IRON-SULFUR 1 (4FE-4S).
FT METAL 14 14 IRON-SULFUR 1 (4FE-4S).
FT METAL 18 18 IRON-SULFUR 2 (4FE-4S).
FT METAL 37 37 IRON-SULFUR 2 (4FE-4S).
FT METAL 40 40 IRON-SULFUR 2 (4FE-4S).
FT METAL 43 43 IRON-SULFUR 2 (4FE-4S).
FT METAL 47 47 IRON-SULFUR 1 (4FE-4S).
FT STRAND 4 4
FT TURN 6 7
FT TURN 13 17
FT TURN 19 20
FT TURN 23 25
FT STRAND 30 32
FT TURN 34 36
FT TURN 42 46
FT TURN 48 49
FT STRAND 52 52
SQ SEQUENCE 55 AA; 5499 MW; AA4C17E5D3E7A495 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 55;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 35 DTCID 39

RESULT 37
FER_CLOPE STANDARD; PRT; 55 AA.
AC P22846;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ferredoxin.
GN FER OR CPE2447.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RA Seki Y., Seki S., Ishimoto M.;
RL "The primary structure of Clostridium perfringens ferredoxin.";
RL J. Gen. Appl. Microbiol. 35:167-172(1989).
RP SEQUENCE.
RN SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Oshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -!- FUNCTION: Ferredoxins are iron-sulfur proteins that transfer
CC electrons in a wide variety of metabolic reactions.
CC -!- COPACTOR: Binds 2 4Fe-4S clusters.
CC -!- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
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CC use by non-profit institutions as long as its content is in no way
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CC -----
DR EMBL; AP003194; BAB82153.1; -.
DR PIR; JX0144; JX0144.
DR HSP; P00195; 1CLF.
DR InterPro; IPR001450; 4FE4S_ferredoxin.
DR InterPro; IPR000813; 7Fe_ferredoxin.
DR Pfam; PF00037; fer4; 2.
DR PRINTS; PR00354; 7FE8SFRDOXIN.
DR PROSITE; PS00198; 4FE4S FERREDOXIN; 2.
KW Electron transport; Iron-sulfur; Repeat; 4Fe-4S;
KW Complete proteome.
FT INIT MET 0 0
FT METAL 8 8 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 11 11 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 14 14 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 18 18 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 37 37 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 40 40 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 43 43 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 47 47 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 55 AA; 5569 MW; 29C77283E6CE948C CRC64;

Query Match 100.0%; Score 23; DB 1; Length 55;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 35 DTCID 39

RESULT 38
FER_CLOPE STANDARD; PRT; 55 AA.
AC P00197;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ferredoxin.
OS Clostridium sp. (strain M-E).
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1506;
RN [1]
RA MEDLINE=75054829; PubMed=4433520;
RA Tanaka M., Haniu M., Yasunobu K.T., Jones J.B., Stadman T.C.;
RT "Amino acid sequence determination of the Clostridium M-E ferredoxin
RT and a comment on the role of the aromatic residues in the clostridial
RT ferredoxins.";
RL Biochemistry 13:5284-5289(1974).
CC -!- FUNCTION: Ferredoxins are iron-sulfur proteins that transfer
CC electrons in a wide variety of metabolic reactions.
CC -!- COPACTOR: Binds 2 4Fe-4S clusters.
CC -!- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
DR HSP; P00198; 2FDN.
DR InterPro; IPR001450; 4FE4S_ferredoxin.
DR InterPro; IPR000813; 7Fe_ferredoxin.
DR Pfam; PF00037; fer4; 2.
DR PRINTS; PR00353; 4FE4SFRDOXIN.
DR PROSITE; PS00198; 4FE4S FERREDOXIN; 2.
KW Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
FT METAL 8 8 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 11 11 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 14 14 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 18 18 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 37 37 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 40 40 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 43 43 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 47 47 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 55 AA; 5622 MW; 418B37657B4FF082 CRC64;
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RA Arcangeli A., Olivetto M., Possani L.D., Wanke E.;
RT "A toxin to nervous, cardiac, and endocrine ERG K+ channels isolated
RL from Centruroides noxius scorpion venom.";
RN FASEB J. 13:953-962(1999).
RX [3]
RP REVISION TO 54 AND 61-62, AND MASS SPECTROMETRY.
RX MEDLINE=20466069; PubMed=11023354;
RA Scatoni A., Bottiglieri C., Ferrara L., Corona M., Gurrola G.B.,
RA Batista C., Wanke E., Possani L.D.;
RT "Disulfide bridges of ergotoxin, a member of a new sub-family of
RL peptide blockers of the ether-a-go-go-related K+ channel.";
RN FEBS Lett. 479:156-157(2000).
RX [4]
RP ERRATUM.
RA Scatoni A., Bottiglieri C., Ferrara L., Corona M., Gurrola G.B.,
RA Batista C., Wanke E., Possani L.D.;
RL FEBS Lett. 481:308-308(2000).
CC -!- FUNCTION: Blocks ERG-potassium channels of nerve, heart and
CC endocrine cells of different species. Is more toxic than CseKergl.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=4730.8; MW ERR=0.4.
CC -!- SIMILARITY: Belongs to the ergotoxin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY164271; AAO22234.1; -.
DR EMBL; AF288205; AAG38523.1; -.
KW Toxin; Ionic channel inhibitor; Neurotoxin;
KW Potassium channel inhibitor; Signal.
FT SIGNAL 1 20
FT CHAIN 21 62 ERGTOXIN.
FT DISULFID 25 43
FT DISULFID 31 54
FT DISULFID 40 59
FT DISULFID 44 61
FT SEQUENCE 62 AA; 6970 MW; 53F88F4B9F187E37 CRC64;
Query Match 100.0%; Score 23; DB 1; Length 62;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
DB 23 DSCVD 27
RESULT 42
SCXV_CENSC ID SCXV_CENSC STANDARD; PRT; 63 AA.
AC P46066;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neurotoxin V (Cse-V) (CSEV) (B140-1).
OS Centruroides sculpturatus (Bark scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Centruroides.
OX NCBI_TaxID=218467;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=92023284; PubMed=1926166;
RA David R.M., Krishna N.R., Watt D.D.;
RT "Characterization of cationic binding sites of neurotoxins from venom
RT of the scorpion (Centruroides sculpturatus Ewing) using lanthanides
RT as binding probes.";

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RL Toxicon 29:645-662(1991).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=95257401; PubMed=7739052;
RA Jablonsky M.J., Watt D.D., Krishna N.R.;
RT "Solution structure of an Old World-like neurotoxin from the venom of
RT the New World scorpion Centruroides sculpturatus Ewing.";
RL J. Mol. Biol. 248:449-458(1995).
CC -!- FUNCTION: Binds to sodium channels and inhibits the inactivation
CC of the activated channels, thereby blocking neuronal transmission.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
CC Alpha-toxin subfamily.
DR PDB; 1NRA; 27-FEB-95.
DR PDB; 1NRB; 27-FEB-95.
DR InterPro; IPR003614; Knot1.
DR InterPro; IPR002061; Scorpion_toxinL.
DR Pfam; PF00537; toxin3; 1.
DR ProDom; PD000908; Scorpion_toxinL; 1.
DR SMART; SM00505; Knot1; 1.
KW Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor;
KW 3D-structure.
FT DISULFID 12 60
FT DISULFID 16 36
FT DISULFID 22 43
FT DISULFID 26 45
FT SEQUENCE 63 AA; 7076 MW; 8BFEB36915AD8467 CRC64;
Query Match 100.0%; Score 23; DB 1; Length 63;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
DB 20 DYCND 24
RESULT 43
IBBI_COILA ID IBBI_COILA STANDARD; PRT; 64 AA.
AC P07679;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Bowman-Birk type trypsin inhibitor T11.
OS Coix lachryma-jobi (Jobs'tears).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Coix.
OX NCBI_TaxID=4505;
RN [1]
RP SEQUENCE.
RX MEDLINE=86152203; PubMed=3162215;
RA Ary M.B., Shewry P.R., Richardson M.;
RT "The amino acid sequence of a cereal Bowman-Birk type trypsin
RT inhibitor from seeds of Jobs' tears (Coix lachryma-jobi L.).";
RL FEBS Lett. 229:111-118(1988).
CC -!- SIMILARITY: Belongs to the Bowman-Birk serine protease inhibitor
CC family.
DR PIR; S00349; TIOAB.
DR HSSP; P56679; 1PBI.
DR InterPro; IPR000877; Bowman-Birk_leg.
DR Pfam; PF00228; Bowman-Birk_leg; 2.
DR ProDom; PD002168; Bowman-Birk_leg; 1.
DR SMART; SM00269; BowB; 1.
DR PROSITE; PS00281; BOWMAN_BIRK; 1.
KW Serine protease inhibitor.
FT ACT_SITE 17 18 INTERACTION WITH TRYPSIN (BY SIMILARITY).
FT DISULFID 9 61 BY SIMILARITY.
FT DISULFID 10 25 BY SIMILARITY.
FT DISULFID 15 23 BY SIMILARITY.
FT DISULFID 32 39 BY SIMILARITY.

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FT DISULFID 36 49 BY SIMILARITY.
SQ SEQUENCE 64 AA; 7270 MW; 2ED0BEFF063E891 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 64;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 30 DRCS D 34

RESULT 44
ID SIX1 BUTOC STANDARD; PRT; 65 AA.
AC P55902;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Insect toxin 1 (BotT1).
OS Buthus occitanus tunetanus (Common European scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butoidea; Buthidae; Buthus.
OX NCBI_TaxID=6871;
RN [1]_TaxID=6871;
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=97235474; PubMed=9080593;
RA Borhani L., Stankiewicz M., Kopeyan C., Mansuelle P., Kharat R.,
RA Cestele S., Karoui H., Rochat H., Pelhate M., el Ayeb M.;
RT "Purification, structure and activity of three insect toxins from
RT Buthus occitanus tunetanus venom.";
RL Toxicon 35:365-382(1997).
CC -!- FUNCTION: Binds to sodium channels and inhibits the inactivation
CC of the activated channels, thereby blocking neuronal transmission.
CC This contractive toxin is highly toxic to insects and barely toxic
CC to mammals.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=7334.93; MW_ERR=0.23; METHOD=Electrospray.
CC -!- MISCELLANEOUS: LD(50) is 50 mug/kg in mouse by
CC intracerebroventricular injection and 600 ng/g in Blatella
CC germanica.
CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
CC Alpha-toxin subfamily.
CC HSP; P01487; ILQ.
DR InterPro; IPR003614; Knot1.
DR InterPro; IPR001219; Neurotoxin.
DR InterPro; IPR002061; Scorpion_toxinL.
DR Pfam; PF00537; toxin_3; 1.
DR PRINTS; PR00284; TOXIN.
DR ProDom; PD000908; Scorpion_toxinL; 1.
DR SMART; SM00505; Knot1; 1.
FT Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor.
FT DISULFID 12 63 BY SIMILARITY.
FT DISULFID 16 36 BY SIMILARITY.
FT DISULFID 22 45 BY SIMILARITY.
FT DISULFID 26 48 BY SIMILARITY.
SQ SEQUENCE 65 AA; 7343 MW; 93A1371D877D7123 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 65;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 20 DYCD N 24

RESULT 45
Y777 TREPA
ID Y777 TREPA STANDARD; PRT; 74 AA.
AC O83756;

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DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein TP0777.
GN TP0777.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL Science 281:375-388(1998).
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CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; AE001249; AAC65750.1; --
DR PIR; B71282; B71282.
DR TIGR; TP0777; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 74 AA; 9018 MW; 299EB9E2CEC22DE5 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 74;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 29 DYCD N 33

RESULT 46
ID 15E1 HUMAN STANDARD; PRT; 76 AA.
AC O43715;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein 15E1.1 (Protein HSPC132).
GN 15E1.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy L.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=20499367; PubMed=11042152;
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells.";

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Genome Res. 10:1546-1560(2000).
[3]
SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datcher K.L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.K., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SIMILARITY: BELONGS TO THE UPF0203 (15E1.1) FAMILY.
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CC -----
DR EMBL; AL021546; CAA16495.1; -
DR EMBL; AF161481; AAF29096.1; -
DR EMBL; BC002638; AAO02638.1; -
DR PIR; T09476; T09476.
DR InterPro; IPR007918; UPF0203.
DR Pfam; PF05254; UPF0203; 1.
SQ SEQUENCE 76 AA; 8786 MW; 00B41AC399D76590 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 76;
Best Local Similarity 60.0%; Pred. No. 2.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 35 DPCTD 39

RESULT 47
15E1_MOUSE COMA CONMA STANDARD; PRT; 76 AA.
AC Q9D822;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein 15E1.1.
GN 15E1.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

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RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustineich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilmig L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- SIMILARITY: BELONGS TO THE UPF0203 (15E1.1) FAMILY.
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CC -----
DR EMBL; AK007514; BAB25082.1; -
DR MGD; MGI:1916326; 1810015M01Rik.
DR InterPro; IPR007918; UPF0203.
DR Pfam; PF05254; UPF0203; 1.
SQ SEQUENCE 76 AA; 8756 MW; 00B41AC389862094 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 76;
Best Local Similarity 60.0%; Pred. No. 2.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 35 DPCTD 39

RESULT 48
COMA CONMA STANDARD; PRT; 77 AA.
AC Q9TWL9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Conodipine-M alpha chain (EC 3.1.1.4).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=95181300; PubMed=7876086;
RA McIntosh J.M., Ghomashchi F., Gelb M.H., Dooley D.J., Stoehr S.J.,
RA Giordani A.B., Naisbitt S.R., Olivera B.M.;
RT "Conodipine-M, a novel phospholipase A2 isolated from the venom of the
RT marine snail Conus magus.";
RL J. Biol. Chem. 270:3518-3526(1995).
CC -!- FUNCTION: Conodipine-M catalyzes the calcium-dependent hydrolysis
CC of the 2-acyl groups in 3-sn-phosphoglycerides. This activity may
CC be supported by the alpha chain. Conodipine-M inhibits the binding
CC of isradipine (a ligand specific for L-type calcium channel) to L-
CC type calcium channels. It is inhibited by linoleoyl amide and
CC MG14.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Calcium.
CC -!- SUBUNIT: Conodipine-M consists of 2 subunits alpha and beta, which

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CC may be linked to each other through one or more disulfide bonds.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=8571; METHOD=Electrospray.
 CC -1- SIMILARITY: DISTANTLY RELATED TO THE PHOSPHOLIPASE A2 FAMILY.
 DR InterPro: IPR001211; PhospholipaseA2.
 KW Toxin; Hydrolase; Lipid degradation; Calcium;
 KW Pyrrolidone carboxylic acid.
 FT ACT SITE 36 36 POTENTIAL.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT SEQUENCE 77 AA; 8486 MW; 73861D7587479D8C CRC64;
 SQ
 Query Match 100.0%; Score 23; DB 1; Length 77;
 Best Local Similarity 60.0%; Pred. No. 2.8e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DXCXD 5
 Db 51 DDCDD 55
 RESULT 49
 FER_BACSC STANDARD; PRT; 77 AA.
 ID AC Q45560;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ferredoxin 7Fe (Seven-iron ferredoxin).
 GN FDXA.
 OS Bacillus schlegelii.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1484;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 43741;
 RX MEDLINE=94271256; PubMed=8003034;
 RA Aono S., Nakamura S., Aono R., Okura I.;
 RT "Cloning and expression of the gene encoding the 7Fe type ferredoxin
 RT from a thermophilic hydrogen oxidizing bacterium, Bacillus
 RT schlegelii.";
 RL J. Biochem. 112:792-795 (1992).
 RN [2]
 RN Biochem. Biophys. Res. Commun. 201:938-942 (1994).
 RN CHARACTERIZATION.
 RP MEDLINE=93203149; PubMed=1338329;
 RA Aono S., Kurita H., Uno S., Okura I.;
 RT "Purification and characterization of a 7Fe ferredoxin from a
 RT thermophilic hydrogen-oxidizing bacterium, Bacillus schlegelii.";
 RL J. Biochem. 112:792-795 (1992).
 RN [3]
 RP STRUCTURE BY NMR.
 RC STRAIN=ATCC 43741;
 RX MEDLINE=98322084; PubMed=9657695;
 RA Aono S., Bentrop D., Bertini I., Donaire A., Luchinat C., Nikura Y.,
 RA Rosato A.;
 RT "Solution structure of the oxidized Fe7S8 ferredoxin from the
 RT thermophilic bacterium Bacillus schlegelii by 1H NMR spectroscopy.";
 RL Biochemistry 37:9812-9826 (1998).
 RN [4]
 RP MUTAGENESIS OF ASP-13.
 RC MEDLINE=97420469; PubMed=9276454;
 RA Aono S., Bentrop D., Bertini I., Luchinat C., Macinai R.;
 RT "The D13C variant of Bacillus schlegelii 7Fe ferredoxin is an 8Fe
 RT ferredoxin as revealed by 1H-NMR spectroscopy.";
 RL FEBS Lett. 412:501-505 (1997).
 CC -1- COFACTOR: Binds 1 4Fe-4S cluster and a 3Fe-4S cluster.
 CC -1- SUBUNIT: Monomer.
 CC -1- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
 CC
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 CC -----
 DR EMBL: D29804; BAA06187.1; -
 DR PIR: J2496; JC2496.
 DR PDB: 1BC6; 17-JUN-98.
 DR PDB: 1BD6; 17-JUN-98.
 DR PDB: 1BQX; 26-AUG-98.
 DR PDB: 1BWE; 30-SEP-98.
 DR InterPro: IPR001450; 4Fe4S_ferredoxin.
 DR InterPro: IPR000813; 7Fe_ferredoxin.
 DR Pfam: PF00037; fer4; 2.
 DR PRINTS: PR00354; 7FE8SFRDXIN.
 DR PROSITE: PS00198; 4Fe4S_FERREDOXIN; 1.
 KW Electron transport; Iron-sulfur; 4Fe-4S; 3Fe-4S; 3D-structure.
 FT INIT MET 0 0
 FT METAL 8 8 IRON-SULFUR 1 (3FE-4S).
 FT METAL 16 16 IRON-SULFUR 1 (3FE-4S).
 FT METAL 20 20 IRON-SULFUR 2 (4FE-4S).
 FT METAL 39 39 IRON-SULFUR 2 (4FE-4S).
 FT METAL 42 42 IRON-SULFUR 2 (4FE-4S).
 FT METAL 45 45 IRON-SULFUR 2 (4FE-4S).
 FT METAL 49 49 IRON-SULFUR 1 (3FE-4S).
 FT MUTAGEN 13 13 D->C: TRANSFORMATION FROM A 7S TO 8S
 FT STRAND 2 3 FERREDOXIN.
 FT HELIX 6 8
 FT TURN 9 11
 FT HELIX 17 19
 FT TURN 21 22
 FT STRAND 25 27
 FT STRAND 32 34
 FT TURN 36 38
 FT HELIX 44 48
 FT STRAND 50 52
 FT STRAND 55 56
 FT TURN 57 59
 FT HELIX 62 75
 SQ SEQUENCE 77 AA; 8743 MW; 4CSA06AB2ED34D93 CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 77;
 Best Local Similarity 60.0%; Pred. No. 2.8e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DXCXD 5
 Db 37 DVCID 41
 RESULT 50
 FER_ALIAC STANDARD; PRT; 78 AA.
 ID AC P03941;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ferredoxin.
 OS Alicyclobacillus acidocaldarius (Bacillus acidocaldarius).
 OC Bacteria; Firmicutes; Bacillales; Alicyclobacillaceae;
 OC Alicyclobacillus.
 OX NCBI_TaxID=1388;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85225952; PubMed=2988582;
 RA Schlatter D., Walldvogel S., Zulli F., Suter F., Portmann W.,
 RA Zuber H.;
 RT "Purification, amino-acid sequence and some properties of the
 RT ferredoxin isolated from Bacillus acidocaldarius.";
 RL Biol. Chem. Hoppe-Seyler 366:223-231 (1985).
 CC -1- FUNCTION: Ferredoxins are iron-sulfur proteins that transfer
 CC electrons in a wide variety of metabolic reactions.
 CC -1- COFACTOR: Binds 1 3Fe-4S and 1 4Fe-4S cluster (probable).
 CC

CC -!- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
 DR PIR; A00215; FEBSA.
 DR HSP; Q45560; 1BD6.
 DR InterPro; IPR001450; 4Fe4S ferredoxin.
 DR InterPro; IPR000813; 7Fe_ferredoxin.
 DR Pfam; PF00037; fer4; 1
 DR PRINTS; PR00354; 7FE8SFRDXXIN.
 DR PROSITE; PS00198; 4FE4S_FERREDXXIN; 1.
 KW Electron transport; Iron-sulfur; Repeat; 4Fe-4S; 3Fe-4S.
 FT METAL 8
 FT METAL 16
 FT METAL 20
 FT METAL 39
 FT METAL 42
 FT METAL 45
 FT METAL 49
 FT METAL 49
 SQ SEQUENCE 78 AA; 8872 MW; AF09FE2C4D7D2F0E CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 78;
 Best Local Similarity 60.0%; Pred. No. 2.8e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DXCXD 5
 DB 37 DLICID 41
 RESULT 51
 SAP_PIG STANDARD; PRT; 80 AA.
 AC P81405;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Saposin B (Cerebroside sulfate activator) (CS-ACT) (Non-specific
 DE activator) (Sphingolipid activator protein 1) (SAP-1).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE OF 1-79.
 RC TISSUE=Kidney;
 RX MEDLINE=93229506; PubMed=8471613;
 RA Stevens R.L., Faull K.F., Conklin K.A., Green B.N., Fluharty A.L.;
 RT "Porcine cerebroside sulfate activator: further structural
 RT characterization and disulfide identification.";
 RL Biochemistry 32:4051-4059(1993).
 RN [2]
 RP SEQUENCE OF 1-64.
 RC TISSUE=Kidney;
 RX MEDLINE=92222651; PubMed=1562358;
 RA Fluharty A.L., Katona Z., Meek W.E., Frei K., Fowler A.V.;
 RT "The cerebroside sulfate activator from pig kidney: purification and
 RT molecular structure.";
 RL Biochem. Med. Metab. Biol. 47:66-85(1992).
 RN [3]
 RP STRUCTURE OF CARBOHYDRATE ON ASN-21.
 RX MEDLINE=21110404; PubMed=11180632;
 RA Faull K.F., Johnson J., Kim M.J., To T., Whitelegge J.P.,
 RA Stevens R.L., Fluharty C.B., Fluharty A.L.;
 RT "Structure of the asparagine-linked sugar chains of porcine kidney and
 RT human urine cerebroside sulfate activator protein.";
 RL J. Mass Spectrom. 35:1416-1424(2000).
 RN [4]
 RP MASS SPECTROMETRY.
 RC TISSUE=Kidney;
 RX MEDLINE=99441404; PubMed=10510427;
 RA Faull K.F., Whitelegge J.P., Higginson J., To T., Johnson J.,
 RA Krutchinsky A.N., Standing K.G., Waring A.J., Stevens R.L.,
 RA Fluharty C.B., Fluharty A.L.;
 RT "Cerebroside sulfate activator protein (Saposin B): chromatographic
 RT and electrospray mass spectrometric properties.";

J. Mass Spectrom. 34:1040-1054(1999).
 -!- FUNCTION: Saposin B stimulates the hydrolysis of galacto-
 CC cerebroside sulfate by arylsulfatase A (EC 3.1.6.8), GM1
 CC ganglioside by beta-galactosidase (EC 3.2.1.23) and
 CC globosiosylceramide by alpha-galactosidase A (EC 3.2.1.22).
 CC Saposin B forms a solubilizing complex with the substrates of the
 CC sphingolipid hydrolases.
 CC -!- SUBUNIT: Saposin B is a homodimer (By similarity).
 CC -!- PTM: The one residue extended Saposin B-Val is only found in a
 CC minority of the chains.
 CC -!- SIMILARITY: Contains 1 saposin B-type domain.
 DR GlycoSuiteDB; P81405; -
 DR InterPro; IPR007856; SapB_1.
 DR InterPro; IPR008138; SapB_2.
 DR InterPro; IPR008373; Saposin.
 DR InterPro; IPR008139; SaposinB.
 DR Pfam; PF05184; SapB_1; 1.
 DR Pfam; PF03489; SapB_2; 1.
 DR PRINTS; PR01797; SAPOSIN.
 DR SMART; SMO0118; SAPB; 1.
 KW Glycoprotein; Sphingolipid metabolism.
 FT CHAIN 1 79
 FT CHAIN 1 80
 FT DOMAIN 1 80
 FT DISULFID 4 77
 FT DISULFID 7 71
 FT DISULFID 36 47
 FT CARBOHYD 21 21
 FT N-LINKED (GLCNAC. . .) (COMPLEX).
 FT /FTID=CAR_000177.
 SQ SEQUENCE 80 AA; 8949 MW; EF7BA249B63E789C CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 80;
 Best Local Similarity 60.0%; Pred. No. 2.9e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DXCXD 5
 DB 2 DVCQD 6
 RESULT 52
 NUML_HUMAN STANDARD; PRT; 81 AA.
 AC O00483;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE NADH-ubiquinone oxidoreductase MLRQ subunit (EC 1.6.5.3) (EC 1.6.99.3)
 DE (Complex I-MLRQ) (CI-MLRQ).
 GN NDUF44.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98013339; PubMed=9352085;
 RA Kim J.W., Lee Y., Kang H.B., Chose Y.K., Chung T.W., Chang S.Y.,
 RA Lee K.S., Choe I.S.;
 RT "Cloning of the human cDNA sequence encoding the NADH:ubiquinone
 RT oxidoreductase MLRQ subunit.";
 RL Biochem. Mol. Biol. Int. 43:669-675(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kanagarajan D., Raha S., Scherer S., Robinson B.H.;
 RT "Genomic sequence, cDNA sequence and chromosomal localization of the
 RT NDUF44 human gene coding for the MLRQ subunit of NADH:ubiquinone
 RT oxidoreductase and its pseudogene.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Transfer of electrons from NADH to the respiratory
 CC chain. The immediate electron acceptor for the enzyme is believed
 CC to be ubiquinone.

CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
 CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane; matrix side.
 CC -!- SIMILARITY: Belongs to the complex I NDUF4 subunit family.
 CC -----
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 CC -----
 CC EMBL; U94586; AAB52726.1; -
 CC EMBL; AF201077; AAF09253.1; -
 CC MIM; 603833; -
 CC DR GO; 0008137; F:NADH dehydrogenase (ubiquinone) activity; TAS.
 CC Oxidoreductase; NAD, Ubiquinone; Mitochondrion.
 CC KW OXIDOREDUCTASE; NAD, Ubiquinone; Mitochondrion.
 CC SQ SEQUENCE 81 AA; 9370 MW; 2FAID1115EDE24C7 CRC64;
 CC -----
 CC Query Match 100.0%; Score 23; DB 1; Length 81;
 CC Best Local Similarity 60.0%; Pred. No. 2.9e+02;
 CC Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 1 DXCXD 5
 CC |::|
 CC Db 42 DVCWD 46
 CC -----
 CC RESULT 53
 CC PORD METH
 CC ID PORD METH STANDARD; PRT; 81 AA.
 CC AC PS6815;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Pyruvate synthase subunit pord [EC 1.2.7.1] (Pyruvate oxidoreductase
 CC delta chain) (POR) (Pyruvate-ferredoxin oxidoreductase delta subunit).
 CC GN PORD OR MTH1740.1.
 CC OS Methanobacterium thermoautotrophicum.
 CC OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 CC OC Methanobacteriaceae; Methanothermobacter.
 CC OX NCBI_TaxID=187420;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=Delta H;
 CC RX MEDLINE=98037514; PubMed=9371463;
 CC RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 CC RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 CC RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 CC RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 CC RA Jiawani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 CC RA McDougall S., Shiner G., Goyal A., Pietrowski S., Church G.M.,
 CC RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 CC RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 CC deltaH: functional analysis and comparative genomics."; J.
 CC RL J. Bacteriol. 179:7135-7155(1997)
 CC CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
 CC CoA + CO(2) + reduced ferredoxin.
 CC CC -!- COFACTOR: Binds 2 4Fe-4S clusters.
 CC CC -!- SUBUNIT: Heterotrimer of one alpha, one beta, one delta and one
 CC gamma chain.
 CC CC -!- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
 CC CC -!- CAUTION: THERE SEEMS TO BE A SEQUENCING ERROR THAT FUSES TOGETHER
 CC PORC AND PORD. WE HAVE CUT THE ORF INTO ITS TWO CONSTITUENTS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AE000929; AAB86210.1; ALT_INIT.
 CC DR HSSP; P00195; 1CLF.
 CC DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 CC DR Pfam; PF00037; fe4; 2.
 CC DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
 CC KW Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S;
 CC KW Complete proteome.
 CC FT METAL 34 34 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).
 CC FT METAL 37 37 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).
 CC FT METAL 40 40 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).
 CC FT METAL 44 44 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).
 CC FT METAL 60 60 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).
 CC FT METAL 63 63 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).
 CC FT METAL 66 66 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).
 CC FT METAL 70 70 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).
 CC SQ SEQUENCE 81 AA; 9121 MW; 219A9CCEA8A41604 CRC64;
 CC -----
 CC Query Match 100.0%; Score 23; DB 1; Length 81;
 CC Best Local Similarity 60.0%; Pred. No. 2.9e+02;
 CC Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 1 DXCXD 5
 CC |::|
 CC Db 32 DKCID 36
 CC -----
 CC RESULT 54
 CC IT15 ARATH
 CC ID IT15 ARATH STANDARD; PRT; 85 AA.
 CC AC O22867;
 CC DT 15-JUL-1998 (Rel. 36, Created)
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Putative trypsin inhibitor At2g43530 precursor.
 CC GN AT2G43530 OR T01024.27.
 CC OS Arabidopsis thaliana (Mouse-ear cress).
 CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 CC OX NCBI_TaxID=3702;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=cv. Columbia;
 CC RX MEDLINE=20083487; PubMed=10617197;
 CC RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 CC RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 CC RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
 CC RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 CC RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 CC RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 CC RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 CC RA Venter J.C.;
 CC RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 CC thaliana."; J.
 CC RL Nature 402:761-768(1999).
 CC CC -!- SIMILARITY: BELONGS TO THE RTI/MTI-2 PROTEASE INHIBITORS FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; ACO02335; AAB64336.1; -
 CC PIR; C84867; C84867.
 CC DR InterPro; IPR003614; Knot1.
 CC DR InterPro; IPR008679; MTI-2.
 CC Pfam; PF05828; MTI-2; 1.


```
DR SMART; SM00505; Knot1; 1.
KW Serine protease inhibitor; signal; Multigene family.
FT SIGNAL 1 29
FT CHAIN 30 85 PUTATIVE TRYPSIN INHIBITOR AT2G43530.
FT DISULFID 34 80 BY SIMILARITY.
FT DISULFID 46 70 BY SIMILARITY.
FT DISULFID 55 75 BY SIMILARITY.
FT DISULFID 59 77 BY SIMILARITY.
FT ACT SITE 49 50 REACTIVE-BOND (BY SIMILARITY).
SQ SEQUENCE 85 AA; 9596 MW; C96D38F723D35BD5 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 85;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 78 DFCSD 82

RESULT 55
TXM2 DENAN STANDARD; PRT; 86 AA.
AC P18328;
DT 01-NOV-1990 (Rel. 16, Created)
DT 28-FEB-2003 (Rel. 16, Last sequence update)
DE Muscarinic toxin 2 precursor.
OS Dendroaspis angusticeps (Eastern green mamba).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Dendroaspis.
OX NCBI_TaxID=8618;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=91320365; PubMed=1862524;
RA Duncanson F., Rowan E.G., Caesar E., Harvey A.L., Menez A.,
RA Boulain J.-C.;
RT "Amino acid sequence of a muscarinic toxin deduced from the cDNA
RT nucleotide sequence.";
RL Toxicon 29:516-520(1991).
RN [2]
RP SEQUENCE OF 22-86.
RC TISSUE=Venom;
RX MEDLINE=91320366; PubMed=1862525;
RA Karlsson E., Risinger C., Jolkonen M., Wernstedt C., Adam A.;
RT "Amino acid sequence of a snake venom toxin that binds to the
RT muscarinic acetylcholine receptor.";
RL Toxicon 29:521-526(1991).
CC -!- FUNCTION: Binds to the muscarinic acetylcholine receptor.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the snake toxin family.
CC -----
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CC -----
DR EMBL; X52292; CAA36541.1; -.
DR PIR; A37910; A37910.
DR HSP; P01382; INTN.
DR InterPro; IPR003572; Cytotoxin.
DR Pfam; PF00087; toxin.1.
DR PRINTS; PR00282; CYTOTOXIN.
DR ProDom; PD000206; Snake_toxin; 1.
DR PROSITE; PS00272; SNAKE_TOXIN; 1.
KW Toxin; Neurotoxin; Signal.
```

```
FT SIGNAL 1 21
FT CHAIN 22 86 MUSCARINIC TOXIN 2.
FT DISULFID 24 45 BY SIMILARITY.
FT DISULFID 38 63 BY SIMILARITY.
FT DISULFID 67 78 BY SIMILARITY.
FT DISULFID 79 84 BY SIMILARITY.
SQ SEQUENCE 86 AA; 9375 MW; 6F062C970074D653 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 86;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 82 DKCND 86

RESULT 56
NUOS HUMAN STANDARD; PRT; 87 AA.
ID NUOS_HUMAN
AC Q9NRX3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NADH:ubiquinone oxidoreductase MLRQ subunit homolog (NUOMS).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal gland;
RX MEDLINE=20402571; PubMed=10931946;
RA Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,
RA Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,
RA Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,
RA Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,
RA Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;
RT "Gene expression profiling in the human hypothalamus-pituitary-adrenal
RT axis and full-length cDNA cloning.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SIMILARITY: Belongs to the complex 1 NUFA4 subunit family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF164796; AAF80760.1; -.
DR EMBL; BC011910; AAH11910.1; -.
SQ SEQUENCE 87 AA; 9566 MW; A08D7182A0A3CA87 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 87;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 47 DVCWD 51

RESULT 57
Y898 MYCTU
ID Y898 MYCTU STANDARD; PRT; 87 AA.
AC Q10566;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein Rv0898c/MT0921.1/Nb0922c.
GN Rv0898c OR MT0921.1 OR MTCV31.26C OR Mb0922c.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekle A.F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL J. Bacteriol. 184:5479-5490(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
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CC -----
DR EMBL; Z73101; CAA37373.1; -.
DR EMBL; AE006979; AAK45168.1; -.
DR EMBL; BX248337; CAD93783.1; -.
DR PIR; G70782; G70782.
DR TIGR; MT0921.1; -.
DR TubercuList; Rv0898c; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 87 AA; 9920 MW; 79D055AB95C09BB2 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 87;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 52 DQCWD 56

RESULT 58
Y06G BPT4
ID Y06G BPT4 STANDARD; PRT; 88 AA.
AC P13314;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 10.2 kDa protein in regA-denv intergenic region.
GN Y06G OR VS.4 OR 62.5.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=10665;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87066735; PubMed=3024113;
RA Valerie K., Stevens J., Lynch M., Henderson E.E., de Riel J.K.;
RT "Nucleotide sequence and analysis of the 58.3 to 65.5-kb early region
RT of bacteriophage T4."
RL Nucleic Acids Res. 14:8637-8654(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22514363; PubMed=12626685;
RA Miller E.S., Kutter E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
RT "Bacteriophage T4 genome."
RL Microbiol. Mol. Biol. Rev. 67:86-156(2003).
CC
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```
Query Match 100.0%; Score 23; DB 1; Length 88;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 45 DNCED 49

RESULT 59
IT12 ARATH
ID IT12 ARATH STANDARD; PRT; 89 AA.
AC Q42328; O22865;
```

FT	DISULFID	58	81
FT	ACT_SITE	48	49.
FT	CONFLICT	85	
SQ	SEQUENCE	89 AA; 9885 MW;	C4FA5D0B3ABB03D5 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 89;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY	1 DXCXD 5
Db	82 DFCD 86

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RESULT 60
IT16 ARATH
ID IT16 ARATH STANDARD; PRT; 89 AA.
AC Q22869;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative trypsin inhibitor AT2G43550 precursor.
GN AT2G43550 OR T01024.29.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid I; Brassicales; Brassicaceae; Arabidopsids.
NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X.C., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RA thaliana.";
RL Nature 402:761-768(1999).
CC -! SIMILARITY: BELONGS TO THE RTI/MTI-2 PROTEASE INHIBITORS FAMILY.
CC -----
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CC -----
CC EMBL; AC002335; AAB64322.2; ALT_INIT.
DR PIR; E84867; E84867.
DR GO; GO:0030304; F:trypsin inhibitor activity; NAS.
DR InterPro; IPR003614; Knot1.
DR InterPro; IPR008679; MTI-2.
DR Pfam; PF05828; MTI-2; 1.
DR SMART; SM00505; Knot1; 1.
DR Serine protease inhibitor; Signal; Multigene family.
KW SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 89 PUTATIVE TRYP SIN INHIBITOR AT2G43550.
FT FT DISULFID 33 86 BY SIMILARITY.
FT FT DISULFID 46 70 BY SIMILARITY.
FT FT DISULFID 55 81 BY SIMILARITY.
FT FT DISULFID 59 83 BY SIMILARITY.
FT ACT SITE 49 50 REACTIVE-BOND (BY SIMILARITY).
SQ SEQUENCE 89 AA; 10192 MW; C0964810F33099A3 CRC64;

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Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 89;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY      1 DXCD 5
DB      84 DYCD 88

RESULT 61
IT14_ARATH
ID      IT14_ARATH      STANDARD;      PRT;      90 AA.
AC      O22866;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Putative trypsin inhibitor At2g43520 precursor.
GN      AT2g43520 OR T01024.26.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsids.
ON      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=cv. Columbia;
RX      MEDLINE=20083487; PubMed=10611717;
RA      Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA      Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA      Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA      Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA      Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA      Goodman H.M., Somerville C.R., Coppenhaver G.P., Preuss D.,
RA      Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA      Venter J.C.;
RT      "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT      thaliana.";
RL      Nature 402:761-768(1999).
CC      -1- SIMILARITY: BELONGS TO THE RT1/MTI-2 PROTEASE INHIBITORS FAMILY.
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-----
EMBL; AC002335; AB864324.1; -
DR      PIR; B84867; B84867.
DR      InterPro; IPR003614; Knot1.
DR      InterPro; IPR008679; MTI-2.
DR      Pfam; PF05828; MTI-2; 1.
DR      SMART; SM00505; Knot1; 1.
KW      Serine protease inhibitor; Signal; Multigene family.
FT      SIGNAL      1      27
FT      CHAIN      28      90
FT      DISULFID      32      86
FT      DISULFID      45      69
FT      DISULFID      54      81
FT      DISULFID      58      83
FT      ACT_SITE      48      49
SQ      SEQUENCE      90 AA; 9660 MW; 405F8A927F5A9F6A CRC64;
Query Match      100.0%; Score 23; DB 1; Length 90;
Best Local Similarity      60.0%; Pred. No. 3.3e+02;
Matches      3; Conservative      2; Mismatches      0; Indels      0; Gaps      0;
QY      1 DXCD 5
DB      84 DYCD 88

RESULT 62
YORK_TTV1
ID      YORK_TTV1      STANDARD;      PRT;      90 AA.
AC      O22866;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Putative trypsin inhibitor At2g43520 precursor.
GN      AT2g43520 OR T01024.26.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsids.
ON      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=cv. Columbia;
RX      MEDLINE=20083487; PubMed=10611717;
RA      Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA      Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA      Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA      Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA      Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA      Goodman H.M., Somerville C.R., Coppenhaver G.P., Preuss D.,
RA      Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA      Venter J.C.;
RT      "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT      thaliana.";
RL      Nature 402:761-768(1999).
CC      -1- SIMILARITY: BELONGS TO THE RT1/MTI-2 PROTEASE INHIBITORS FAMILY.
-----
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-----
EMBL; AC002335; AB864324.1; -
DR      PIR; B84867; B84867.
DR      InterPro; IPR003614; Knot1.
DR      InterPro; IPR008679; MTI-2.
DR      Pfam; PF05828; MTI-2; 1.
DR      SMART; SM00505; Knot1; 1.
KW      Serine protease inhibitor; Signal; Multigene family.
FT      SIGNAL      1      27
FT      CHAIN      28      90
FT      DISULFID      32      86
FT      DISULFID      45      69
FT      DISULFID      54      81
FT      DISULFID      58      83
FT      ACT_SITE      48      49
SQ      SEQUENCE      90 AA; 9660 MW; 405F8A927F5A9F6A CRC64;
Query Match      100.0%; Score 23; DB 1; Length 90;
Best Local Similarity      60.0%; Pred. No. 3.3e+02;
Matches      3; Conservative      2; Mismatches      0; Indels      0; Gaps      0;
QY      1 DXCD 5
DB      84 DYCD 88

RESULT 63
GATC_HALN1
ID      GATC_HALN1      STANDARD;      PRT;      91 AA.
AC      Q9HR44;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Glucamyl-CRGA (Gln) amidotransferase subunit C (EC 6.3.5.-) (Glu-ADT
DE      subunit C).
GN      GATC OR VNG0870G.
OS      Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC      Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC      Halobacteriaceae; Halobacterium.
ON      NCBI_TaxID=64091;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20504483; PubMed=11016950;
NG      W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA      Shukla H.D., Lasky S.R., Baliga N.S., Thorsen V., Sbrogna J.,
RA      Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA      Leithausen B., Keller K., Cruz R., Danon M.J., Hough D.W.,
RA      Maddocks D.G., Jablonka P.E., Krebs M.P., Angevine C.M., Dale H.,
RA      Isenbarger T.A., Beck R.F., Pohlenschroder M., Spudich J.L., Jung K.-H.,
RA      Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA      Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT      "Genome sequence of Halobacterium species NRC-1.";
RT      Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC      -1- FUNCTION: Allows the formation of correctly charged Asn-tRNA(Asn)
CC      or Gln-tRNA(Gln) through the transamidation of misacylated Asp-
CC      tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both
CC      of asparaginyl-tRNA or glutamyl-tRNA synthetases. The reaction
CC      takes place in the presence of glutamine and ATP through an
CC      activated phospho-Asp-tRNA(Asn) or phospho-Glu-tRNA(Gln) (By
CC      similarity).
CC      -1- CATALYTIC ACTIVITY: ATP + L-glutamyl-tRNA(Gln) + L-glutamine = ADP
CC      + phosphate + L-glutamyl-tRNA(Gln) + L-glutamate.
CC      -1- CATALYTIC ACTIVITY: ATP + L-aspartyl-tRNA(Asn) + L-glutamine = ADP
CC      + phosphate + L-asparaginyl-tRNA(Asn) + L-glutamate.

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CC -!- SUBUNIT: Heterotrimer of A, B and C subunits (By similarity).
CC -!- SIMILARITY: Belongs to the gatC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE005026; AAG19314.1; ALT_INIT.
CC HAMAP; MF_00122; -. 1.
CC InterPro; IPR003837; Glu-trnAGln.
CC Pfam; PF02686; Glu-trnAGln; 1.
CC Protein biosynthesis; Ligase; Complete proteome.
CC SEQUENCE 91 AA; 10129 MW; 721DCE34F1A8ECD4 CRC64;
CC -----
Query Match 100.0%; Score 23; DB 1; Length 91;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
DB 31 DHCGD 35
-----
RESULT 64
SY22_MOUSE STANDARD; PRT; 92 AA.
AC O88430;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-WAR-2004 (Rel. 43, Last annotation update)
DE Small inducible cytokine A22 precursor (CCL22) (CC chemokine ABCD-1)
DE (Activated B and dendritic cell-derived).
GN CCL22 OR SCYA22 OR ABCD1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98353531; PubMed=9687523;
RA Schaniel C., Pardali E., Sallusto F., Spelietas M., Ruedl C.,
RA Shimizu T., Seidl T., Andersson J., Melchers F., Rolink A.G.,
RA Sideras P.;
RT "Activated murine B lymphocytes and dendritic cells produce a novel
RT C chemokine which acts selectively on activated T cells.";
RL J. Exp. Med. 188:451-463(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length

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RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Chemotactic for activated T lymphocytes. May play an
CC important role in the collaboration of dendritic cells and B
CC lymphocytes with T cells in immune responses.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by activated splenic B lymphocytes
CC and dendritic cells. Low expression in lung, thymocytes, lymph
CC node, and unstimulated splenic cells.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC -----
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CC -----
CC EMBL; AF052505; AAC40200.1; -.
CC EMBL; BC012658; AAH12658.1; -.
CC HSSP; Q98157; 1CM9.
CC MGD; MGI:1306779; Ccl22
CC InterPro; IPR000827; CC_chemokine_sml.
CC InterPro; IPR001811; Chemokine_IL8.
CC Pfam; PF00048; IL8; 1.
CC SMART; SM00199; SCY; 1.
CC PROSITE; PS00472; SMALL_CYTOKINES_CC; FALSE NEG.
KW Cytokine; Chemotaxis; Signal; Inflammatory Response.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 92 SMALL INDUCIBLE CYTOKINE A22.
FT DISULFID 36 60 BY SIMILARITY.
FT DISULFID 37 76 BY SIMILARITY.
SQ SEQUENCE 92 AA; 10302 MW; 39859881CDAE07CA CRC64;
Query Match 100.0%; Score 23; DB 1; Length 92;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DXCXD 5
DB 74 DICAD 78
-----
RESULT 65
FER1_AFIPE
ID FER1_AFIPE STANDARD; PRT; 93 AA.
AC Q44037;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ferredoxin 1 (Fragment).
GN PDXA
CN Afipia felis (Cat scratch disease bacillus).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Afipia.
OX NCBI_TaxID=1035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49716;
RX MEDLINE=95222000; PubMed=7535830;
RA Bergmans A.M.C., Groothedde J.W., Schellekens J.F.P.,
RA van Embden J.M.C., Osewaarde J.M., Schouls L.M.;
RA "Etology of cat scratch disease: comparison of polymerase chain
RT reaction detection of Bartonella (formerly Rochalimaea) and Afipia
RT felis DNA with serology and skin tests.";
RL J. Infect. Dis. 171:916-923(1995).
CC -!- COFACTOR: Binds 1 4Fe-4S cluster and 1 3Fe-4S cluster.
CC -!- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
CC -----
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DR EMBL; X01826; CAA57420.1; -.
DR HSP; P00214; IFRH.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR Pfam; PF00037; fer4_2; ferredoxin.
DR PRINTS; PR00354; 7FE8SFPROXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW Electron transport; Iron-sulfur; Repeat; 4Fe-4S; 3Fe-4S.
FT METAL 9
FT METAL 17 17 IRON-SULFUR 1 (3FE-4S) (BY SIMILARITY).
FT METAL 21 21 IRON-SULFUR 1 (3FE-4S) (BY SIMILARITY).
FT METAL 40 40 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 43 43 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 46 46 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 50 50 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT NON_TER 93
SQ SEQUENCE 93 AA; 10556 MW; 429C09DADF6368BE2 CRC64;

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Query Match 100.0%; Score 23; DB 1; Length 93;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
   |::|
DB 38 DECID 42

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RESULT 66
SI10_PIG
ID SI10_PIG STANDARD; PRT; 94 AA.
AC P05943;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calpactin I light chain (p10 protein) (P11) (Cellular ligand of
DE annexin II) (Nerve growth factor induced protein 42C).
GN SI00A10.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88125019; PubMed=3422491;
RA Maslakowski P.; Shooter E.M.;
RT "Nerve growth factor induces the genes for two proteins related to a
RT family of calcium-binding proteins in PC12 cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1277-1281(1988).
CC -!- FUNCTION: Because p10 induces the dimerization of annexin II
CC in that the p36 monomer is the preferred target (in vitro) of
CC tyrosine-specific kinase.
CC -!- SUBUNIT: Tetramer of 2 light chains (p10) and 2 heavy chains
CC (annexin II).
CC -!- INDUCTION: By nerve growth factor.
CC -!- MISCELLANEOUS: p10 does not appear to bind calcium.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC -----
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DR EMBL; J03627; AAA42097.1; -.
DR PIR; A31373; A31373.
DR HSP; P08206; IA4P.
DR InterPro; IPR001751; CaBP_S100.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00303; S100_CABP; 1.
FT INIT_MET 0
FT DOMAIN 59 70 ANCESTRAL CALCIUM SITE.
SQ SEQUENCE 94 AA; 10944 MW; 8C8B9F9CE8F5221 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 94;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
   |::|
DB 59 DQCRD 63

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RESULT 67
SI10_PIG
ID SI10_PIG STANDARD; PRT; 95 AA.
AC P04163;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calpactin I light chain (p10 protein) (P11) (Cellular ligand of
DE annexin II).
GN SI00A10.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=86055730; PubMed=2998764;
RA Gerke V.; Weber K.;
RT "The regulatory chain in the p36-kd substrate complex of viral
RT tyrosine-specific protein kinases is related in sequence to the
RL S-100 protein of glial cells.";
RL EMBO J. 4:2917-2920(1985).
CC -!- FUNCTION: Because p10 induces the dimerization of annexin II
CC (p36), it may function as a regulator of protein phosphorylation
CC in that the p36 monomer is the preferred target (in vitro) of
CC tyrosine-specific kinase.
CC -!- SUBUNIT: Tetramer of 2 light chains (p10) and 2 heavy chains
CC (annexin II).
CC -!- MISCELLANEOUS: p10 does not appear to bind calcium.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
DR PIR; A03079; LUPG10.
DR HSP; P08206; IA4P.
DR InterPro; IPR001751; CaBP_S100.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00303; S100_CABP; 1.
FT DOMAIN 59 70 ANCESTRAL CALCIUM SITE.
SQ SEQUENCE 95 AA; 10944 MW; 67933FEE4D837D2C CRC64;

Query Match 100.0%; Score 23; DB 1; Length 95;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
   |::|
DB 59 DQCRD 63

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RESULT 68
S110 CHICK
ID S110 CHICK STANDARD; PRT; 96 AA.
AC P27003;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calpactin I light chain (P10 protein) (P11) (Cellular ligand of
DE annexin II).
GN S100A10.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91340161; PubMed=1831433;
RA Kube E., Weber K., Gerke V.;
RT "Primary structure of human, chicken, and Xenopus laevis p11, a
RT cellular ligand of the Src-kinase substrate, annexin II."
RL Gene 102:255-259(1991).
CC -!- FUNCTION: Because p10 induces the dimerization of annexin II
CC (p36), it may function as a regulator of protein phosphorylation
CC in that the p36 monomer is the preferred target (in vitro) of
CC tyrosine-specific kinase.
CC -!- SUBUNIT: Tetramer of 2 light chains (p10) and 2 heavy chains
CC (annexin II).
CC -!- MISCELLANEOUS: p10 does not appear to bind calcium.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC
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CC
DR EMBL; M38592; AAA48690.1; -.
DR FIR; JH0663; JH0663.
DR HSP; P08206; IAP4.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF01023; S_100_1.
DR ProDom; PD003407; CaBP_S100; 1.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00303; S100_CaBP; 1.
FT INIT MET 0 0
FT DOMAIN 59 70 ANCESTRAL CALCIUM SITE.
SQ SEQUENCE 96 AA; 11159 MW; 2C0B0CD68CF9885B CRC64;

Query Match 100.0%; Score 23; DB 1; Length 96;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 59 DQCRD 63

RESULT 69
S110 HUMAN
ID S110 HUMAN STANDARD; PRT; 96 AA.
AC P08206;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calpactin I light chain (P10 protein) (P11) (Cellular ligand of
DE annexin II).
GN S100A10 OR CAL1L OR ANX2LG OR CLP11.

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OS Homo sapiens (Human), and
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91340161; PubMed=1831433;
RA Kube E., Weber K., Gerke V.;
RT "Primary structure of human, chicken, and Xenopus laevis p11, a
RT cellular ligand of the Src-kinase substrate, annexin II."
RL Gene 102:255-259(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES=Human;
RX MEDLINE=92241679; PubMed=1533380;
RA Harder T., Kube E., Gerke V.;
RT "Cloning and characterization of the human gene encoding p11:
RT structural similarity to other members of the S-100 gene family."
RL Gene 113:269-274(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX SPECIES=Human; TISSUE=Keratinocytes;
RX MEDLINE=92347895; PubMed=1386341;
RA Dooley T.P., Weiland K.L., Simon M.;
RT "cDNA sequence of human p11 calpactin I light chain."
RL Genomics 13:866-868(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX SPECIES=Human; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX SPECIES=Bovine;
RX MEDLINE=87280130; PubMed=3038891;
RA Saris C.J.M., Kristensen T., D'Eustachio P., Hicks L.J., Noonan D.J.,
RA Glenney J.R. Jr., Hunter T., Tack B.F.;
RT "cDNA sequence and tissue distribution of the mRNA for bovine and
RT murine p11, the S100-related light chain of the protein-tyrosine
RT kinase substrate p36 (calpactin I)."
RL J. Biol. Chem. 262:10663-10671(1987).
RN [6]
RP SEQUENCE OF 1-56.
RX SPECIES=Bovine;
RX MEDLINE=86068007; PubMed=2415974;
RA Glenney J.R. Jr., Tack B.F.;
RT "Amino-terminal sequence of p36 and associated p10: identification of
RT the site of tyrosine phosphorylation and homology with S-100."
RL Proc. Natl. Acad. Sci. U.S.A. 82:7884-7888(1985).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.25 ÅNGSTRÖMS).
RX SPECIES=Human;

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RX MEDLINE=99101388; PubMed=9886297;
RA Rety S., Sopkova J., Renouard M., Osterloh D., Gerke V., Tabaries S.,
RA Russo-Marie F., Lewit-Bentley A.;
RT "The crystal structure of a complex of p11 with the annexin II N-
RL terminal peptide.";
RL Nat. Struct. Biol. 6:89-95(1999).
CC -!- FUNCTION: Because p10 induces the dimerization of annexin II
CC (p36), it may function as a regulator of protein phosphorylation
CC in that the p36 monomer is the preferred target (in vitro) of
CC tyrosine-specific kinase.
CC -!- SUBUNIT: Tetramer of 2 light chains (p10) and 2 heavy chains
CC (annexin II).
CC -!- MISCELLANEOUS: p10 does not appear to bind calcium.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC
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CC
CC EMBL; M81457; AAA58404.1; -
CC EMBL; M38591; AAA58426.1; -
CC EMBL; M77483; -; NOT_ANNOTATED CDS.
CC EMBL; BC015973; AAH15973.1; -
CC EMBL; M16464; AAA30423.1; -
CC PIR; B28489; B28489.
CC PIR; JC1139; JC1139.
CC PDB; 1A4P; 27-MAY-98.
CC PDB; 1BT6; 27-JAN-99.
CC Genew; HGNC:10487; S100A10.
CC MIM; 114085; -
CC InterPro; IPR001751; CaBP_S100.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF01023; S_100; 1.
CC ProDom; PD003407; CaBP_S100; 1.
CC ProDom; PD000012; EF-hand; 1.
CC PROSITE; PS00303; S100_CABP; 1.
KW 3D-structure.
FT INIT MET 0 0
FT DOMAIN 59 70 ANCESTRAL CALCIUM SITE.
FT HELIX 3 19
FT HELIX 20 22
FT STRAND 25 25
FT HELIX 27 37
FT HELIX 39 44
FT TURN 48 49
FT HELIX 50 58
FT TURN 60 61
FT STRAND 66 66
FT HELIX 68 89
SQ SEQUENCE 96 AA; 11072 MW; 5E77933FEE4D837D CRC64;

Query Match 100.0%; Score 23; DB 1; Length 96;
Best Local Similarity 60.0%; Pred. No. 3 5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
DB 59 DQCRD 63

RESULT 70
S110_MOUSE
ID S110_MOUSE STANDARD; PRT; 96 AA.
AC P08207;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calpactin I light chain (P10 protein) (P11) (Cellular ligand of

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DE annexin II).
GN S100A10 OR CALIL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87280130; PubMed=3038891;
RA Saris C.J.M., Kristensen T., D'Eustachio P., Hicks L.J., Noonan D.J.,
RA Glenney J.R. Jr., Hunter T., Tack B.F.;
RT "cDNA sequence and tissue distribution of the mRNA for bovine and
RT murine p11, the S100-related light chain of the protein-tyrosine
RT kinase substrate p36 (calpactin I).";
RL J. Biol. Chem. 263:10663-10671(1987).
CC -!- FUNCTION: Because p10 induces the dimerization of annexin II
CC (p36), it may function as a regulator of protein phosphorylation
CC in that the p36 monomer is the preferred target (in vitro) of
CC tyrosine-specific kinase.
CC -!- SUBUNIT: Tetramer of 2 light chains (p10) and 2 heavy chains
CC (annexin II).
CC -!- MISCELLANEOUS: p10 does not appear to bind calcium.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC
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CC
CC EMBL; M16465; AAA37363.1; -
CC PIR; A28489; A28489.
CC HSP; P08206; 1A4P.
CC MGD; MGI:1339468; S100a10.
CC InterPro; IPR001751; CaBP_S100.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF01023; S_100; 1.
CC ProDom; PD003407; CaBP_S100; 1.
CC ProDom; PD000012; EF-hand; 1.
CC PROSITE; PS00303; S100_CABP; 1.
FT INIT MET 0 0
FT DOMAIN 59 70 ANCESTRAL CALCIUM SITE.
FT SEQUENCE 96 AA; 11055 MW; 8709024DD3664DCE CRC64;

Query Match 100.0%; Score 23; DB 1; Length 96;
Best Local Similarity 60.0%; Pred. No. 3 5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
DB 59 DQCRD 63

RESULT 71
ECOTA_HUMAN
ID ECOTA_HUMAN STANDARD; PRT; 97 AA.
AC P51671; P50877; Q92490; Q92491;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ecotaxin precursor (Small inducible cytokine A11) (CCL11) (Eosinophil
DE chemotactic protein).
GN CCL11 OR SCV11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96181758; PubMed=8597956;

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FT DISULFID 33 73
FT CARBOHYD 94 94
FT VARIANT 7 7
FT  O-LINKED (GALNAC. .).
FT  L -> P (IN CLONE 34).
FT  /FTId=VAR_001634. 34).
FT  A -> T (IN CLONE 53).
FT  /FTId=VAR_001635.
FT  R -> S (IN CLONE 34).
FT  /FTId=VAR_001636.
FT  K -> R (IN CLONE 53).
FT  /FTId=VAR_001637.
FT  VARIANT 23 23
FT  VARIANT 51 51
FT  VARIANT 79 79
FT  TURN 44 45
FT  STRAND 46 52
FT  STRAND 61 66
FT  TURN 67 68
FT  STRAND 71 74
FT  TURN 76 77
FT  HELIX 79 91
SQ SEQUENCE 97 AA; 10732 MW; B433C30FDA4C71A7 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 97;
Best Local Similarity 60.0%; Pred. NO. 3.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD.5
   |.:|
Db 71 DICAD 75

RESULT 72
XPA_CRIGR STANDARD; PRT; 97 AA.
AC Q64029;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE DNA-repair protein complementing XP-A cells homolog (Xeroderma
  pigmentosum group A complementing protein homolog) (Fragment).
GN XPA OR XPAC.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OC NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Ovary;
RX MEDLINE=95064305; PubMed=7974007;
RA Cleaver J.E., McDowell M., Jones C., Wood R., Karentz D.;
RT "Mutation and expression of the XPA gene in revertants and hybrids of
  a Xeroderma pigmentosum cell line."
RL Somat. Cell Mol. Genet. 20:327-337(1994).
CC -!- FUNCTION: Involved in DNA excision repair. Initiates repair by
  binding to damaged sites with various affinities, depending on the
  photoproduct and the transcriptional state of the region.
CC -!- SUBUNIT: Interacts with XAB1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the XPA family.
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CC EMBL: S74024; AAP21086.1; -.
DR InterPro: IPR000465; XPA_protein.
DR Pfam: PF05181; XPA_C; 1.
DR Pfam: PF01286; XPA_N; 1.
DR TIGRfams: TIGR00598; rad14; 1.
DR PROSITE: PS00752; XPA_1; PARTIAL.
DR PROSITE: PS00753; XPA_2; 1.

KW DNA repair; DNA-binding; Zinc-finger; Nuclear protein.
FT NON TER 1 1
FT ZN FING <1 15
FT NON TER 97 97
SQ SEQUENCE 97 AA; 11519 MW; B55360D5C5C24BEE CRC64;

Query Match 100.0%; Score 23; DB 1; Length 97;
Best Local Similarity 60.0%; Pred. NO. 3.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
   |.:|
Db 13 DSCRD 17

RESULT 73
BXEL_BOMMO STANDARD; PRT; 98 AA.
AC P21808; O18329;
DT 01-MAY-1991 (Rel. 18, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Bombyxin E-1 precursor (BBX-E1) (Bombyxin IV) (4K-prothoracicotropic
  hormone IV) (4K-PTTH-IV).
GN BBXEL.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OC NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Kinshu X Showa;
RX MEDLINE=97397026; PubMed=9253178;
RA Tsuzuki S., Masuta T., Furuno M., Sakurai S., Iwami M.;
RT "Structure and expression of bombyxin E1 gene: a novel family gene
  that encodes bombyxin-IV, an insect insulin-related neurosecretory
  peptide."
RT Peptide.
RL Comp. Biochem. Physiol. 117B:409-416(1997).
RN [2]
RP SEQUENCE OF 48-67 AND 79-98.
RA Maruyama K., Hietter H., Nagasawa H., Isogai A., Tamura S., Suzuki A.,
RA Ishizaki H.;
RT "Isolation and primary structure of bombyxin-IV, a novel molecular
  species of bombyxin from the silkworm, Bombyx mori."
RL Agric. Biol. Chem. 52:3035-3041(1988).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=92384896; PubMed=1515030;
RA Maruyama K., Nagasawa H., Isogai A., Ishizaki H., Suzuki A.;
RT "Determination of disulfide bond arrangement in bombyxin-IV, an
  insulin superfamily peptide from the silkworm, Bombyx mori, by
  combination of thermolysin digestion of natural peptide and selective
  synthesis of disulfide bond isomers."
RT J. Protein Chem. 11:13-20(1992).
CC -!- FUNCTION: PTTH IS A BRAIN PEPTIDE RESPONSIBLE FOR ACTIVATION OF
  PROTHORACIC GLANDS TO PRODUCE ECDYSONE IN INSECTS.
CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
  disulfide bonds.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: SILK WORM HAS TWO KINDS OF PTTH: 4K-PTTH AND
  22K-PTTH; THERE ARE FOUR FORMS OF 4K-PTTH.
CC -!- SIMILARITY: Belongs to the insulin family.
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CC EMBL: D78138; BAA22159.1; -.
DR
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DR HSP; P26729; LBOM.
DR InterPro; IPR004824; Bombyxin.
DR Pfam; PF00049; Inulin; 1.
DR ProDom; PD001048; Bombyxin; 1.
DR SMART; SM00078; ILGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Hormone; Inulin family; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 19
FT CHAIN 20 47 BOMBYXIN E-1 B CHAIN.
FT PROPEP 50 75 BOMBYXIN E-1 C PEPTIDE-LIKE.
FT CHAIN 79 98 BOMBYXIN E-1 A CHAIN.
FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 29 85 INTERCHAIN.
FT DISULFID 41 98 INTERCHAIN.
FT DISULFID 84 89
SQ SEQUENCE 98 AA; 10987 MW; 8890301EF39AB093 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 98;
Best Local Similarity 60.0%; Pred. No. 3.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 39 DDCWD 43

RESULT 74
IT12 SIGNAL
ID IT12 SIGNAL STANDARD; PRT; 99 AA.
AC P26780;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Trypsin inhibitor 2 precursor (MTI-2).
OS Sinapis alba (white mustard) (Brassica hirta).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Sinapis.
OX NCBI_TaxID=3728;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Albatros; TISSUE=Seed;
RX MEDLINE=95269796; PubMed=7750566;
RA Ceci L.R., Spoto N., de Virgilio M., Gallerani R.;
RT "The gene coding for the mustard trypsin inhibitor-2 is discontinuous
and wound-inducible";
RL FEBS Lett. 364:179-181(1995).
RN [2]
RP SEQUENCE OF 31-93.
RC STRAIN=cv. Albatros; TISSUE=Seed;
RX MEDLINE=93083607; PubMed=1451776;
RA Menegatti E., Tedeschi G., Ronchi S., Bortolotti F., Ascenzi P.,
RA Thomas R.M., Bolognesi M., Palmeri S.;
RT "Purification, inhibitory properties and amino acid sequence of a new
serine proteinase inhibitor from white mustard (Sinapis alba L.)
seed.";
RL FEBS Lett. 301:10-14(1992).
CC -!- FUNCTION: Inhibits bovine beta-trypsin and alpha-chymotrypsin
on a 1:1 molar basis.
CC -!- SIMILARITY: BELONGS TO THE RTI/MTI-2 PROTEASE INHIBITORS FAMILY.
CC
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DR InterPro; IPR008679; MTI-2.
DR Pfam; PF05828; MTI-2; 1.
DR SMART; SM00505; Knot1; 1.
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 30
FT CHAIN 31 93 TRYPSIN INHIBITOR 2.
FT PROPEP 94 99
FT DISULFID 34 86 BY SIMILARITY.
FT DISULFID 47 71 BY SIMILARITY.
FT DISULFID 56 81 BY SIMILARITY.
FT DISULFID 60 83 BY SIMILARITY.
FT ACT_SITE 50 51 REACTIVE-BOND (BY SIMILARITY).
SQ SEQUENCE 99 AA; 10982 MW; SE96C788968EEA9F CRC64;

Query Match 100.0%; Score 23; DB 1; Length 99;
Best Local Similarity 60.0%; Pred. No. 3.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 84 DYCND 88

RESULT 75
RS10 HALMA
ID RS10 HALMA STANDARD; PRT; 99 AA.
AC P23357;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S10P (HmaS10).
GN RPS10P.
OS Haloarcula marismortui (Halo bacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxID=2238;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174971; PubMed=2155402;
RA Baldacci G., Guinet F., Tillit J., Zaccal G., de Recondo A.M.;
RT "Functional implications related to the gene structure of the
elongation factor EF-Tu from Halobacterium marismortui.";
RL Nucleic Acids Res. 18:507-511(1990).
CC -!- FUNCTION: Involved in the binding of tRNA to the ribosomes (By
similarity).
CC -!- SIMILARITY: Belongs to the S10P family of ribosomal proteins.
CC
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Db          18 DICAD 22
|:|:|
RESULT 76
SY08_BOVIN
ID SY08_BOVIN STANDARD; PRT; 99 AA.
AC Q09141;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemoattractant protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
GN CCL8 OR SCYAS OR MCP2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94114084; PubMed=8286035;
RA Wempe F., Hanes J., Scheit K.H.;
RT "Cloning of the gene for bovine monocyte chemoattractant protein-2.";
RL DNA Cell Biol. 13:1-8(1994).
CC -!- FUNCTION: Chemoattractant factor that attracts monocytes. This protein
CC can bind heparin.
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC -----
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CC -----
DR EMBL; S67954; AAD14005.1; -.
DR EMBL; S67956; AAB29750.1; -.
DR HSSP; P51671; 1EOT.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR01811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response;
KW Pyroglutamate carboxylic acid.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 99 SMALL INDUCIBLE CYTOKINE A8.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT DISULFID 34 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
SQ SEQUENCE 99 AA; 10900 MW; 01974CDB3FF9119B CRC64;

Query Match 100.0%; Score 23; DB 1; Length 99;
Best Local Similarity 60.0%; Pred. No. 3.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 73 DVCAD 77
```

Search completed: May 6, 2004, 10:45:50
Job time : 12 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2004, 10:43:51 ; Search time 20 Seconds
(without alignments)
24.048 Million cell updates/sec

Title: SEQ1
Perfect score: 23
Sequence: 1 dxcxd 5

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 78

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	18	B61110	68K collagen-bindi
2	23	100.0	24	A05134	neurotoxin V - sco
3	23	100.0	28	JT0412	bombyxin-IV chain
4	23	100.0	30	C32946	serine proteinase
5	23	100.0	33	S65599	hevein - Para rubb
6	23	100.0	36	A05135	neurotoxin VIII -
7	23	100.0	36	C82694	hypothetical prote
8	23	100.0	37	C41933	mating pheromone E
9	23	100.0	38	A45588	kunitz trypsin inh
10	23	100.0	40	T08107	nonenzymatic prote
11	23	100.0	42	A82802	hypothetical prote
12	23	100.0	43	A70231	hypothetical prote
13	23	100.0	44	D82579	hypothetical prote
14	23	100.0	47	I48943	cellular disintegr
15	23	100.0	54	FEME	ferredoxin 2[4Fe-4
16	23	100.0	54	F86583	hypothetical prote
17	23	100.0	54	C84292	hypothetical prote
18	23	100.0	54	G72040	hypothetical prote
19	23	100.0	55	FEPE	ferredoxin 2[4Fe-4
20	23	100.0	55	FEQFR	ferredoxin 2[4Fe-4
21	23	100.0	55	FECLCB	ferredoxin 2[4Fe-4
22	23	100.0	55	FECLCE	ferredoxin 2[4Fe-4
23	23	100.0	55	FECLCU	ferredoxin 2[4Fe-4
24	23	100.0	55	FECLCT	ferredoxin 2[4Fe-4
25	23	100.0	55	JX0144	ferredoxin - Clost
26	23	100.0	56	FECLCP	ferredoxin 2[4Fe-4
27	23	100.0	57	T03654	glyceraldehyde-3-p
28	23	100.0	58	B81202	hypothetical prote
29	23	100.0	60	G81777	probable periplasm

30	23	100.0	62	2	G84271	50S ribosomal prot
31	23	100.0	63	2	A23727	neurotoxin V - bar
32	23	100.0	64	1	TIOAB	trypsin inhibitor
33	23	100.0	65	2	S74702	hypothetical prote
34	23	100.0	65	2	A86027	hypothetical prote
35	23	100.0	67	2	S33873	glyceraldehyde-3-p
36	23	100.0	67	2	G84255	hypothetical prote
37	23	100.0	68	2	E97420	hypothetical prote
38	23	100.0	70	2	A83982	hypothetical prote
39	23	100.0	70	2	E72171	K8R protein - vari
40	23	100.0	74	2	B71282	hypothetical prote
41	23	100.0	75	2	T25370	hypothetical prote
42	23	100.0	76	2	B91110	ferredoxin - Metha
43	23	100.0	76	2	T03860	TA20 protein - com
44	23	100.0	76	2	T09476	hypothetical prote
45	23	100.0	77	2	A82086	hypothetical prote
46	23	100.0	78	1	FEBSA	ferredoxin [3Fe-4S
47	23	100.0	78	2	JC2496	ferredoxin [3Fe-4S
48	23	100.0	79	2	A49475	cerebroside sulfat
49	23	100.0	79	2	C87028	hypothetical prote
50	23	100.0	79	2	C84308	hypothetical prote
51	23	100.0	79	2	C84381	hypothetical prote
52	23	100.0	80	2	T45327	hypothetical prote
53	23	100.0	83	2	A82769	hypothetical prote
54	23	100.0	85	2	C84867	probable trypsin i
55	23	100.0	85	2	T47563	kinetochore-like p
56	23	100.0	86	2	A37910	muscarinic toxin 2
57	23	100.0	87	2	E81063	hypothetical prote
58	23	100.0	87	2	G70782	hypothetical prote
59	23	100.0	89	2	A84867	probable trypsin i
60	23	100.0	89	2	E84867	probable trypsin i
61	23	100.0	89	2	S71555	proteinase inhibit
62	23	100.0	89	2	JQ2361	wheat aluminum ind
63	23	100.0	90	2	B84867	probable trypsin i
64	23	100.0	92	2	A87600	conserved hypotet
65	23	100.0	93	2	S49260	ferredoxin 2[4Fe-4
66	23	100.0	95	1	L0FG10	calpactin I light
67	23	100.0	95	2	A31373	calpactin I light
68	23	100.0	95	2	G81901	hypothetical prote
69	23	100.0	97	1	JH0663	calpactin I light
70	23	100.0	97	2	JC4912	eotaxin precursor
71	23	100.0	97	2	JC1139	calpactin I light
72	23	100.0	97	2	B28489	calpactin I light
73	23	100.0	97	2	A28489	calpactin I light
74	23	100.0	99	2	S65661	trypsin inhibitor
75	23	100.0	99	2	T32227	hypothetical prote
76	23	100.0	99	2	AD2270	hypothetical prote
77	23	100.0	100	2	D71962	hypothetical prote
78	23	100.0	100	2	T16810	hypothetical prote

ALIGNMENTS

RESULT 1

B61110
68K collagen-binding protein, light form - chicken (fragments)
C:Species: Gallus gallus (chicken)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Oct-1994
C:Accession: B61110
R:Tidball, J.G.
J. Biol. Chem. 267, 21211-21219, 1992
A:Title: Identification and distribution of a novel, collagen-binding protein in the deve
A:Reference number: A61110; MUID:93016046; PMID:1328225
A:Accession: B61110
A:Molecule type: protein
A:Residues: 1-18 <TID>
C:Keywords: collagen binding

Query Match 100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 0;

QY 1 DXCXD 5
Db 1 DVCXD 5

RESULT 2
A05134
neurotoxin V - scorpion (Buthus occitanus) (fragment)
C/Species: Buthus occitanus tunetanus
C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 07-Feb-1997
C/Accession: A05134
R/Martin, M.F.; Rochat, H.
Toxicon 22, 279-291, 1984
A/Title: Purification of thirteen toxins active on mice from the venom of the North African scorpion Buthus occitanus tunetanus
A/Reference number: A94316; PMID:84224814; PMID:6729843
A/Accession: A05134
A/Molecule type: protein
A/Residues: 1-24 <MAR>
C/Superfamily: scorpion neurotoxin
C/Keywords: neurotoxin

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 24;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 20 DVCND 24

RESULT 3
JT0412
bombyxin-IV chain B - silkworm
C/Species: Bombyx mori (silkworm)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Mar-1998
C/Accession: JT0412
R/Maruyama, K.; Hietter, H.; Nagaawa, H.; Isogai, A.; Tamura, S.; Suzuki, A.; Ishizaki, A.; Agric. Biol. Chem. 52, 3035-3041, 1988
A/Title: Isolation and primary structure of bombyxin-IV, a novel molecular species of bombyxin
A/Reference number: JT0410
A/Accession: JT0412
A/Molecule type: protein
A/Residues: 1-28 <MAR>
C/Superfamily: insulin
C/Keywords: pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/10/Disulfide bonds: interchain (to chain A-7) #status predicted
F/22/Disulfide bonds: interchain (to chain A-20) #status predicted

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 28;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 20 DLQWD 24

RESULT 4
C32946
serine proteinase (EC 3.4.21.-) 3 - nematode (Anisakis simplex) (fragments)
C/Species: Anisakis simplex
C/Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change 20-Sep-1999
C/Accession: C32946
R/Sakanari, J.A.; Staunton, C.E.; Eakin, A.E.; Craik, C.S.; McKerrow, J.H.
Proc. Natl. Acad. Sci. U.S.A. 86, 4863-4867, 1989
A/Title: Serine proteinases from nematode and protozoan parasites: isolation of sequence homologies
A/Reference number: A32946; PMID:89296904; PMID:2662185
A/Accession: C32946
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-30 <SAK>
C/Keywords: hydrolase; serine proteinase

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 30;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 9 DRCSL 13

RESULT 5
S65599
hevein - Para rubber tree (fragments)
C/Species: Hevea brasiliensis (Para rubber tree)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C/Accession: S65599
R/Soedjantamadja, U.M.S.; Subroto, T.; Beintema, J.J.
FEBS Lett. 363, 211-213, 1995
A/Title: Processed products of the hevein precursor in the latex of the rubber tree (Hevea brasiliensis)
A/Reference number: S65599; PMID:95255547; PMID:7737403
A/Accession: S65599
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-15,16-33 <SOE>
C/Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 33;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 14 DSCGD 18

RESULT 6
A05135
neurotoxin VIII - scorpion (Buthus occitanus) (fragment)
C/Species: Buthus occitanus tunetanus
C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 07-Feb-1997
C/Accession: A05135
R/Martin, M.F.; Rochat, H.
Toxicon 22, 279-291, 1984
A/Title: Purification of thirteen toxins active on mice from the venom of the North African scorpion Buthus occitanus tunetanus
A/Reference number: A94316; PMID:84224814; PMID:6729843
A/Accession: A05135
A/Molecule type: protein
A/Residues: 1-36 <MAR>
C/Superfamily: scorpion neurotoxin
C/Keywords: neurotoxin

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 36;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 20 DYCND 24

RESULT 7
C82694
hypothetical protein XF1342 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C/Accession: C82694
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; PMID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: C82694
A/Status: preliminary

A:Molecule type: DNA
A:Residues: 1-36 <SIM>
A:Cross-references: GB:AE003966; GB:AE003849; NID:g9106327; PIDN:AAF84151.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1342

Query Match 100.0%; Score 23; DB 2; Length 36;
Best Local Similarity 60.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 14 DDCLD 18

RESULT 8
C41933
N:Alternate names: Euplotes raikovi
C:Species: Euplotes raikovi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 07-Dec-1999
C:Accession: C41933
R:Raffioni, S.; Miceli, C.; Vallesi, A.; Chowdhury, S.K.; Chait, B.T.; Luporini, P.; Bra
Proc. Natl. Acad. Sci. U.S.A. 89, 2071-2075, 1992
A:Title: Primary structure of Euplotes raikovi pheromones: comparison of five sequences
A:Reference number: A41933; MUID:92196059; PMID:1549567
A:Accession: C41933
A:Molecule type: protein
A:Residues: 1-37 <RAF>
A:Cross-references: PIDN:AAB21809.1; PID:g247247
A:Note: sequence extracted from NCBI backbone (NCBIP:104633)
C:Genetics:
A:Genetic code: SGC9
A:Keywords: pheromone
F:3-18,10-32,15-24/Disulfide bonds: #status predicted

Query Match 100.0%; Score 23; DB 2; Length 37;
Best Local Similarity 60.0%; Pred. No. 5.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 1 DICDD 5

RESULT 9
A45588
kunitz trypsin inhibitor beta chain - Prosopsis juliflora
C:Species: Prosopsis juliflora
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 17-Mar-2000
C:Accession: A45588
R:Negreiros, A.N.; Carvalho, M.M.; Xavier Filho, J.; Blanco-Labra, A.; Shewry, P.R.; Ric
Phytochemistry 30, 2829-2833, 1991
A:Title: The complete amino acid sequence of the major Kunitz trypsin inhibitor from the
A:Reference number: A45588; MUID:92118295; PMID:1367792
A:Contents: seeds
A:Accession: A45588
A:Status: preliminary

A:Molecule type: protein
A:Residues: 1-38 <NEG>
A:Note: sequence extracted from NCBI backbone (NCBIP:78370)
C:Superfamily: plant Kunitz-type proteinase inhibitor

Query Match 100.0%; Score 23; DB 2; Length 38;
Best Local Similarity 60.0%; Pred. No. 5.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 2 DRCKD 6

RESULT 10
T08107
nonenzymatic protein CP12 - Chlamydomonas reinhardtii (fragment)
C:Species: Chlamydomonas reinhardtii
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 21-Jul-2000
C:Accession: T08107
R:Wedel, N.; Soll, J.
Proc. Natl. Acad. Sci. U.S.A. 95, 9699-9704, 1998
A:Title: Evolutionary conserved light regulation of Calvin cycle activity by NADPH-mediat
A:Reference number: Z16360; MUID:98356221; PMID:9689144
A:Accession: T08107
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-40 <WED>
A:Cross-references: EMBL:AJ005284; NID:g3123344; PIDN:CAA06467.1; PID:g3123345
A:Experimental source: strain cw15
C:Comment: It is supposed that light regulation of Calvin cycle activity via NADPH-mediat
. The two key enzymes of the Calvin cycle, phosphoribulokinase (EC 2.7.1.19) and glyceral
dehydrotic acid 3-phosphate dehydrogenase (EC 1.1.1.29) are involved in the regulation of
enzymatic peptide CP12.
C:Genetics:
A:Gene: cp12

Query Match 100.0%; Score 23; DB 2; Length 40;
Best Local Similarity 60.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
DB 35 DYCKD 39

RESULT 11
A82802
hypothetical protein XF0471 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: A82802
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: A82802
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-42 <SIM>
A:Cross-references: GB:AE003897; GB:AE003849; NID:g9105313; PIDN:AAF83281.1; GSPDB:GN0012
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0471

Query Match 100.0%; Score 23; DB 2; Length 42;
Best Local Similarity 60.0%; Pred. No. 6.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 13 DLCCD 17

RESULT 12
A70231
hypothetical protein BBP28 - Lyme disease spirochete plasmid F/1p28-1
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C:Accession: A70231
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Surton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A>Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: A70231
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-43 <KLB>
A:Cross-references: GB:AE000794; NID:G2689981; PIDN:AAC66389.1; PID:G2690006; TIGR:BBP28
A:Experimental source: strain B31
C:Genetics:
A:Genome: plasmid

Query Match 100.0%; Score 23; DB 2; Length 43;
Best Local Similarity 60.0%; Pred. No. 6.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 20 DMCRD 24

RESULT 13
D82579
hypothetical protein XF2254 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82579
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: D82579
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-44 <SIM>
A:Cross-references: GB:AE0004038; GB:AE003849; NID:G9107408; PIDN:AAF85053.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF2254

Query Match 100.0%; Score 23; DB 2; Length 44;
Best Local Similarity 60.0%; Pred. No. 6.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 9 DLCLD 13

RESULT 14
I48943
cellular disintegrin-related protein 16-2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 20-Sep-1999
C:Accession: I48943
R:Weskamp, G.; Blobel, C.P.
Proc. Natl. Acad. Sci. U.S.A. 91, 2748-2751, 1994
A>Title: A new family of cellular proteins related to snake venom disintegrins.
A:Reference number: A53476; MUID:94195820; PMID:8146185
A:Accession: I48943
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-47 <RES>
A:Cross-references: EMBL:U06145; NID:G487138; PIDN:AAA18424.1; PID:G487139
C:Superfamily: unassigned disintegrins; disintegrin.homology

Query Match 100.0%; Score 23; DB 2; Length 47;
Best Local Similarity 60.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 28 DCCXD 32

RESULT 15
FEME
ferredoxin 2[4Fe-4S] - Megaspheara eladenii
C:Species: Megaspheara eladenii
C>Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 18-Sep-1998
R:Azari, P.; Giantz, M.; Tsunoda, J.; Yasunobu, K.T.
unpublished results, cited by Yasunobu, K.T., and Tanaka, M., Syst. Zool. 22, 570-589, 19
A:Reference number: A00203
A:Accession: A00203
A:Molecule type: protein
A:Residues: 1-54 <AZA>
C:Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
C:Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein
F:1-54/Domain: ferredoxin 2[4Fe-4S] homology <FER>
F:8,11,14,46/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F:18,36,39,42/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 100.0%; Score 23; DB 1; Length 54;
Best Local Similarity 60.0%; Pred. No. 7.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 34 DSCID 38

RESULT 16
F86583
hypothetical protein CPJ0745 [imported] - Chlamydomydia pneumoniae (strain J138)
C:Species: Chlamydomydia pneumoniae, Chlamydia pneumoniae

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
 C:Accession: F86583
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise,
 Nucleic Acids Res. 28, 2311-2314, 2000
 A>Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A:Reference number: A86491; MUID:20330349; PMID:10871362
 A:Accession: F86583
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-54 <STO>
 A:Cross-references: GB:BA000008; NID:g8979117; PIDN:BAA98952.1; GSPDB:GN00142
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: CPJ0745

Query Match 100.0%; Score 23; DB 2; Length 54;
 Best Local Similarity 60.0%; Pred. No. 7.5e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 DB 2 DSCFD 6

RESULT 17

C84292

hypothetical protein Vngl376h [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: C84292

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
 ; Leibhauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniel, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A>Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: C84292

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-54 <STO>

A:Cross-references: GB:AE004437; NID:g10580885; PIDN:AAG19703.1; GSPDB:GN00138

C:Genetics:

A:Gene: VNG1376H

Query Match 100.0%; Score 23; DB 2; Length 54;
 Best Local Similarity 60.0%; Pred. No. 7.5e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 DB 6 DGCID 10

RESULT 18

G72040

hypothetical protein CP1127 [imported] - Chlamydia pneumoniae (strains CWL029 and AR

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000

C:Accession: G72040; B81501

R:Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A>Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A:Reference number: A72000; MUID:99206606; PMID:10192388

A:Accession: G72040

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-54 <ARN>

A:Cross-references: GB:AE001656; GB:AE001363; NID:g4377047; PIDN:AAD18884.1; PID:g437705

A:Experimental source: strain CWL029

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A>Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A:Reference number: A81500; MUID:20150255; PMID:10684935
 A:Accession: B81501
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-54 <REA>
 A:Cross-references: GB:AE002268; GB:AE002161; NID:g7190029; PIDN:AAF38893.1; PID:g719003;
 A:Experimental source: strain AR39, HL cells
 C:Genetics:
 A:Gene: CPn0745; CP1127

Query Match 100.0%; Score 23; DB 2; Length 54;
 Best Local Similarity 60.0%; Pred. No. 7.5e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 DB 2 DSCFD 6

RESULT 19

FEPE

ferredoxin 2[4Fe-4S] [validated] - Peptostreptococcus asaccharolyticus

C:Species: Peptostreptococcus asaccharolyticus

C>Date: 24-Apr-1984 #sequence_revision 23-Mar-1995 #text_change 20-Apr-2000

C:Accession: A00196

R:Tsunoda, J.N.; Yasunobu, K.T.; Whiteley, H.R.

J. Biol. Chem. 243, 6262-6272, 1968

A>Title: Non-heme iron proteins. IX. The amino acid sequence of ferredoxin from Micrococ

A:Reference number: A92040; MUID:69054261; PMID:5723466

A>Note: the source is designated as Micrococcus aerogenes

A:Accession: A00196

A:Molecule type: protein

A:Residues: 1-21,23-24,'O',26-55 <TSU>

R:Backes, G.; Mino, Y.; Loehr, T.M.; Meyer, T.E.; Cusanovich, M.A.; Sweeney, W.V.; Adman,

J. Am. Chem. Soc. 113, 2055-2064, 1991

A>Title: The environment of Fe4S4 clusters in ferredoxins and high-potential iron protei

A:Reference number: A44688

A:Contents: annotation; X-ray crystallography, 2.0 angstroms; sequence revision

A>Note: sequence correction confirmed by peptide sequencing

R:Adman, E.T.; Sieker, L.C.; Jensen, L.H.

submitted to the Brookhaven Protein Data Bank, August 1976

A:Reference number: A50836; PDB:1FDX

A:Contents: annotation; X-ray crystallography, 2.0 angstroms

R:Adman, E.T.; Sieker, L.C.; Jensen, L.H.

J. Biol. Chem. 251, 3801-3806, 1976

A>Title: Structure of Peptococcus aerogenes ferredoxin. Refinement at 2 angstroms resolut

A:Reference number: A92192; MUID:76213238; PMID:932007

A:Contents: annotation; X-ray crystallography, 2.0 angstroms

R:Adman, E.T.; Sieker, L.C.; Jensen, L.H.

J. Biol. Chem. 248, 3987-3996, 1973

A>Title: The structure of a bacterial ferredoxin.

A:Reference number: A92136; MUID:73187389; PMID:4708097

A:Contents: annotation; X-ray crystallography, 2.8 angstroms

C:Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology

C:Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein

F:1-54/Domain: ferredoxin 2[4Fe-4S] homology <FER>

F:8,11,14,46/Binding site: 4Fe-4S cluster (Cys) (covalent) #status experimental

F:18,36,39,42/Binding site: 4Fe-4S cluster (Cys) (covalent) #status experimental

Query Match 100.0%; Score 23; DB 1; Length 55;

Best Local Similarity 60.0%; Pred. No. 7.6e+02;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 DB 34 DSCID 38

RESULT 20

FQ0PR

ferredoxin 2[4Fe-4S] - Rhodospirillum rubrum

C:Species: Rhodospirillum rubrum

C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 18-Sep-1998
 C;Accession: A00197
 R;Matsumura, H.; Inoue, K.; Hase, T.; Hiura, H.; Kakuno, T.; Yamashita, J.; Horio, T.
 J. Biochem. 93, 1385-1390, 1983
 A;Title: Structure of the extracellular ferredoxin from Rhodospirillum rubrum: close similarity to the structure of the ferredoxin from Clostridium acidithiobacillus
 A;Reference number: A00197; PMID:83290779; PMID:6411697
 A;Accession: A00197
 A;Molecule type: protein
 A;Residues: 1-55 <MAT>
 A;Note: This is one of the four ferredoxins, most likely ferredoxin I, of R. rubrum
 C;Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
 C;Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein
 F;1-55/Domain: ferredoxin 2[4Fe-4S] homology <PER>
 F;8,11,14,47/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F;18,37,40,43/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 100.0%; Score 23; DB 1; Length 55;
 Best Local Similarity 60.0%; Pred. No. 7.6e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 35 DTCID 39

RESULT 21
 FECLCB
 ferredoxin 2[4Fe-4S] - Clostridium butyricum
 C;Species: Clostridium butyricum
 C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 18-Sep-1998
 C;Accession: A00199
 R;Benson, A.M.; Mower, H.F.; Yasunobu, K.T.
 Proc. Natl. Acad. Sci. U.S.A. 55, 1532-1535, 1966
 A;Title: The amino acid sequence of Clostridium butyricum ferredoxin.
 A;Reference number: A00199; PMID:67125829; PMID:5227671
 A;Accession: A00199
 A;Molecule type: protein
 A;Residues: 1-55 <BEN>
 C;Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
 C;Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein
 F;1-55/Domain: ferredoxin 2[4Fe-4S] homology <PER>
 F;8,11,14,47/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F;18,37,40,43/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 100.0%; Score 23; DB 1; Length 55;
 Best Local Similarity 60.0%; Pred. No. 7.6e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 35 DTCID 39

RESULT 22
 FECLCE
 ferredoxin 2[4Fe-4S] - Clostridium sp.
 C;Species: Clostridium sp.
 C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 18-Sep-1998
 C;Accession: A00200
 R;Tanaka, M.; Haniu, M.; Yasunobu, K.T.; Jones, J.B.; Stadtman, T.C.
 Biochemistry 13, 5284-5289, 1974
 A;Title: Amino acid sequence determination of the Clostridium M-E ferredoxin and a comparison with the sequence of the Clostridium thermosaccharolyticum ferredoxin
 A;Reference number: A00200; PMID:75054829; PMID:4433520
 A;Accession: A00200
 A;Molecule type: protein
 A;Residues: 1-55 <ATAN>
 A;Experimental source: strain M-E
 C;Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
 C;Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein
 F;1-55/Domain: ferredoxin 2[4Fe-4S] homology <PER>
 F;8,11,14,47/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F;18,37,40,43/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 100.0%; Score 23; DB 1; Length 55;
 Best Local Similarity 60.0%; Pred. No. 7.6e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 35 DTCID 39

RESULT 23
 FECLCU
 ferredoxin 2[4Fe-4S] [validated] - Clostridium acidithiobacillus
 C;Species: Clostridium acidithiobacillus
 C;Date: 24-Apr-1984 #sequence_revision 22-Apr-1995 #text_change 20-Apr-2000
 C;Accession: S36790; A00201
 R;Meyer, J.; Moulis, J.M.; Scherrer, N.; Gagnon, J.; Ulrich, J.
 Biochem. J. 294, 622-623, 1993
 A;Title: Sequences of clostridial ferredoxins: determination of the Clostridium sticklandii ferredoxin
 A;Reference number: S36790; PMID:93384542; PMID:8373379
 A;Accession: S36790
 A;Molecule type: protein
 A;Residues: 1-55 <MEY>
 R;Rall, S.C.; Bolinger, R.E.; Cole, R.D.
 Biochemistry 8, 2486-2496, 1969
 A;Title: The amino acid sequence of ferredoxin from Clostridium acidithiobacillus
 A;Reference number: A00201; PMID:69253175; PMID:5799135
 A;Accession: A00201
 A;Molecule type: protein
 A;Residues: 1-14, 'D', '16-20, 'D', '22-24, 'Q', '26-27, 'S', '29-55 <RAL>
 R;Dues, E.; Fanchon, E.; Vicat, J.; Sieker, L.C.; Meyer, J.; Moulis, J.M.
 submitted to the Brookhaven Protein Data Bank, March 1994
 A;Reference number: A52567; PDB:1FDN
 A;Contents: annotation; X-ray crystallography, 1.84 angstroms, residues 1-55
 A;Notes: ATCC:7906
 R;Tranquil, D.; Jesior, J.C.
 submitted to the Brookhaven Protein Data Bank, September 1994
 A;Reference number: A65570; PDB:1FCA
 A;Contents: annotation; X-ray crystallography, 1.8 angstroms, residues 1-20, 'D', '22-24, 'Q', '26-27, 'S', '29-55 <RAL>
 C;Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
 C;Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein
 F;1-55/Domain: ferredoxin 2[4Fe-4S] homology <PER>
 F;8,11,14,47/Binding site: 4Fe-4S cluster (Cys) (covalent) #status experimental
 F;18,37,40,43/Binding site: 4Fe-4S cluster (Cys) (covalent) #status experimental

Query Match 100.0%; Score 23; DB 1; Length 55;
 Best Local Similarity 60.0%; Pred. No. 7.6e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 35 DTCID 39

RESULT 24
 FECLCT
 ferredoxin 2[4Fe-4S] - Clostridium thermosaccharolyticum
 C;Species: Clostridium thermosaccharolyticum, Clostridium tartarivorum
 C;Date: 24-Apr-1984 #sequence_revision 04-Dec-1985 #text_change 18-Sep-1998
 C;Accession: A92138; A92086; A00202
 R;Tanaka, M.; Haniu, M.; Yasunobu, K.T.; Himes, R.H.; Akagi, J.M.
 J. Biol. Chem. 248, 5215-5217, 1973
 A;Title: The primary structure of the Clostridium thermosaccharolyticum ferredoxin, a heat-labile protein
 A;Reference number: A92138; PMID:74071583; PMID:4768897
 A;Accession: A92138
 A;Molecule type: protein
 A;Residues: 1-55 <ATAN>
 R;Tanaka, M.; Haniu, M.; Matsueda, G.; Yasunobu, K.T.; Himes, R.H.; Akagi, J.M.; Barnes, J. Biol. Chem. 246, 3953-3960, 1971
 A;Title: The primary structure of the Clostridium tartarivorum ferredoxin, a heat-stable protein
 A;Reference number: A92086; PMID:71259897; PMID:4934841
 A;Accession: A92086
 A;Molecule type: protein
 A;Residues: 1-30, 'Q', '32-43, 'Q', '45-55 <ATA>

A>Note: the authors considered C. tartarivorum to be a separate species
 C:Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
 A:Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein
 F:1-55/Domain: ferredoxin 2[4Fe-4S] homology <FER>
 F:8,11,14,47/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F:18,37,40,43/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 100.0%; Score 23; DB 1; Length 55;
 Best Local Similarity 60.0%; Pred. No. 7.6e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 35 DTCID 39

RESULT 25
 JX0144
 ferredoxin - Clostridium perfringens
 C:Species: Clostridium perfringens
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Jun-1999
 C:Accession: JX0144
 R:Seki, Y.; Seki, S.; Ishimoto, M.
 J. Gen. Appl. Microbiol. 35, 167-172, 1989
 A:Title: The primary structure of Clostridium perfringens ferredoxin.
 A:Reference number: JX0144
 A:Accession: JX0144
 A:Molecule type: DNA
 A:Residues: 1-55 <SEK>
 C:Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
 A:Keywords: 4Fe-4S; iron-sulfur protein; metalloprotein
 F:1-55/Domain: ferredoxin 2[4Fe-4S] homology <FER>
 F:8,11,14,47/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F:18,37,40,43/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 100.0%; Score 23; DB 2; Length 55;
 Best Local Similarity 60.0%; Pred. No. 7.6e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 35 DTCID 39

RESULT 26
 F8CLCP
 ferredoxin 2[4Fe-4S] [validated] - Clostridium pasteurianum
 C:Species: Clostridium pasteurianum
 C:Date: 07-May-1981 #sequence_revision 14-Nov-1997 #text_change 20-Apr-2000
 C:Accession: A94028; A90550; A00198
 R:Graves, M.C.; Mullenbach, G.T.; Rabinowitz, J.C.
 Proc. Natl. Acad. Sci. U.S.A. 82, 1653-1657, 1985
 A:Title: Cloning and nucleotide sequence determination of the Clostridium pasteurianum F
 A:Reference number: A94028; MUID:85166189; PMID:3856844
 A:Accession: A94028
 A:Molecule type: DNA
 A:Residues: 1-56 <GRA>
 A:Cross-references: GB:M11214; GB:M13633; GB:M13682; NID:G144805; PIDN:AAA83524.1; PID:G
 A:Experimental source: ATCC:6013; soil spore
 A>Note: Initiator Met not shown
 R:Tanaka, M.; Nakaishima, T.; Benson, A.M.; Mower, H.F.; Yasunobu, K.T.
 Biochemistry 5, 1666-1680, 1966
 A:Title: The amino acid sequence of Clostridium pasteurianum ferredoxin.
 A:Reference number: A90550; MUID:67120720; PMID:5335811
 A:Accession: A90550
 A:Molecule type: protein
 A:Residues: 2-56 <TAN>
 R:Bertini, I.; Donaire, A.; Feinberg, B.A.; Luchinat, C.; Piccioli, M.; Yuan, H.
 submitted to the Brookhaven Protein Data Bank, June 1995
 A:Reference number: A65284; PDB:1CLF
 A:Contents: annotation; conformation by (1)H-NMR, residues 2-56
 R:Bertini, I.; Donaire, A.; Feinberg, B.A.; Luchinat, C.; Piccioli, M.; Yuan, H.

Eur. J. Biochem. 232, 192-205, 1995
 A:Title: Solution structure of the oxidized 2[4Fe-4S] ferredoxin from Clostridium pasteur
 A:Reference number: A58660; MUID:96048047; PMID:7556151
 C:Contents: annotation; conformation by (1)H-NMR
 R:Scrofanis, S.D.B.; Brerston, P.S.; Hamer, A.M.; Lavery, M.J.; McDowell, S.G.; Vincent, C.
 Biochemistry 33, 14486-14495, 1994
 A:Title: Comparison of native and mutant proteins provides a sequence-specific assignment
 A:Reference number: A58659; MUID:95072020; PMID:7981209
 C:Contents: annotation; conformation by (1)H-NMR
 C:Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
 A:Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein
 F:2-56/Product: ferredoxin 2[4Fe-4S] #status experimental <MAT>
 F:2-56/Domain: ferredoxin 2[4Fe-4S] homology <FER>
 F:9,12,15,48/Binding site: 4Fe-4S cluster (Cys) (covalent) #status experimental
 F:19,38,41,44/Binding site: 4Fe-4S cluster (Cys) (covalent) #status experimental

Query Match 100.0%; Score 23; DB 1; Length 56;
 Best Local Similarity 60.0%; Pred. No. 7.8e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 36 DTCID 40

RESULT 27
 T03654
 glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - maize (fragmer
 N:Alternate names: hypothetical protein Q
 C:Species: Zea mays (maize)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 03-Jun-2002
 C:Accession: T03654
 R:Keith, C.S.; Hoang, D.O.; Barrett, B.M.; Feigelman, B.; Nelson, M.C.; Thai, H.; Bayados
 Plant Physiol. 101, 329-332, 1993
 A:Title: Partial sequence analysis of 130 randomly selected maize cDNA clones.
 A:Reference number: Z14989; MUID:94105294; PMID:8278499
 A:Accession: T03654
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-57 <KEI>
 A:Cross-references: EMBL:M95076; NID:G168567; PIDN:AAA72117.1; PID:G168568
 C:Function:
 A:Description: catalyzes the oxidative phosphorylation of D-glyceraldehyde-3-phosphate t
 A:Pathway: glycolysis
 C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
 C:Keywords: oxidoreductase

Query Match 100.0%; Score 23; DB 2; Length 57;
 Best Local Similarity 60.0%; Pred. No. 7.9e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 41 DFCXD 45

RESULT 28
 E81202
 hypothetical protein NMB0417 [imported] - Neisseria meningitidis (strain MC58 serogroup E
 C:Species: Neisseria meningitidis
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C:Accession: E81202
 R:Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A:Reference number: A81000; MUID:20175755; PMID:10710307
 A:Accession: E81202
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-58 <TET>

A;Cross-references: GB:AE002397; GB:AE002098; NID:g7225631; PIDN:AAF40855.1; PID:g7225631
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NM0417

Query Match 100.0%; Score 23; DB 2; Length 58;
Best Local Similarity 60.0%; Pred. No. 8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
33 DLCLD 37

Db

RESULT 29
G81777
probable periplasmic protein NMA2067 [imported] - Neisseria meningitidis (strain Z2491)
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: G81777
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jogle, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: G81777
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-60 <PAR>
A;Cross-references: GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB85285.1; PID:g7380672
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA2067

Query Match 100.0%; Score 23; DB 2; Length 60;
Best Local Similarity 60.0%; Pred. No. 8.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
35 DLCLD 39

Db

RESULT 30
G84271
50S ribosomal protein L24E [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
C;Accession: G84271
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: G84271
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-62 <STO>
A;Cross-references: GB:AE004437; NID:g10580695; PIDN:AAG19539.1; GSPDB:GN00138
C;Genetics:
A;Gene: rpl24e
C;Superfamily: Haloarcula ribosomal protein HU21

Query Match 100.0%; Score 23; DB 2; Length 62;
Best Local Similarity 60.0%; Pred. No. 8.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
8 DYCGD 12

Db

RESULT 31

A23727

neurotoxin V - bark scorpion

C;Species: Centruroides sculpturatus (bark scorpion)

C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 07-Feb-1997

C;Accession: A23727

R;David, R.M.; Krishna, N.R.; Watt, D.D.

Toxicon 29, 645-662, 1991

A;Title: Characterization of cationic binding sites of neurotoxins from venom of the scorpion

A;Reference number: A23727; MUID:92023284; PMID:1926166

A;Accession: A23727

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-63 <DAV>

C;Superfamily: scorpion neurotoxin

C;Keywords: neurotoxin

Query Match

Best Local Similarity 100.0%; Score 23; DB 2; Length 63;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5

|:|:
20 DYCNL 24

Db

RESULT 32

TIOAB

trypsin inhibitor (Bowman-Birk) - Job's tears

C;Species: Coix lachryma-jobi (Job's tears)

C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 31-Dec-1993

C;Accession: S00349

R;Ary, M.B.; Shewry, P.R.; Richardson, M.

FEBS Lett. 229, 111-118, 1988

A;Title: The amino acid sequence of a cereal Bowman-Birk type trypsin inhibitor from seed

A;Reference number: S00349; MUID:88152203; PMID:3162215

A;Accession: S00349

A;Molecule type: protein

A;Residues: 1-64 <ARY>

C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology

C;Keywords: duplication; proteinase inhibitor

F;10-35/Domain: Bowman-Birk inhibitor repeat homology <BB1>

F;36-59/Domain: Bowman-Birk inhibitor repeat homology #status atypical <BB2>

F;9-61,10-25,15-23,32-39,36-49/Disulfide bonds: #status predicted

F;17/inhibitory site: Arg (trypsin) #status predicted

Query Match

Best Local Similarity 100.0%; Score 23; DB 1; Length 64;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5

|:|:
30 DRCSL 34

Db

RESULT 33

S74702

hypothetical protein srr2153 - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C;Accession: S74702

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

s.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S74702

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-65 <KAN>

A;Cross-references: EMBL:D90901; GB:AB001339; NID:gl1651897; PIDN:BAAL6853.1; PID:dl01758
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 100.0%; Score 23; DB 2; Length 65;
 Best Local Similarity 60.0%; Pred. No. 8.8e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 61 DDCRD 65

RESULT 34

hypothetical protein Z4950 [imported] - Escherichia coli (strain O157:H7, substrain EDL93)
 C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C;Accession: A86027

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: A86027

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-65 <STO>

A;Cross-references: GB:AE005174; NID:gl12518254; PIDN:AAG58677.1; GSPDB:GN00145; UWGP:Z49
 A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:
 A;Gene: Z4950

Query Match 100.0%; Score 23; DB 2; Length 65;
 Best Local Similarity 60.0%; Pred. No. 8.8e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 37 DACPD 41

RESULT 35

glyceraldhyde-3-phosphate dehydrogenase (NADP) (phosphorylating) (EC 1.2.1.13) B, chloro
 C;Species: Spinacia oleracea (spinach)

C;Date: 19-Mar-1997 #sequence_revision 30-Jan-1998 #text_change 03-Jun-2002

C;Accession: S33873

R;Zapponi, M.C.; Iadarola, P.; Stoppini, M.; Ferri, G.

Biol. Chem. Hoppe-Seyler 374, 395-402, 1993

A;Title: Limited proteolysis of chloroplast glyceraldhyde-3-phosphate dehydrogenase (NA
 A;Reference number: S33872; MUID:93363226; PMID:8357535

A;Accession: S33873

A;Molecule type: protein

A;Residues: 1-67 <ZAP>

A;Experimental source: leaf

C;Genetics:

A;Genome: nuclear

C;Superfamily: glyceraldhyde-3-phosphate dehydrogenase

C;Keywords: Calvin cycle; chloroplast; NADP; oxidoreductase; tetramer

Query Match 100.0%; Score 23; DB 2; Length 67;
 Best Local Similarity 60.0%; Pred. No. 9e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 52 DPCDK 56

RESULT 36

G84255

hypothetical protein Vng0994h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 18-Jul-2001
 C;Accession: G84255; F84181; F84317; C84257

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
 ; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: G84255

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-67 <STO>

A;Cross-references: GB:AE004437; NID:gl0580549; PIDN:AAG19411.1; GSPDB:GN00138

A;Accession: F84181

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-67 <ST2>

A;Cross-references: GB:AE004437; NID:gl0579856; PIDN:AAG18818.1; GSPDB:GN00138

A;Accession: F84317

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-67 <ST3>

A;Cross-references: GB:AE004437; NID:gl0581122; PIDN:AAG19906.1; GSPDB:GN00138

A;Accession: C84257

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-67 <ST4>

A;Cross-references: GB:AE004437; NID:gl0580563; PIDN:AAG19423.1; GSPDB:GN00138

C;Genetics:

A;Gene: VNG0994H; VNG0210H; VNG1651H; VNG1007H

Query Match 100.0%; Score 23; DB 2; Length 67;
 Best Local Similarity 60.0%; Pred. No. 9e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 23 DECSD 27

RESULT 37

E97420

hypothetical protein AGR_C_892 [imported] - Agrobacterium tumefaciens (strain C58, Cersor

C;Species: Agrobacterium tumefaciens

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002

C;Accession: E97420

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: E97420

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-68 <KUR>

A;Cross-references: GB:AE007869; PIDN:AAK86318.1; PID:gl5155436; GSPDB:GN00169

C;Genetics:

A;Gene: AGR_C_892

A;Map position: circular chromosome

Query Match 100.0%; Score 23; DB 2; Length 68;
 Best Local Similarity 60.0%; Pred. No. 9.1e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 3 DPCGD 7

RESULT 38

A83982

hypothetical protein BH2657 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C;Accession: A83982
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: A83982
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-70 <STO>
 A;Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06376.1; GSPDB:GN00
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH2657

Query Match 100.0%; Score 23; DB 2; Length 70;
 Best Local Similarity 60.0%; Pred. No. 9.3e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |::|
 Db 7 DGCFD 11

RESULT 39
 E72171
 K8R protein - variola minor virus (strain Garcia-1966)
 C;Species: variola minor virus
 C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999
 C;Accession: E72171
 R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopax
 submitted to GenBank, March 1998
 A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
 A;Reference number: A72150
 A;Accession: E72171
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-70 <SHC>
 A;Cross-references: GB:Y16780; NID:G5830555; PIDN:CAB54767.1; PID:61542723; PID:G5830728
 A;Experimental source: strain Garcia-1966
 C;Genetics:
 A;Gene: K8R

Query Match 100.0%; Score 23; DB 2; Length 70;
 Best Local Similarity 60.0%; pred. No. 9.3e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |::|
 Db 27 DTCTD 31

RESULT 40
 B71282
 hypothetical protein TP0777 - syphilis spirochete
 C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
 C;Accession: B71282
 R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 zson, J.; Khatak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A;Reference number: A71250; MUID:98332770; PMID:9665876
 A;Accession: B71282
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-74 <COL>
 A;Cross-references: GB:AE001249; GB:AE000520; NID:g3323083; PIDN:AAC65750.1; PID:g332309
 A;Experimental source: strain Nichols
 C;Genetics:
 A;Gene: TP0777

Query Match 100.0%; Score 23; DB 2; Length 74;
 Best Local Similarity 60.0%; Pred. No. 9.8e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |::|
 Db 29 DVCED 33

RESULT 41
 T25370
 hypothetical protein T27E9.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 27-Oct-2003
 C;Accession: T25370
 R;Lloyd, C.
 submitted to the EMBL Data Library, November 1996
 A;Reference number: Z20024
 A;Accession: T25370
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-75 <WIL>
 A;Cross-references: EMBL:Z82059; PIDN:CAB04873.1; GSPDB:GN00021; CESP:T27E9.2
 A;Experimental source: clone T27E9
 C;Genetics:
 A;Gene: CESP:T27E9.2
 A;Map position: 3
 C;Superfamily: ubiquinol-cytochrome-c reductase (cytochrome c1), nonheme 11 kDa protein;

Query Match 100.0%; Score 23; DB 2; Length 75;
 Best Local Similarity 60.0%; Pred. No. 9.9e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |::|
 Db 35 DECND 39

RESULT 42
 B69110
 ferredoxin - Methanobacterium thermoautotrophicum (strain Delta H)
 C;Species: Methanobacterium thermoautotrophicum
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jun-1999
 C;Accession: B69110
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; F.
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A;Reference number: A69000; MUID:98037514; PMID:9371463
 A;Accession: B69110
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-76 <MTH>
 A;Cross-references: GB:AE000935; GB:AE000666; NID:g2622945; PIDN:AAB86285.1; PID:g262295;
 A;Experimental source: strain Delta H
 C;Genetics:
 A;Gene: MTH1819
 C;Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
 F;4-69/Domain: ferredoxin 2[4Fe-4S] homology <FER>

Query Match 100.0%; Score 23; DB 2; Length 76;
 Best Local Similarity 60.0%; Pred. No. 1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |::|
 Db 19 DSCPD 23

RESULT 43
 T03860

TA20 protein - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C:Accession: T03860
R:Beals, T.P.; Goldberg, R.B.
Submitted to the EMBL Data Library, October 1996
A:Description: Nicotiana tabacum gene expressed in anther.
A:Reference number: Z15122
A:Accession: T03860
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-76 <BEA>
A:Cross-references: EMBL:U73164; NID:G1657813; PIDN:AAB18190.1; PID:G1657814
A:Experimental source: tissue-type anther
C:Genetics:
A:Gene: TA20

Query Match 100.0%; Score 23; DB 2; Length 76;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
DB 34 DSCTD 38

RESULT 44
T09476
hypothetical protein - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: T09476
R:Murphy, L.
Submitted to the EMBL Data Library, January 1998.
A:Reference number: Z16683
A:Accession: T09476
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-76 <MUR>
A:Cross-references: EMBL:AL021546; NID:e1248287; PID:e1248289
C:Genetics:
A:Gene: 15E1.1
A:Map position: 12
A:Introns: 49/3

Query Match 100.0%; Score 23; DB 2; Length 76;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
DB 35 DPCDT 39

RESULT 45
AB2086
hypothetical protein VC2357 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: AB2086
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.
L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833; PMID:10952301
A:Accession: AB2086
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-77 <HEI>
A:Cross-references: GB:AE004306; GB:AE003852; NID:G9656924; PIDN:AAF95500.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:

A:Gene: VC2357
A:Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 77;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
DB 67 DVCID 71

RESULT 46
FEBSA
ferredoxin [3Fe-4S][4Fe-4S] - Alicyclobacillus acidocaldarius
C:Species: Alicyclobacillus acidocaldarius
C:Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Sep-1998
C:Accession: A00215
R:Schlatter, D.; Waldvogel, S.; Zulli, F.; Suter, F.; Portmann, W.; Zuber, H.
Biol. Chem. Hoppe-Seyler 366, 223-231, 1985
A:Title: Purification, amino-acid sequence and some properties of the ferredoxin isolated
A:Reference number: A00215; MUID:85225952; PMID:2988582
A:Accession: A00215
A:Molecule type: protein
A:Residues: 1-78 <SCH>
C:Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
C:Keywords: 3Fe-4S; 4Fe-4S; duplication; electron transfer; iron-sulfur protein; metallo
F:1-57/Domain: ferredoxin 2[4Fe-4S] homology <FER>
F:8,16,49/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted
F:20,39,42,45/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 100.0%; Score 23; DB 1; Length 78;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
DB 37 DVCID 41

RESULT 47
JC2496
ferredoxin [3Fe-4S][4Fe-4S] - Bacillus schlegelii
C:Species: Bacillus schlegelii
C:Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: JC2496
R:Aono, S.; Nakamura, S.; Aono, R.; Okura, I.
Biochem. Biophys. Res. Commun. 201, 938-942, 1994
A:Title: Cloning and expression of the gene encoding the 7Fe type ferredoxin from a therm
A:Reference number: JC2496; MUID:94271256; PMID:8003034
A:Accession: JC2496
A:Molecule type: DNA
A:Residues: 1-78 <AON>
C:Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
C:Keywords: 3Fe-4S; 4Fe-4S; iron-sulfur protein; metalloprotein
F:2-58/Domain: ferredoxin 2[4Fe-4S] homology <FER>
F:9,17,50/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted
F:21,40,43,46/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 100.0%; Score 23; DB 2; Length 78;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
DB 38 DVCID 42

RESULT 48
A49475
cerebroside sulfate activator - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 17-May-1996

C;Accession: A49475
R;Stevens, R.L.; Faull, K.F.; Conklin, K.A.; Green, B.N.; Fluharty, A.L.
Biochemistry 32, 4051-4059, 1993
A;Title: Porcine cerebroside sulfate activator: further structural characterization and
A;Reference number: A49475; MUID:93229506; PMID:8471613
A;Accession: A49475
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-79 <STE>
A;Experimental source: kidney
A;Note: sequence extracted from NCBI backbone (NCBIP:129597)
C;Superfamily: saposin; saposin repeat homology
F;1-79/Domain: saposin repeat homology <SAP>

Query Match 100.0%; Score 23; DB 2; Length 79;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXND 5
|:|:
Db 2 DVCQD 6

RESULT 49
C87028
hypothetical protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: C87028
R;Cole, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
sam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: C87028
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-79 <STO>
A;Cross-references: GB:AL450380; NID:gl3093004; PIDN:CAC31334.1; GSPDB:GN00147
C;Genetics:
A;Gene: ML0953

Query Match 100.0%; Score 23; DB 2; Length 79;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXND 5
|:|:
Db 73 DHCD 77

RESULT 50
C84308
hypothetical protein Vng1546h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84308
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: C84308
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-79 <STO>
A;Cross-references: GB:AE004437; NID:gl0581035; PIDN:AAG19831.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG1546H

Query Match 100.0%; Score 23; DB 2; Length 80;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXND 5
|:|:
Db 33 DPCID 37

RESULT 53
A82769
hypothetical protein XF0756 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: A82769

Query Match 100.0%; Score 23; DB 2; Length 79;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXND 5
|:|:
Db 9 DDCPD 13

RESULT 51
C84381
hypothetical protein Vng2304h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84381
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: C84381
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-79 <STO>
A;Cross-references: GB:AE004437; NID:gl0581716; PIDN:AAG20415.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG2304H

Query Match 100.0%; Score 23; DB 2; Length 79;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXND 5
|:|:
Db 10 DWCGD 14

RESULT 52
T45327
hypothetical protein MCB1779.39c [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 31-Jan-2000
C;Accession: T45327
R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z22864
A;Accession: T45327
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-80 <PAR>
A;Cross-references: EMBL:Z98271; PIDN:CAB11020.1
A;Experimental source: cosmid B1779
C;Genetics:
A;Note: MCB1779.39c

Query Match 100.0%; Score 23; DB 2; Length 80;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXND 5
|:|:
Db 33 DPCID 37

RESULT 53
A82769
hypothetical protein XF0756 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: A82769

R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing 406, 151-157, 2000
 A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A; Reference number: A82515; MUID:20365717; PMID:10910347
 A; Note: for a complete list of authors see reference number A59328 below
 A; Accession: A82769
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-83 <SIM>
 A; Cross-references: GB:AE003916; GB:AE003849; NID:g9105626; PIDN:AAF83566.1; GSPDB:GN001
 A; Experimental source: strain 9a5c
 R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, R
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A; Reference number: A59328
 A; Contents: annotation
 C; Genetics:
 A; Gene: XF0756

Query Match 100.0%; Score 23; DB 2; Length 83;
 Best Local Similarity 60.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 | : | : |
 Db 38 DGCND 42

RESULT 54

C84867
 probable trypsin inhibitor [imported] - Arabidopsis thaliana
 C; Species: Arabidopsis thaliana (mouse-ear cress)
 C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C; Accession: C84867
 R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vannken, S.E.; Umayam, L.; Tallon, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
 Nature 402, 761-768, 1999
 A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A; Reference number: A84420; MUID:20083487; PMID:10617197
 A; Accession: C84867
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-85 <STO>
 A; Cross-references: GB:AE002093; NID:g2289007; PIDN:AAB64336.1; GSPDB:GN00139
 C; Genetics:
 A; Gene: At2g43530
 A; Map position: 2

Query Match 100.0%; Score 23; DB 2; Length 85;
 Best Local Similarity 60.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 | : | : |
 Db 78 DFCSD 82

RESULT 55

T47563
 kinetochore-like protein - Arabidopsis thaliana
 N; Alternate names: protein F8J2.230
 C; Species: Arabidopsis thaliana (mouse-ear cress)
 C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C; Accession: T47563
 R; Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weicheelgartner, M.; N
 Mayer, K.F.X.
 submitted to the Protein Sequence Database, April 2000
 A; Reference number: Z24458
 A; Accession: T47563
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-85 <NYA>
 A; Cross-references: EMBL:AL132969
 A; Experimental source: cultivar Columbia; BAC clone F8J2
 C; Genetics:
 A; Map position: 3
 A; Introns: 58/3
 A; Note: F8J2.230

Query Match 100.0%; Score 23; DB 2; Length 85;
 Best Local Similarity 60.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 | : | : |
 Db 4 DDCAD 8

RESULT 56

A37910
 muscarinic toxin 2 precursor - eastern green mamba
 N; Alternate names: MTX2
 C; Species: Dendroaspis angusticeps (eastern green mamba)
 C; Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 17-Mar-2000
 C; Accession: A37910; A37911; S66418
 R; Ducancel, F.; Rowan, E.G.; Cassar, E.; Harvey, A.L.; Menez, A.; Boulain, J.C.
 Toxicon 29, 516-520, 1991
 A; Title: Amino acid sequence of a muscarinic toxin deduced from the cDNA nucleotide sequ
 A; Reference number: A37910; MUID:91320365; PMID:1862524
 A; Accession: A37910
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-86 <DUC>
 A; Cross-references: GB:X52292; NID:g62765; PIDN:CAA36541.1; PID:g62766
 R; Karlsson, E.; Risinger, C.; Jolkonen, M.; Wernstedt, C.; Adem, A.
 Toxicon 29, 521-526, 1991
 A; Title: Amino acid sequence of a snake venom toxin that binds to the muscarinic acetylch
 A; Reference number: A37911; MUID:91320366; PMID:1862525
 A; Accession: A37911
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 'K', 23-86 <KAR>
 R; Segalae, I.; Thai, R.; Menez, R.; Vita, C.
 FEBS Lett. 371, 171-175, 1995
 A; Title: A particularly labile Asp-Pro bond in the green mamba muscarinic toxin MTX2. Bf1
 A; Reference number: S66418; MUID:95402203; PMID:7672121
 A; Accession: S66418
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 22-27, 29-86 <SEG>
 C; Superfamily: snake toxin
 C; Keywords: toxin; venom
 F; 1-21/Domain: signal sequence #status predicted <SIG>
 F; 22-86/Product: muscarinic toxin 2 #status experimental <MAT>

Query Match 100.0%; Score 23; DB 2; Length 86;
 Best Local Similarity 60.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 | : | : |
 Db 82 DXCND 86

RESULT 57

E81063

```

hypothetical protein NMB1615 [imported] - Neisseria meningitidis (strain MC58 serogroup
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: E81063
R:Tetrelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.B.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Ri, H.; Qln, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masiagnani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: E81063
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-87 <TET>
A:Cross-references: GB:AE002511; GB:AE002098; NID:G7226857; PIDN:AAF41967.1; PID:G722686
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1615

Query Match 100.0%; Score 23; DB 2; Length 87;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 72 DCLD 76

RESULT 58
G70782
hypothetical protein RV0898c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: G70782
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: G70782
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-87 <COL>
A:Cross-references: GB:Z73101; GB:AL123456; NID:G3261565; PIDN:CAA97373.1; PID:e241996;
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV0898c

Query Match 100.0%; Score 23; DB 2; Length 87;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 52 DQWD 56

RESULT 59
A84867
probable trypsin inhibitor [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: A84867
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84867

```

```

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <STO>
A:Cross-references: GB:AE002093; NID:G2288996; PIDN:AAB64325.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g943510
A:Map position: 2

```

```

Query Match 100.0%; Score 23; DB 2; Length 89;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 82 DFCDD 86

```

```

RESULT 60
E84867
probable trypsin inhibitor [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: E84867
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: E84867
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <STO>
A:Cross-references: GB:AE002093; NID:G2288993; PIDN:AAB64322.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g943550
A:Map position: 2

```

```

Query Match 100.0%; Score 23; DB 2; Length 89;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 84 DYCDD 88

```

```

RESULT 61
S71555
protease inhibitor-related protein bs11 precursor - barley
C:Species: Hordeum vulgare (barley)
C>Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 21-Jul-2000
C:Accession: S71555; S53102
R:Stevens, C.; Titarenko, E.; Hargreaves, J.A.; Gurr, S.J.
Plant Mol. Biol. 31, 741-749, 1996
A:Title: Defence-related gene activation during an incompatible interaction between Stagg
A:Reference number: S71554; MUID:96400029; PMID:8806405
A:Accession: S71555
A:Molecule type: DNA
A:Residues: 1-89 <STG>
A:Cross-references: EMBL:Z48729; NID:G732808; PIDN:CAA8619.1; PID:G732809
C:Genetics:
A:Gene: bs11
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-89/Product: proteinase inhibitor-related protein bs11 #status predicted <MAT>

```

```

Query Match 100.0%; Score 23; DB 2; Length 89;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 43 DVCDD 47

```

RESULT 62
JQ2361
wheat aluminum induced protein wali 5 - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 29-Oct-1999
C:Accession: JQ2361
R:Snowden, K.C.; Gardner, R.C.
A:Title: Five genes induced by aluminum in wheat (*Triticum aestivum* L.) roots.
A:Reference number: JQ2358; MUID:94294563; PMID:8022939
A:Accession: JQ2361
A:Molecule type: mRNA
A:Residues: 1-89 <SNO>
A:Cross-references: GB:L11882; NID:g170794; PIDN:AAA50850.1; PID:g170795
A:Experimental source: root, cv. Warigal
C:Keywords: metal binding

Query Match 100.0%; Score 23; DB 2; Length 89;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
|:|:
DB 43 DVCDD 47

RESULT 63
B84867
probable trypsin inhibitor [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: B84867
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: B84420; MUID:20083487; PMID:1061197
A:Accession: B84867
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STO>
A:Cross-references: GB:AE002093; NID:g2288995; PIDN:AAB64324.1; GSPDB:GN00139
A:Gene: At2g43520
A:Map position: 2

Query Match 100.0%; Score 23; DB 2; Length 90;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
|:|:
DB 84 DYCS 88

RESULT 64
B87600
conserved hypothetical protein CC2833 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: B87600
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.;
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: B87249; MUID:21173698; PMID:11255647
A:Accession: B87600
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-92 <STO>
A:Cross-references: GB:AE005673; NID:g13424443; PIDN:AAK24797.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC2833

Query Match 100.0%; Score 23; DB 2; Length 92;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
|:|:
DB 41 DLCPD 45

RESULT 65
S49260
ferredoxin 2[4Fe-4S] - *Afipia felis* (ATCC 49716) (fragment)
C:Species: *Afipia felis*
A:Variety: ATCC 49716
C:Date: 19-Mar-1997 #sequence_revision 24-Oct-1997 #text_change 11-Jun-1999
C:Accession: S49260
R:Bergmans, A.M.C.; Groothedde, J.W.; Schellekens, J.F.P.; van Embden, J.D.A.; Ossewaarde
submitted to the EMBL Data Library, September 1994
A:Description: A comparative study on the etiology of cat scratch disease: PCR detection
A:Reference number: S49260
A:Accession: S49260
A:Molecule type: DNA
A:Residues: 1-93 <BER>
A:Cross-references: EMBL:X81826; NID:g550301; PIDN:CAA57420.1; PID:g550302
A:Experimental source: ATCC 49716
C:Genetics:
A:Gene: fdx4

C:Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
C:Keywords: electron transfer; iron-sulfur protein
F:2-58/Domain: ferredoxin 2[4Fe-4S] homology <FER>

Query Match 100.0%; Score 23; DB 2; Length 93;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCX 5
|:|:
DB 38 DECID 42

RESULT 66
LUPG10
calpactin I light chain - pig
N:Alternate names: p10 protein; p11 protein
C:Species: *Sus scrofa domestica* (domestic pig)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 18-Jul-1997
C:Accession: A03079; A24063
R:Gerke, V.; Weber, K.
EMBO J. 4, 2917-2920, 1985
A:Title: The regulatory chain in the p36-kd substrate complex of viral tyrosine-specific
A:Reference number: A03079; MUID:86055730; PMID:2998764
A:Accession: A03079
A:Molecule type: protein
A:Residues: 1-95 <GER>
R:Hexham, J.M.; Totty, N.F.; Waterfield, M.D.; Crumpton, M.J.
Biochem. Biophys. Res. Commun. 134, 248-254, 1986
A:Title: Homology between the subunits of S100 and A 10kDa polypeptide associated with p;
A:Reference number: A24063; MUID:86130472; PMID:2936341
A:Accession: A24063
A:Molecule type: protein
A:Residues: 1-51, 'XX', '54-55 <HEX>
C:Comment: Calpactin I light does not appear to bind calcium.
C:Complex: Calpactin I is a tetramer of two light chains and two heavy chains (annexin I;
C:Function:
A:Description: found in lamina beneath plasma membrane where it may cross-link plasma men
A:Pathway: exocytosis
A:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: EF hand; intestine

F16-37/Domain: calmodulin repeat homology <EF1>
F146-78/Domain: calmodulin repeat homology <EF2>

Query Match 100.0%; Score 23; DB 1; Length 95;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 59 DQCRD 63

RESULT 67

A31373
calpactin I light chain - rat
N/Alternate names: p11
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 13-Aug-1999
C/Accession: A31373

R/Masiakowski, P.; Shooter, E.M.
Proc. Natl. Acad. Sci. U.S.A. 85, 1277-1281, 1988
A/Title: Nerve growth factor induces the genes for two proteins related to a family of
A/Reference number: A94189; MUID:88125019; PMID:3422491

A/Accession: A31373
A/Molecule type: mRNA
A/Residues: 1-95 <MAS>
A/Cross-references: GB:J03627; NID:g206827; PIDN:AAA42097.1; PID:g206828
C/Superfamily: S-100 protein; calmodulin repeat homology
C/Keywords: calcium binding; EF hand
F147-79/Domain: calmodulin repeat homology <EFH>

Query Match 100.0%; Score 23; DB 2; Length 95;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 60 DQCRD 64

RESULT 68

G81901
hypothetical protein NMA1327 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C/Species: Neisseria meningitidis
C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C/Accession: G81901

R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A/Reference number: A81775; MUID:20222556; PMID:10761919

A/Accession: G81901
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-95 <PAR>
A/Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84578.1; PID:g738000
A/Experimental source: serogroup A, strain Z2491
C/Genetics:

A/Gene: NMA1327

Query Match 100.0%; Score 23; DB 2; Length 95;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 37 DVCDF 41

RESULT 69

JH0663
calpactin I light chain - chicken
N/Alternate names: p10 protein; p11 protein

C/Species: Gallus gallus (chicken)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: JH0663
R/Kube, E.; Weber, K.; Gerke, V.
Gene 102, 255-259, 1991

A/Title: Primary structure of human, chicken, and Xenopus laevis p11, a cellular ligand
A/Reference number: JH0662; MUID:91340161; PMID:1831433

A/Accession: JH0663
A/Molecule type: mRNA
A/Residues: 1-97 <KUB>

A/Cross-references: GB:M38592; NID:g211531; PIDN:AAA48690.1; PID:g211532
C/Comment: This protein interacts with annexin II.

C/Superfamily: S-100 protein; calmodulin repeat homology
C/Keywords: calcium binding; EF hand

F12-97/Product: p11 protein #status predicted <P11>
F18-29/Domain: calcium binding #status predicted <CA1>
F147-79/Domain: calmodulin repeat homology <EFH>

F159-70/Domain: calcium binding #status predicted <CA2>

Query Match 100.0%; Score 23; DB 1; Length 97;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 60 DQCRD 64

RESULT 70

JC4912

eotaxin precursor - human

C/Species: Homo sapiens (man)

C/Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 20-Jun-2000

C/Accession: JC4912

R/Bartels, J.; Schlueter, C.; Richter, E.; Noso, N.; Kulke, R.; Christophers, E.; Schroeder

Biochem. Biophys. Res. Commun. 225, 1045-1051, 1996

A/Title: Human dermal fibroblasts express eotaxin: Molecular cloning, mRNA expression, ar

A/Reference number: JC4912; MUID:96374440; PMID:8780731

A/Accession: JC4912

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-97 <BAR>

A/Cross-references: EMBL:Z75668; NID:g1531982; PIDN:CAA99997.1; PID:g1531983

A/Experimental source: dermal fibroblast

C/Comment: This protein has eosinophil specific chemotactic activity.

C/Superfamily: macrophage inflammatory protein

C/Keywords: fibroblast

F11-18/Domain: signal sequence #status predicted <SIG>

F19-97/Product: eotaxin #status predicted <MAT>

Query Match 100.0%; Score 23; DB 2; Length 97;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 71 DICAD 75

RESULT 71

JC1139

calpactin I light chain - human

N/Alternate names: p11 protein

C/Species: Homo sapiens (man)

C/Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 13-Aug-1999

C/Accession: JC1139; JH0662; A42833

R/Harder, T.; Kube, E.; Gerke, V.

Gene 113, 269-274, 1992

A/Title: Cloning and characterization of the human gene encoding p11: Structural similar

A/Reference number: JC1139; MUID:92241679; PMID:1533380

A/Accession: JC1139

A/Molecule type: DNA

A/Residues: 1-97 <HAR>

A:Cross-references: GB:M77483
 R:Kube, E.; Weber, K.; Gerke, V.
 Gene 102, 255-259, 1991
 A:Title: Primary structure of human, chicken, and *Xenopus laevis* p11, a cellular ligand
 A:Reference number: JH0662; MUID:91340161; PMID:1831433
 A:Accession: JH0662
 A:Molecule type: mRNA
 A:Residues: 1-97 <KUB>
 A:Cross-references: GB:M38591; NID:g180595; PIDN:AAA58426.1; PID:g180596
 R:Dooley, T.P.; Weiland, K.L.; Simon, M.
 Genomics 13, 866-868, 1992
 A:Title: cDNA sequence of human p11 calpactin I light chain.
 A:Reference number: A42833; MUID:92347895; PMID:1386341
 A:Accession: A42833
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-97 <DOO>
 A:Cross-references: GB:M81457; NID:g179874; PIDN:AAA58404.1; PID:g179875
 A:Experimental source: foreskin keratinocyte
 A:Note: sequence extracted from NCBI backbone (NCBIN:109818, NCBIP:109819)
 C:Comment: Calpactin I light chain does not appear to bind calcium.
 C:Genetics:
 A:Gene: GDB:S100A10; ANX2LG; CALIL
 A:Cross-references: GDB:134557; OMIM:114085
 A:Map position: 1q21-1q21
 C:Introns: 44/3
 C:Complex: Calpactin I is a tetramer of two light chains and two heavy chains (annexin I
 C:Function:
 A:Description: found in lamina beneath plasma membrane where it may cross-link plasma me
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: EF hand; heterotetramer
 F:2-97/Product: calpactin I light chain #status predicted <MAT>
 F:7-38/Domain: calmodulin repeat homology <EF1>
 F:47-79/Domain: calmodulin repeat homology <EF2>
 F:79-97/Region: annexin II binding #status predicted

Query Match 100.0%; Score 23; DB 2; Length 97;
 Best Local Similarity 60.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 60 DQCRD 64

RESULT 72
 B28489
 calpactin I light chain - bovine
 N:Alternate names: p10 protein; p11 protein
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 13-Aug-1999
 C:Accession: B28489; A23564; S02478
 R:Saris, C.J.M.; Kristensen, T.; D'Eustachio, P.; Hicks, L.J.; Noonan, D.J.; Hunter, T.;
 J. Biol. Chem. 262, 10663-10671, 1987
 A:Title: cDNA sequence and tissue distribution of the mRNA for bovine and murine p11, th
 A:Reference number: A92603; MUID:87280130; PMID:3038891
 A:Accession: B28489
 A:Molecule type: mRNA
 A:Residues: 1-97 <SAR>
 A:Cross-references: GB:M16464; NID:g162784; PIDN:AAA30423.1; PID:g162785
 A:Experimental source: intestinal epithelium
 R:Glenney Jr., J.R.; Tack, B.F.
 Proc. Natl. Acad. Sci. U.S.A. 82, 7884-7888, 1985
 A:Title: Amino-terminal sequence of p36 and associated p10: identification of the site o
 A:Reference number: A23564; MUID:86068007; PMID:2415974
 A:Accession: A23564
 A:Molecule type: protein
 A:Residues: 2-57 <GLE>
 A:Experimental source: intestinal epithelium
 R:Martin, F.; Derancourt, J.; Capony, J.P.; Watrin, A.; Cavadore, J.C.
 Biochem. J. 251, 777-785, 1988
 A:Title: A 36 kDa monomeric protein and its complex with a 10 kDa protein both isolated
 n-severing properties.

A:Reference number: S02477; MUID:88326216; PMID:2970844
 A:Accession: S02478
 A:Molecule type: protein
 A:Residues: 2-3, 'E', 'S', 'Q', '7-9', 'Q', '11-21 <MAR>
 A:Experimental source: aorta
 C:Comment: Calpactin I is a tetramer of two light chains (p11) and two heavy chains (anne
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: calcium binding; EF hand; heterotetramer
 F:2-97/Product: calpactin I light chain #status predicted <MAT>
 F:47-79/Domain: calmodulin repeat homology <EFH>
 F:79-97/Region: annexin II binding #status predicted

Query Match 100.0%; Score 23; DB 2; Length 97;
 Best Local Similarity 60.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 60 DQCRD 64

RESULT 73
 A28489
 calpactin I light chain - mouse
 N:Alternate names: p11
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
 C:Accession: A28489
 R:Saris, C.J.M.; Kristensen, T.; D'Eustachio, P.; Hicks, L.J.; Noonan, D.J.; Hunter, T.;
 J. Biol. Chem. 262, 10663-10671, 1987
 A:Title: cDNA sequence and tissue distribution of the mRNA for bovine and murine p11, the
 A:Reference number: A92603; MUID:87280130; PMID:3038891
 A:Accession: A28489
 A:Molecule type: mRNA
 A:Residues: 1-97 <SAR>
 A:Cross-references: GB:M16465; GB:J02779; NID:g192360; PIDN:AAA37363.1; PID:g309134
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: calcium binding; EF hand
 F:47-79/Domain: calmodulin repeat homology <EFH>

Query Match 100.0%; Score 23; DB 2; Length 97;
 Best Local Similarity 60.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
 |:|:
 Db 60 DQCRD 64

RESULT 74
 S65661
 trypsin inhibitor 2 precursor - white mustard
 C:Species: Sinapis alba (white mustard)
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
 C:Accession: S65661; S21120
 R:Ceci, L.R.; Spoto, N.; de Virgilio, M.; Gallerani, R.
 FEBS Lett. 364, 179-181, 1995
 A:Title: The gene coding for the mustard trypsin inhibitor-2 is discontinuous and wound-i
 A:Reference number: S65661; MUID:95269796; PMID:7750566
 A:Accession: S65661
 A:Molecule type: DNA
 A:Residues: 1-99 <CEC>
 A:Cross-references: EMBL:X84208; NID:g4902896; PIDN:CAA58994.1; PID:g1054853
 A:Note: the authors translated the codon GCC for residue 2 as Gly
 R:Menegatti, E.; Tedeschi, G.; Ronchi, S.; Bortolotti, F.; Ascenzi, P.; Thomas, R.M.; Boi
 FEBS Lett. 301, 10-14, 1992
 A:Title: Purification, inhibitory properties and amino acid sequence of a new serine prot
 A:Reference number: S21120; MUID:93083607; PMID:1451776
 A:Accession: S21120
 A:Molecule type: protein
 A:Residues: 31-93 <MEN>
 C:Genetics:
 A:Gene: mti-2

```

A;Introns: 23/1
C;Function:
A;Description: serine proteinase inhibitor; strongly inhibits beta-trypsin and alpha-chy
C;Keywords: disulfide bond; serine proteinase inhibitor
F;1-29/Domains: signal sequence #status predicted <SIG>
F;30-93/Product: trypsin inhibitor 2 #status experimental <MAT>

Query Match          100.0%; Score 23; DB 2; Length 99;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
   |:|:|
Db 84 DYCND 88

RESULT 75
T32227
hypothetical protein T23B12.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32227
R;Davidson, S.; Wohldmann, P.; Gillam, B.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid T23B12.
A;Reference number: Z21137
A;Accession: T32227
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-99 <DAV>
A;Cross-references: EMBL:AF022982; PIDN:AB69939.1; GSPDB:GN00023; CESP:T23B12.8
A;Experimental source: strain Bristol N2; clone T23B12
C;Genetics:
A;Gene: CESP:T23B12.8
A;Map position: 5
A;Introns: 37/3

Query Match          100.0%; Score 23; DB 2; Length 99;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
   |:|:|
Db 66 DDCDD 70

RESULT 76
AD2270
hypothetical protein alr3715 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AD2270
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2270
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA675414.1; PID:g17132849; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr3715

Query Match          100.0%; Score 23; DB 2; Length 99;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
   |:|:|

```

Db 57 DICGD 61

RESULT 77

D71962

hypothetical protein jhp0189 - Helicobacter pylori (strain J99)

C;Species: Helicobacter pylori

A;Variety: strain J99

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999

C;Accession: D71962

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric patho

A;Reference number: A71800; MUID:99120557; PMID:9923682

A;Accession: D71962

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-100 <ARN>

A;Cross-references: GB:AE001457; GB:AE001439; NID:g4154703; PIDN:AA05772.1; PID:g4154701

A;Experimental source: strain J99

C;Genetics:

A;Gene: jhp0189

Query Match

Best Local Similarity 100.0%; Score 23; DB 2; Length 100;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5

:|:|

Db 20 DYCSD 24

RESULT 78

Ti6810

hypothetical protein T05C1.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: Ti6810

R;Geisel, C.

submitted to the EMBL Data Library, June 1995

A;Description: The sequence of C. elegans cosmid T05C1.

A;Reference number: Z18581

A;Accession: Ti6810

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-100 <GEI>

A;Cross-references: EMBL:U28992; NID:g861370; PID:g861374; PIDN:AAA68392.1; CESP:T05C1.5

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:T05C1.5

A;Introns: 42/1; 88/1

Query Match

Best Local Similarity 100.0%; Score 23; DB 2; Length 100;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5

:|:|

Db 50 DLCED 54

Search completed: May 6, 2004, 10:47:15

Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2004, 10:45:57 ; Search time 41 Seconds
(without alignments)
33.850 Million cell updates/sec

Title: SEQ1

Perfect score: 23
Sequence: 1 dxcxd 5

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 632

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	23	100.0	9	12	US-10-363-791-27
5	23	100.0	9	12	US-10-253-286-518
6	23	100.0	9	15	US-10-245-871-518
7	23	100.0	9	16	US-10-447-161-67
8	23	100.0	10	10	US-09-572-270A-819
9	23	100.0	10	14	US-10-155-922-76
10	23	100.0	10	14	US-10-062-109A-630
11	23	100.0	10	14	US-10-005-480A-630
12	23	100.0	10	10	US-09-809-391-649
13	23	100.0	11	10	US-09-882-171-649
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269	23	100.0	47	14	US-10-162-435-32	Sequence 32, Appl	342	23	100.0	60	12	US-10-425-114-40059	Sequence 40059, A
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271	23	100.0	48	10	US-09-969-730-206	Sequence 206, App	344	23	100.0	60	14	US-10-040-862-1067	Sequence 1067, App
272	23	100.0	48	10	US-09-948-495A-2	Sequence 2, Appl	345	23	100.0	60	15	US-10-057-475B-1067	Sequence 1067, Ap
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281	23	100.0	51	9	US-09-972-484-7	Sequence 7, Appl	354	23	100.0	62	9	US-09-796-692-1079	Sequence 1079, Ap
282	23	100.0	51	10	US-09-933-767-583	Sequence 583, App	355	23	100.0	62	9	US-09-796-692-1645	Sequence 1645, Ap
283	23	100.0	51	12	US-10-004-860-583	Sequence 583, App	356	23	100.0	62	12	US-10-424-599-214204	Sequence 214204,
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391	23	100.0	67	12	US-10-424-599-227966	Sequence 227966, App	464	23	100.0	78	10	US-09-498-272-56	Sequence 56, Appl
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395	23	100.0	68	12	US-10-424-599-209263	Sequence 209263, App	468	23	100.0	78	12	US-10-424-599-244518	Sequence 244518, App
396	23	100.0	68	12	US-10-424-599-242288	Sequence 242288, App	469	23	100.0	78	12	US-10-424-599-248259	Sequence 248259, App
397	23	100.0	68	12	US-10-424-599-242504	Sequence 242504, App	470	23	100.0	78	12	US-10-424-599-274632	Sequence 274632, App
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403	23	100.0	70	9	US-09-894-882-200	Sequence 200, App	476	23	100.0	79	12	US-09-750-972-37	Sequence 37, Appl
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405	23	100.0	70	9	US-09-894-882-215	Sequence 215, App	478	23	100.0	80	9	US-09-864-761-33883	Sequence 33883, App
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412	23	100.0	70	14	US-10-078-090-161	Sequence 161, App	485	23	100.0	80	12	US-09-750-972-31	Sequence 31, Appl
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535	23	100.0	88	11	US-09-864-761-48169	Sequence 48169, A	608	23	100.0	97	13	US-10-114-893-52	Sequence 3, Appli
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539	23	100.0	88	12	US-10-424-599-258372	Sequence 258372,	612	23	100.0	97	14	US-10-050-928-242	Sequence 242, App
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541	23	100.0	89	9	US-09-858-664A-33	Sequence 33, Appl	614	23	100.0	98	12	US-10-424-599-145173	Sequence 145173,
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544	23	100.0	89	12	US-10-697-283-34	Sequence 34, Appl	617	23	100.0	99	12	US-10-424-599-175303	Sequence 175303,
545	23	100.0	90	9	US-09-796-692-1334	Sequence 1334, Ap	618	23	100.0	99	12	US-10-424-599-222335	Sequence 222335,
546	23	100.0	90	9	US-09-796-692-2079	Sequence 2079, Ap	619	23	100.0	99	12	US-10-029-386-29267	Sequence 29267, A
547	23	100.0	90	14	US-10-424-599-231250	Sequence 231250,	620	23	100.0	100	9	US-09-864-761-33949	Sequence 33949, A
548	23	100.0	90	14	US-10-040-862-1334	Sequence 1334, Ap	621	23	100.0	100	9	US-09-872-523-12	Sequence 12, Appl
549	23	100.0	90	14	US-10-040-862-2079	Sequence 2079, Ap	622	23	100.0	100	9	US-09-764-877-1829	Sequence 1829, Ap
550	23	100.0	90	14	US-10-029-386-28294	Sequence 28294, A	623	23	100.0	100	9	US-09-764-868-1122	Sequence 1122, Ap
551	23	100.0	90	15	US-10-057-475B-1334	Sequence 1334, Ap	624	23	100.0	100	11	US-09-764-875-1028	Sequence 1028, Ap
552	23	100.0	90	15	US-10-475B-2079	Sequence 2079, Ap	625	23	100.0	100	12	US-10-424-599-151310	Sequence 151310,
553	23	100.0	90	15	US-10-154-884B-1334	Sequence 1334, Ap	626	23	100.0	100	12	US-10-424-599-173532	Sequence 173532,
554	23	100.0	90	15	US-10-154-884B-2079	Sequence 2079, Ap	627	23	100.0	100	12	US-10-424-599-184733	Sequence 184733,
555	23	100.0	91	10	US-09-978-303-45	Sequence 45, Appl	628	23	100.0	100	12	US-10-424-599-258943	Sequence 258943,
556	23	100.0	91	12	US-10-424-599-151346	Sequence 151346,	629	23	100.0	100	12	US-10-424-599-262984	Sequence 262984,
557	23	100.0	91	12	US-10-424-599-206585	Sequence 206585,	630	23	100.0	100	12	US-10-424-599-282342	Sequence 282342,
558	23	100.0	91	12	US-10-424-599-248330	Sequence 248330,	631	23	100.0	100	14	US-10-178-213-461	Sequence 461, App
559	23	100.0	91	15	US-10-424-599-268340	Sequence 268340,	632	23	100.0	100	15	US-10-242-515-1829	Sequence 1829, Ap
560	23	100.0	91	15	US-10-630-590-191	Sequence 191, Appl							
561	23	100.0	92	9	US-09-354-453-49	Sequence 49, Appl							
562	23	100.0	92	9	US-09-764-877-1203	Sequence 1203, Ap							
563	23	100.0	92	12	US-10-424-599-265516	Sequence 265516,							
564	23	100.0	92	14	US-10-267-718-49	Sequence 49, Appl							
565	23	100.0	92	15	US-10-242-515-1203	Sequence 1203, Ap							
566	23	100.0	93	12	US-10-424-599-170657	Sequence 170657,							
567	23	100.0	93	12	US-10-424-599-196857	Sequence 196857,							
568	23	100.0	93	12	US-10-424-599-256287	Sequence 256287,							
569	23	100.0	93	12	US-10-424-599-270090	Sequence 270090,							
570	23	100.0	93	12	US-10-424-599-273210	Sequence 273210,							
571	23	100.0	94	14	US-10-174-693-346	Sequence 346, App							
572	23	100.0	94	9	US-09-864-761-38043	Sequence 38043, A							
573	23	100.0	94	10	US-09-498-272-22	Sequence 22, Appl							
574	23	100.0	94	12	US-10-424-599-147953	Sequence 147953,							
575	23	100.0	94	12	US-10-424-599-188297	Sequence 188297,							
576	23	100.0	94	12	US-10-424-599-226799	Sequence 226799,							
577	23	100.0	94	12	US-10-424-599-231211	Sequence 231211,							
578	23	100.0	95	9	US-09-350-874-65	Sequence 65, Appl							
579	23	100.0	95	10	US-09-877-843-27	Sequence 27, Appl							
580	23	100.0	95	12	US-10-424-599-167049	Sequence 167049,							
581	23	100.0	95	12	US-10-424-599-226131	Sequence 226131,							
582	23	100.0	95	12	US-10-424-599-247888	Sequence 247888,							
583	23	100.0	95	12	US-10-424-599-254257	Sequence 254257,							
584	23	100.0	95	14	US-10-106-989-65	Sequence 65, Appl							
585	23	100.0	96	10	US-09-877-843-25	Sequence 25, Appl							
586	23	100.0	96	12	US-10-424-599-158771	Sequence 158771,							
587	23	100.0	96	12	US-10-424-599-181974	Sequence 181974,							
588	23	100.0	96	12	US-10-424-599-251499	Sequence 251499,							
589	23	100.0	96	14	US-10-050-704-135	Sequence 135, App							
590	23	100.0	97	8	US-08-927-939-25	Sequence 25, Appl							
591	23	100.0	97	9	US-09-834-795A-26	Sequence 26, Appl							
592	23	100.0	97	10	US-09-834-794A-26	Sequence 26, Appl							
593	23	100.0	97	10	US-09-920-137A-2	Sequence 2, Appli							
594	23	100.0	97	10	US-09-877-843-26	Sequence 26, Appl							
595	23	100.0	97	10	US-09-877-843-28	Sequence 28, Appl							
596	23	100.0	97	10	US-09-877-843-29	Sequence 29, Appl							
597	23	100.0	97	11	US-09-997-003-32	Sequence 32, Appl							
598	23	100.0	97	12	US-10-424-599-156617	Sequence 156617,							
599	23	100.0	97	12	US-10-424-599-158034	Sequence 158034,							

ALIGNMENTS

RESULT 1

US-10-155-922-8
; Sequence 8, Application US/10155922
; Publication NO. US20030086893A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tochigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 467392000220
; CURRENT APPLICATION NUMBER: US/10/155,922
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: JP 2001-347340
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-347338
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-371175
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: JP 2001-371366
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-155-922-8

Query Match      100.0%; Score 23; DB 14; Length 7;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 3 DQCCD 7

RESULT 2
US-10-155-922-65
; Sequence 65, Application US/10155922
; Publication No. US20030086893A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tochigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 467392000220
; CURRENT APPLICATION NUMBER: US/10/155,922
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: JP 2001-347340
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-347338
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-371175
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: JP 2001-371366
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-155-922-65

Query Match      100.0%; Score 23; DB 14; Length 7;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 3 DQCCD 7

RESULT 3
US-09-997-209-39
; Sequence 39, Application US/09997209
; Publication No. US20030096401A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Eukaryotic Expression Libraries and
; FILE REFERENCE: P-IX 5066
; CURRENT APPLICATION NUMBER: US/09/997,209
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 09/724,762

; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: Patencin ver. 2.1
; SEQ ID NO 518
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BRP variant
US-09-997-209-39

Query Match      100.0%; Score 23; DB 10; Length 8;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 1 DFCED 5

RESULT 4
US-10-363-791-27
; Sequence 27, Application US/10363791
; Publication No. US20040029197A1
; GENERAL INFORMATION:
; APPLICANT: TAKIMOTO, Masato
; APPLICANT: KUZUMAKI, No. US20040029197A1oru
; APPLICANT: SATO, No. US20040029197A1lyuki
; APPLICANT: SAHARA, Hiroeki
; TITLE OF INVENTION: A novel human cancer/testis-associated gene thereof
; FILE REFERENCE: 4439-4006
; CURRENT APPLICATION NUMBER: US/10/363,791
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: JP 2000-274218
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-791-27

Query Match      100.0%; Score 23; DB 12; Length 9;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 1 DYCHD 5

RESULT 5
US-10-253-286-518
; Sequence 518, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: Patencin ver. 2.1
; SEQ ID NO 518
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-253-286-518

Query Match 100.0%; Score 23; DB 12; Length 9;
Best Local Similarity 60.0%; Pred. No. 1e+06; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 0;

QY 1 DXCXD 5
|:|:
Db 3 DICTD 7

RESULT 6

US-10-245-871-518
; Sequence 518, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 518
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-871-518

Query Match 100.0%; Score 23; DB 15; Length 9;
Best Local Similarity 60.0%; Pred. No. 1e+06; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 0;

QY 1 DXCXD 5
|:|:
Db 3 DICTD 7

RESULT 7

US-10-447-161-67
; Sequence 67, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-67

Query Match 100.0%; Score 23; DB 16; Length 9;
Best Local Similarity 60.0%; Pred. No. 1e+06; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 0;

QY 1 DXCXD 5
|:|:
Db 3 DICTD 7

RESULT 8

US-09-572-270A-819
; Sequence 819, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 819
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in T01024.26. at 80-89 and may interact with
US-09-572-270A-819

Query Match 100.0%; Score 23; DB 10; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 5 DYCSD 9

RESULT 9

US-10-155-922-76
; Sequence 76, Application US/10155922
; Publication No. US20030086893A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tochigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 467392000220
; CURRENT APPLICATION NUMBER: US/10/155,922
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: JP 2001-347340
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-347338
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-371175
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: JP 2001-371366
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-155-922-76

Query Match 100.0%; Score 23; DB 14; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5

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Db          3 DCCCD 7

RESULT 10
US-10-062-109A-630
; Sequence 630, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 630
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-630

Query Match          100.0%; Score 23; DB 14; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db          5 DCCAD 9

RESULT 11
US-10-005-480A-630
; Sequence 630, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 630
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-630

Query Match          100.0%; Score 23; DB 14; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db          5 DCCAD 9

RESULT 12
US-09-809-391-649
; Sequence 649, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 649
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-391-649

Query Match          100.0%; Score 23; DB 10; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db          5 DPCGD 9

RESULT 13
US-09-882-171-649
; Sequence 649, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
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1 PRIOR APPLICATION NUMBER: 60/047,617
2 PRIOR FILING DATE: 1997-05-23
3 PRIOR APPLICATION NUMBER: 60/047,618
4 PRIOR FILING DATE: 1997-05-23
5 PRIOR APPLICATION NUMBER: 60/047,503
6 PRIOR FILING DATE: 1997-05-23
7 PRIOR APPLICATION NUMBER: 60/047,592
8 PRIOR FILING DATE: 1997-05-23
9 PRIOR APPLICATION NUMBER: 60/047,581
10 PRIOR FILING DATE: 1997-05-23
11 PRIOR APPLICATION NUMBER: 60/047,584
12 PRIOR FILING DATE: 1997-05-23
13 PRIOR APPLICATION NUMBER: 60/047,500
14 PRIOR FILING DATE: 1997-05-23
15 PRIOR APPLICATION NUMBER: 60/047,587
16 PRIOR FILING DATE: 1997-05-23
17 PRIOR APPLICATION NUMBER: 60/047,492
18 PRIOR FILING DATE: 1997-05-23
19 PRIOR APPLICATION NUMBER: 60/047,598
20 PRIOR FILING DATE: 1997-05-23
21 PRIOR APPLICATION NUMBER: 60/047,613
22 PRIOR FILING DATE: 1997-05-23
23 PRIOR APPLICATION NUMBER: 60/047,582
24 PRIOR FILING DATE: 1997-05-23
25 PRIOR APPLICATION NUMBER: 60/047,596
26 PRIOR FILING DATE: 1997-05-23
27 PRIOR APPLICATION NUMBER: 60/047,612
28 PRIOR FILING DATE: 1997-05-23
29 PRIOR APPLICATION NUMBER: 60/047,632
30 PRIOR FILING DATE: 1997-05-23
31 PRIOR APPLICATION NUMBER: 60/047,601
32 PRIOR FILING DATE: 1997-05-23
33 PRIOR APPLICATION NUMBER: 60/043,580
34 PRIOR FILING DATE: 1997-04-11
35 PRIOR APPLICATION NUMBER: 60/043,568
36 PRIOR FILING DATE: 1997-04-11
37 PRIOR APPLICATION NUMBER: 60/043,314
38 PRIOR FILING DATE: 1997-04-11
39 PRIOR APPLICATION NUMBER: 60/043,569
40 PRIOR FILING DATE: 1997-04-11
41 PRIOR APPLICATION NUMBER: 60/043,311
42 PRIOR FILING DATE: 1997-04-11
43 PRIOR APPLICATION NUMBER: 60/043,671
44 PRIOR FILING DATE: 1997-04-11
45 PRIOR APPLICATION NUMBER: 60/043,674
46 PRIOR FILING DATE: 1997-04-11
47 PRIOR APPLICATION NUMBER: 60/043,669
48 PRIOR FILING DATE: 1997-04-11
49 PRIOR APPLICATION NUMBER: 60/043,312
50 PRIOR FILING DATE: 1997-04-11
51 PRIOR APPLICATION NUMBER: 60/043,313
52 PRIOR FILING DATE: 1997-04-11
53 PRIOR APPLICATION NUMBER: 60/043,672
54 PRIOR FILING DATE: 1997-04-11
55 PRIOR APPLICATION NUMBER: 60/043,315
56 PRIOR FILING DATE: 1997-04-11
57 PRIOR APPLICATION NUMBER: 60/048,974
58 PRIOR FILING DATE: 1997-06-06
59 PRIOR APPLICATION NUMBER: 60/056,886
60 PRIOR FILING DATE: 1997-08-22
61 PRIOR APPLICATION NUMBER: 60/056,877
62 PRIOR FILING DATE: 1997-08-22
63 PRIOR APPLICATION NUMBER: 60/056,889
64 PRIOR FILING DATE: 1997-08-22
65 PRIOR APPLICATION NUMBER: 60/056,893
66 PRIOR FILING DATE: 1997-08-22
67 PRIOR APPLICATION NUMBER: 60/056,630
68 PRIOR FILING DATE: 1997-08-22
69 PRIOR APPLICATION NUMBER: 60/056,878
70 PRIOR FILING DATE: 1997-08-22
71 PRIOR APPLICATION NUMBER: 60/056,662
72 PRIOR FILING DATE: 1997-08-22
73 PRIOR APPLICATION NUMBER: 60/056,872
74 PRIOR FILING DATE: 1997-08-22
75 PRIOR APPLICATION NUMBER: 60/056,882
76 PRIOR FILING DATE: 1997-08-22
77 PRIOR APPLICATION NUMBER: 60/056,637
78 PRIOR FILING DATE: 1997-08-22
79 PRIOR APPLICATION NUMBER: 60/056,903
80 PRIOR FILING DATE: 1997-08-22
81 PRIOR APPLICATION NUMBER: 60/056,888
82 PRIOR FILING DATE: 1997-08-22
83 PRIOR APPLICATION NUMBER: 60/056,879
84 PRIOR FILING DATE: 1997-08-22
85 PRIOR APPLICATION NUMBER: 60/056,880
86 PRIOR FILING DATE: 1997-08-22
87 PRIOR APPLICATION NUMBER: 60/056,894
88 PRIOR FILING DATE: 1997-08-22
89 PRIOR APPLICATION NUMBER: 60/056,911
90 PRIOR FILING DATE: 1997-08-22
91 PRIOR APPLICATION NUMBER: 60/056,636
92 PRIOR FILING DATE: 1997-08-22
93 PRIOR APPLICATION NUMBER: 60/056,874
94 PRIOR FILING DATE: 1997-08-22
95 PRIOR APPLICATION NUMBER: 60/056,910
96 PRIOR FILING DATE: 1997-08-22
97 PRIOR APPLICATION NUMBER: 60/056,864
98 PRIOR FILING DATE: 1997-08-22
99 PRIOR APPLICATION NUMBER: 60/056,631
100 PRIOR FILING DATE: 1997-08-22
101 PRIOR APPLICATION NUMBER: 60/056,845
102 PRIOR FILING DATE: 1997-08-22
103 PRIOR APPLICATION NUMBER: 60/056,892
104 PRIOR FILING DATE: 1997-08-22
105 PRIOR APPLICATION NUMBER: 60/057,761
106 PRIOR FILING DATE: 1997-08-22
107 PRIOR APPLICATION NUMBER: 60/047,595
108 PRIOR FILING DATE: 1997-05-23
109 PRIOR APPLICATION NUMBER: 60/047,599
110 PRIOR FILING DATE: 1997-05-23
111 PRIOR APPLICATION NUMBER: 60/047,588
112 PRIOR FILING DATE: 1997-05-23
113 PRIOR APPLICATION NUMBER: 60/047,585
114 PRIOR FILING DATE: 1997-05-23
115 PRIOR APPLICATION NUMBER: 60/047,586
116 PRIOR FILING DATE: 1997-05-23
117 PRIOR APPLICATION NUMBER: 60/047,590
118 PRIOR FILING DATE: 1997-05-23
119 PRIOR APPLICATION NUMBER: 60/047,594
120 PRIOR FILING DATE: 1997-05-23
121 PRIOR APPLICATION NUMBER: 60/047,589
122 PRIOR FILING DATE: 1997-05-23
123 PRIOR APPLICATION NUMBER: 60/047,593
124 PRIOR FILING DATE: 1997-05-23
125 PRIOR APPLICATION NUMBER: 60/047,614
126 PRIOR FILING DATE: 1997-05-23
127 PRIOR APPLICATION NUMBER: 60/043,578
128 PRIOR FILING DATE: 1997-04-11
129 PRIOR APPLICATION NUMBER: 60/043,576
130 PRIOR FILING DATE: 1997-04-11
131 PRIOR APPLICATION NUMBER: 60/047,501
132 PRIOR FILING DATE: 1997-05-23
133 PRIOR APPLICATION NUMBER: 60/043,670
134 PRIOR FILING DATE: 1997-04-11
135 PRIOR APPLICATION NUMBER: 60/056,632
136 PRIOR FILING DATE: 1997-08-22
137 PRIOR APPLICATION NUMBER: 60/056,664
138 PRIOR FILING DATE: 1997-08-22
139 PRIOR APPLICATION NUMBER: 60/056,876
140 PRIOR FILING DATE: 1997-08-22
141 PRIOR APPLICATION NUMBER: 60/056,881
142 PRIOR FILING DATE: 1997-08-22
143 PRIOR APPLICATION NUMBER: 60/056,909
144 PRIOR FILING DATE: 1997-08-22
145 PRIOR APPLICATION NUMBER: 60/056,875
146 PRIOR FILING DATE: 1997-08-22
147 PRIOR APPLICATION NUMBER: 60/056,872
148 PRIOR FILING DATE: 1997-08-22

; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Query Match 100.0%; Score 23; DB 10; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 5 DPCGD 9

RESULT 14

US-10-164-861-649
; Sequence 649, Application US/10164861
; Publication No. US2003025249A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 649
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-861-649

Query Match 100.0%; Score 23; DB 12; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 5 DPCGD 9

RESULT 15

US-10-209-323-41
; Sequence 41, Application US/10209323
; Publication No. US2003011907A1
; GENERAL INFORMATION:
; APPLICANT: Schaeffer, Andrew T.
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Thornton, Jeffrey R.
; APPLICANT: Van Epps, Dennis E.
; TITLE OF INVENTION: Reagents For Cell Selection and Methods
; FILE REFERENCE: P-NT4360
; CURRENT APPLICATION NUMBER: US/10/209,323
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/09/659,469A
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/578,784
; PRIOR FILING DATE: 2000-05-23

; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-209-323-41

Query Match 100.0%; Score 23; DB 14; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 6 DFCND 10

RESULT 16

US-10-256-277-41
; Sequence 41, Application US/10256277
; Publication No. US20030219445A1
; GENERAL INFORMATION:
; APPLICANT: Schaeffer, Andrew T.
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Thornton, Jeffrey R.
; TITLE OF INVENTION: Reagents For Cell Selection and Methods
; FILE REFERENCE: P-NT 3773
; CURRENT APPLICATION NUMBER: US/10/256,277
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/09/578,784
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-256-277-41

Query Match 100.0%; Score 23; DB 15; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 6 DFCND 10

RESULT 17

US-10-253-286-483
; Sequence 483, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 483
; LENGTH: 12
; TYPE: PRT


```
; ORGANISM: Homo sapiens
US-10-253-286-483

Query Match
Best Local Similarity 100.0%; Score 23; DB 12; Length 12;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 6 DICTD 10

RESULT 18
US-10-253-286-522
; Sequence 522, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: I1-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 522
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-286-522

Query Match
Best Local Similarity 100.0%; Score 23; DB 12; Length 12;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 6 DICTD 10

RESULT 19
US-10-245-871-483
; Sequence 483, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: I1-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 483
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-871-483

Query Match
Best Local Similarity 100.0%; Score 23; DB 15; Length 12;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 6 DICTD 10

RESULT 20
US-10-245-871-522
; Sequence 522, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: I1-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 522
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-871-522

Query Match
Best Local Similarity 100.0%; Score 23; DB 15; Length 12;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 6 DICTD 10

RESULT 21
US-10-158-847-107
; Sequence 107, Application US/10158847
; Publication No. US20030091557A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PFS57
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-107

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 13;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 2 DMCDF 6

RESULT 22
US-10-158-847-109
; Sequence 109, Application US/10158847
; Publication No. US20030091557A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PFS57
; CURRENT APPLICATION NUMBER: US/10/158,847
```

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; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-109

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 13;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 2 DFCFD 6

RESULT 23
US-10-158-825-107
; Sequence 107, Application US/10158825
; Publication No. US20030138894A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF555
; CURRENT APPLICATION NUMBER: US/10/158,825
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/294,976
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-825-107

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 13;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 2 DFCFD 6

RESULT 24
US-10-158-825-109
; Sequence 109, Application US/10158825
; Publication No. US20030138894A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF555
; CURRENT APPLICATION NUMBER: US/10/158,825
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/294,976
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-825-109

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 13;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 DXCXD 5
Db 2 DFCFD 6

RESULT 25
US-10-209-323-45
; Sequence 45, Application US/10209323
; Publication No. US20030119070A1
; GENERAL INFORMATION:
; APPLICANT: Schaeffer, Andrew T.
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Thornton, Jeffrey R.
; APPLICANT: Van Epps, Dennis E.
; TITLE OF INVENTION: Reagents For Cell Selection and Methods
; FILE REFERENCE: P-NT4360
; CURRENT APPLICATION NUMBER: US/10/209,323
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/09/559,469A
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/578,784
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-209-323-45

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 14;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 6 DFCND 10

RESULT 26
US-10-256-277-45
; Sequence 45, Application US/10256277
; Publication No. US2003021945A1
; GENERAL INFORMATION:
; APPLICANT: Schaeffer, Andrew T.
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Thornton, Jeffrey R.
; TITLE OF INVENTION: Reagents For Cell Selection and Methods
; FILE REFERENCE: P-NT 3773
; CURRENT APPLICATION NUMBER: US/10/256,277
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/09/578,784
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-256-277-45

Query Match
Best Local Similarity 100.0%; Score 23; DB 15; Length 14;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 6 DFCND 10
```

```
Db          6 DFCND 10

RESULT 27
US-10-186-229-34
; Sequence 34, Application US/10186229
; Publication No. US20040001827A1
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING PEPTIDES FOR TUMOR TARGETING
; FILE REFERENCE: 11669.108US01
; CURRENT APPLICATION NUMBER: US/10/186,229
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides
US-10-186-229-34

Query Match          100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DXCXD 5
       |:|:|
Db      1 DTCVD 5

RESULT 28
US-10-186-229-149
; Sequence 149, Application US/10186229
; Publication No. US20040001827A1
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING PEPTIDES FOR TUMOR TARGETING
; FILE REFERENCE: 11669.108US01
; CURRENT APPLICATION NUMBER: US/10/186,229
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 149
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides
US-10-186-229-149

Query Match          100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DXCXD 5
       |:|:|
Db      1 DTCVD 5

RESULT 29
US-10-186-229-151
; Sequence 151, Application US/10186229
; Publication No. US20040001827A1
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING PEPTIDES FOR TUMOR TARGETING
; FILE REFERENCE: 11669.108US01
; CURRENT APPLICATION NUMBER: US/10/186,229
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 151
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides
US-10-186-229-151

Query Match          100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DXCXD 5
       |:|:|
Db      1 DTCDD 5

RESULT 30
US-10-186-229-152
; Sequence 152, Application US/10186229
; Publication No. US20040001827A1
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING PEPTIDES FOR TUMOR TARGETING
; FILE REFERENCE: 11669.108US01
; CURRENT APPLICATION NUMBER: US/10/186,229
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 152
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides
US-10-186-229-152

Query Match          100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DXCXD 5
       |:|:|
Db      1 DTCDD 5

RESULT 31
US-10-186-229-153
; Sequence 153, Application US/10186229
; Publication No. US20040001827A1
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING PEPTIDES FOR TUMOR TARGETING
; FILE REFERENCE: 11669.108US01
; CURRENT APPLICATION NUMBER: US/10/186,229
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 153
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides
US-10-186-229-153

Query Match          100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DXCXD 5
       |:|:|
Db      1 DTCED 5

RESULT 32
US-10-186-229-154
; Sequence 154, Application US/10186229
; Publication No. US20040001827A1
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING PEPTIDES FOR TUMOR TARGETING
; FILE REFERENCE: 11669.108US01
; CURRENT APPLICATION NUMBER: US/10/186,229
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 154
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides
US-10-186-229-154

Query Match          100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DXCXD 5
       |:|:|
Db      1 DTCED 5
```

```
RESULT 32
US-10-186-229-154
; Sequence 154, Application US/10186229
; Publication No. US20040001827A1
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING PEPTIDES FOR TUMOR TARGETING
; FILE REFERENCE: 11669.108US01
; CURRENT APPLICATION NUMBER: US/10/186,229
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 154
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides
US-10-186-229-154

Query Match
Best Local Similarity 100.0%; Score 23; DB 15; Length 15;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 1 DTCSD 5

RESULT 33
US-10-158-847-63
; Sequence 63, Application US/10158847
; Publication No. US20030091557A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 16
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-63

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 16;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 11 DYCFLD 15

RESULT 34
US-10-158-847-71
; Sequence 71, Application US/10158847
; Publication No. US20030091557A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 16
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-71

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 16;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 11 DYCFLD 15

RESULT 35
US-10-158-847-72
; Sequence 72, Application US/10158847
; Publication No. US20030091557A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 16
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-72

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 16;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 11 DYCFLD 15

RESULT 36
US-10-072-602B-444
; Sequence 444, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 444
; LENGTH: 16
; TYPE: PRT
```

```
; ORGANISM: Conus emaciatus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(16)
; OTHER INFORMATION: Xaa at residues 6, 7 and 13 is Pro or hydroxy-Pro
US-10-072-602B-444

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 16;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DCCSD 5

RESULT 37
US-10-072-602B-617
; Sequence 617, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 617
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-10-072-602B-617

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 16;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DCCSD 5

RESULT 38
US-10-158-825-63
; Sequence 63, Application US/10158825
; Publication No. US20030138894A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF555
; CURRENT APPLICATION NUMBER: US/10/158,825
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/294,976
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 16
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-825-63

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 16;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DCCSD 5

RESULT 39
US-10-158-825-71
; Sequence 71, Application US/10158825
; Publication No. US20030138894A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF555
; CURRENT APPLICATION NUMBER: US/10/158,825
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/294,976
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 16
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-825-71

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 16;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DCCSD 5

RESULT 40
US-10-158-825-72
; Sequence 72, Application US/10158825
; Publication No. US20030138894A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF555
; CURRENT APPLICATION NUMBER: US/10/158,825
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/294,976
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 16
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-825-72

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 16;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DCCSD 5

RESULT 41
US-10-300-699-45
; Sequence 45, Application US/10300699
```

```
; ORGANISM: homo sapiens
US-10-158-825-63

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 16;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DCCSD 5

RESULT 39
US-10-158-825-71
; Sequence 71, Application US/10158825
; Publication No. US20030138894A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF555
; CURRENT APPLICATION NUMBER: US/10/158,825
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/294,976
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 16
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-825-71

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 16;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DCCSD 5

RESULT 40
US-10-158-825-72
; Sequence 72, Application US/10158825
; Publication No. US20030138894A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF555
; CURRENT APPLICATION NUMBER: US/10/158,825
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/294,976
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 16
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-825-72

Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 16;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
Db 1 DCCSD 5

RESULT 41
US-10-300-699-45
; Sequence 45, Application US/10300699
```

```

; Publication No. US20030161845A1
; GENERAL INFORMATION:
; APPLICANT: Verheije, Monique H.
; APPLICANT: Meulenbergh, Johanna J.M.
; TITLE OF INVENTION: Chimeric Arterivirus-like particles
; FILE REFERENCE: P53321US00
; CURRENT APPLICATION NUMBER: US/10/300,699
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: EP 00201780.4
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: PCT/NL01/00382
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 45
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GP5-M protein
; OTHER INFORMATION: construct pABV437
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(16)
US-10-300-699-45

Query Match          100.0%; Score 23; DB 14; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
   |:|:|
Db 6 DFCND 10

RESULT 42
US-10-209-323-47
; Sequence 47, Application US/10209323
; Publication No. US20030119070A1
; GENERAL INFORMATION:
; APPLICANT: Schaeffer, Andrew T.
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Thornton, Jeffrey R.
; APPLICANT: Van Epps, Dennis E.
; TITLE OF INVENTION: Reagents For Cell Selection and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: P-NT4360
; CURRENT APPLICATION NUMBER: US/10/209,323
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/09/659,469A
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/578,784
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-209-323-47

Query Match          100.0%; Score 23; DB 14; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
   |:|:|
Db 6 DFCND 10

RESULT 43

```

```

US-10-300-699-48
; Sequence 48, Application US/10300699
; Publication No. US20030161845A1
; GENERAL INFORMATION:
; APPLICANT: Verheije, Monique H.
; APPLICANT: Meulenbergh, Johanna J.M.
; TITLE OF INVENTION: Chimeric Arterivirus-like particles
; FILE REFERENCE: P53321US00
; CURRENT APPLICATION NUMBER: US/10/300,699
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: EP 00201780.4
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: PCT/NL01/00382
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 48
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GP5-M protein
; OTHER INFORMATION: construct pABV857
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(17)
US-10-300-699-48

Query Match          100.0%; Score 23; DB 14; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
   |:|:|
Db 7 DFCND 11

RESULT 44
US-10-291-241-82
; Sequence 82, Application US/10291241
; Publication No. US20030206905A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Aya Jakobovits
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert
; APPLICANT: Wangmao Ge
; APPLICANT: Karen Jane Meyrick Morrison
; APPLICANT: Robert Kendall Morrison
; APPLICANT: Pia M. Challita-Eid
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 51158-20062.20
; CURRENT APPLICATION NUMBER: US/10/291,241
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-291-241-82

Query Match          100.0%; Score 23; DB 15; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;

```

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 11 DCCAD 15

RESULT 45

US-10-256-277-47
; Sequence 47, Application US/10256277
; Publication No. US20030219445A1
; GENERAL INFORMATION:
; APPLICANT: Schaeffer, Andrew T.
; APPLICANT: Thornton, Jeffrey R.
; TITLE OF INVENTION: Reagents For Cell Selection and Methods
; FILE REFERENCE: P-NT 3773
; CURRENT APPLICATION NUMBER: US/10/256,277
; PRIOR FILING DATE: 2002-09-25
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-256-277-47

Query Match 100.0%; Score 23; DB 15; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 6 DFCND 10

RESULT 46

US-09-932-613-92
; Sequence 92, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-92

Query Match 100.0%; Score 23; DB 10; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 2 DMCDF 6

RESULT 47

US-09-932-613-105
; Sequence 105, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-105

Query Match 100.0%; Score 23; DB 10; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 2 DGCYD 6

RESULT 48

US-09-932-322-92
; Sequence 92, Application US/09932322
; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Ladner, Robert Charles
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (Blys)
; FILE REFERENCE: Dyx-018.1 PCT; DYX-018.1 US
; CURRENT APPLICATION NUMBER: US/09/932,322
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-322-92

Query Match 100.0%; Score 23; DB 10; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 2 DMCDF 6

RESULT 49

US-09-932-322-105
; Sequence 105, Application US/09932322
; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.

; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Ladner, Robert Charles
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (Blys)
; FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
; CURRENT APPLICATION NUMBER: US/09/932.322
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-322-105

Query Match 100.0%; Score 23; DB 10; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCYD 5
|:|:
Db 2 DGCYD 6

RESULT 50
US-10-104-440-5
; Sequence 5, Application US/10104440
; Publication No. US20020132774A1
; GENERAL INFORMATION:
; APPLICANT: KLAGSBRUN, Michael
; APPLICANT: SOKER, Shay
; APPLICANT: MIAO, Hua Quan
; TITLE OF INVENTION: ANTAGONISTS OF NEUROPILIN RECEPTOR FUNCTION AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 48802 C
; CURRENT APPLICATION NUMBER: US/10/104,440
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/580,803
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/069,155
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: 60/069,687
; PRIOR FILING DATE: 1997-12-29
; PRIOR APPLICATION NUMBER: 60/078,541
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: human
US-10-104-440-5

Query Match 100.0%; Score 23; DB 13; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCYD 5
|:|:
Db 4 DECYD 8

RESULT 51
US-10-094-401-209
; Sequence 209, Application US/10094401
; Publication No. US20030069395A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ley, Arthur C.

; APPLICANT: Cohen, Edward H.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING MOIETIES
; FILE REFERENCE: DYX-026.2 PCT; DYX-026.2 US
; CURRENT APPLICATION NUMBER: US/10/094,401
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/331,352
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/292,975
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 209
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: albumin binding peptide
US-10-094-401-209

Query Match 100.0%; Score 23; DB 14; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCYD 5
|:|:
Db 2 DGCYD 6

RESULT 52
US-10-104-610-9
; Sequence 9, Application US/10104610
; Publication No. US20030104532A1
; GENERAL INFORMATION:
; APPLICANT: KLAGSBRUN, Michael
; APPLICANT: SOKER, Shay
; APPLICANT: GAGNON, Michael L.
; TITLE OF INVENTION: SOLUBLE INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH
; TITLE OF INVENTION: FACTOR
; TITLE OF INVENTION: AND USE THEREOF
; FILE REFERENCE: 48801 C
; CURRENT APPLICATION NUMBER: US/10/104,610
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/580,989
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/069,155
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: 60/069,687
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: human
US-10-104-610-9

Query Match 100.0%; Score 23; DB 14; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCYD 5
|:|:
Db 4 DECYD 8

RESULT 53
US-10-462-262-177
; Sequence 177, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS


```

; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: example of serum albumin-binding agent
US-10-462-262-177

```

```

Query Match      100.0%; Score 23; DB 15; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DXCXD 5
   |:|
Db 2 DGCTD 6

```

```

RESULT 54
US-10-291-241-83
; Sequence 83, Application US/10291241
; Publication No. US20030206905A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Aya Jakobovits
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert
; APPLICANT: Wangmao Ge
; APPLICANT: Karen Jane Meyrick Morrison
; APPLICANT: Robert Kendall Morrison
; APPLICANT: Pia M. Challita-Eid
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 51158-20062.20
; CURRENT APPLICATION NUMBER: US/10/291,241
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-291-241-83

```

```

Query Match      100.0%; Score 23; DB 15; Length 19;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DXCXD 5
   |:|
Db 12 DCCAD 16

```

```

RESULT 55
US-10-186-229-39
; Sequence 39, Application US/10186229
; Publication No. US20040001827A1
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.

```

```

; TITLE OF INVENTION: SERUM ALBUMIN BINDING PEPTIDES FOR TUMOR TARGETING
; FILE REFERENCE: 11669.108US01
; CURRENT APPLICATION NUMBER: US/10/186,229
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides
US-10-186-229-39

```

```

Query Match      100.0%; Score 23; DB 15; Length 20;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DXCXD 5
   |:|
Db 13 DLCDG 17

```

```

RESULT 56
US-09-962-756-591
; Sequence 591, Application US/09962756
; Publication No. US20030195147A1
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 591
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-962-756-591

```

```

Query Match      100.0%; Score 23; DB 10; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DXCXD 5
   |:|
Db 5 DCCQD 9

```

```

RESULT 57
US-10-062-109A-740
; Sequence 740, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.

```

; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Jakobovits, Aya
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 ; TITLE OF INVENTION: Cancer
 ; FILE REFERENCE: 51158-20062.01
 ; CURRENT APPLICATION NUMBER: US/10/062,109A
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: US 10/005,480
 ; NUMBER OF SEQ ID NOS: 765
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 740
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-062-109A-740

Query Match 100.0%; Score 23; DB 14; Length 21;
 Best Local Similarity 60.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
 Db 12 DCCWD 16

RESULT 58
 US-10-062-109A-741
 ; Sequence 741, Application US/10062109A
 ; Publication No. US20030165505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys
 ; APPLICANT: Challita-Eid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Jakobovits, Aya
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 ; TITLE OF INVENTION: Cancer
 ; FILE REFERENCE: 51158-20062.01
 ; CURRENT APPLICATION NUMBER: US/10/062,109A
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: US 10/005,480
 ; NUMBER OF SEQ ID NOS: 765
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 741
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-062-109A-741

Query Match 100.0%; Score 23; DB 14; Length 21;
 Best Local Similarity 60.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
 Db 12 DCCWD 16

RESULT 59
 US-10-005-480A-740
 ; Sequence 740, Application US/10005480A
 ; Publication No. US20030191073A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys
 ; APPLICANT: Challita-Eid, Pia M.

; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Jakobovits, Aya
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 ; TITLE OF INVENTION: Cancer
 ; FILE REFERENCE: 51158-20062.00
 ; CURRENT APPLICATION NUMBER: US/10/005,480A
 ; CURRENT FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 765
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 740
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-005-480A-740

Query Match 100.0%; Score 23; DB 14; Length 21;
 Best Local Similarity 60.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
 Db 12 DCCWD 16

RESULT 60
 US-10-005-480A-741
 ; Sequence 741, Application US/10005480A
 ; Publication No. US20030191073A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys
 ; APPLICANT: Challita-Eid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Jakobovits, Aya
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 ; TITLE OF INVENTION: Cancer
 ; FILE REFERENCE: 51158-20062.00
 ; CURRENT APPLICATION NUMBER: US/10/005,480A
 ; CURRENT FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 765
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 741
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-005-480A-741

Query Match 100.0%; Score 23; DB 14; Length 21;
 Best Local Similarity 60.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
 Db 12 DCCWD 16

RESULT 61
 US-10-291-241-79
 ; Sequence 79, Application US/10291241
 ; Publication No. US20030206905A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Aya Jakobovits
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Mary Paris
 ; APPLICANT: Rene S. Hubert

; APPLICANT: Wangmao Ge
; APPLICANT: Karen Jane Meyrick Morrison
; APPLICANT: Robert Kendall Morrison
; APPLICANT: Pia M. Challita-Eid
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 51158-20062.20
; CURRENT APPLICATION NUMBER: US/10/291,241
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-291-241-79

Query Match 100.0%; Score 23; DB 15; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 12 DCCWD 16

RESULT 62
US-10-291-241-80
; Sequence 80, Application US/10291241
; Publication No. US20030206905A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Aya Jakobovits
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert
; APPLICANT: Wangmao Ge
; APPLICANT: Karen Jane Meyrick Morrison
; APPLICANT: Robert Kendall Morrison
; APPLICANT: Pia M. Challita-Eid
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 51158-20062.20
; CURRENT APPLICATION NUMBER: US/10/291,241
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-291-241-80

Query Match 100.0%; Score 23; DB 15; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|

Db 12 DCCAD 16
RESULT 63
US-10-253-471-591
; Sequence 591, Application US/10253471
; Publication No. US20030236190A1
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA et al.
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4057
; CURRENT APPLICATION NUMBER: US/10/253,471
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 591
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-253-471-591

Query Match 100.0%; Score 23; DB 15; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 5 DGCQD 9

RESULT 64
US-10-253-493-591
; Sequence 591, Application US/10253493
; Publication No. US20040023887A1
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA et al.
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4056
; CURRENT APPLICATION NUMBER: US/10/253,493
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 591
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-253-493-591

Query Match 100.0%; Score 23; DB 16; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:|
Db 5 DGCQD 9

RESULT 65
US-09-948-495A-4
; Sequence 4, Application US/09948495A
; Publication No. US20030105304A1
; GENERAL INFORMATION:
; APPLICANT: Acey, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated
; FILE REFERENCE: 21089-11
; CURRENT APPLICATION NUMBER: US/09/948.495A
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artemia
US-09-948-495A-4

Query Match 100.0%; Score 23; DB 10; Length 22;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCYD 5
Db 2 DCCKD 6

RESULT 66
US-09-997-003-50
; Sequence 50, Application US/09997003
; Publication No. US20030203361A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA003p1
; CURRENT APPLICATION NUMBER: US/09/997,003
; CURRENT FILING DATE: 2001-11-30
; PRIOR FILING DATE: 2001-11-30
; PRIOR FILING DATE: 2001-11-30
; PRIOR FILING DATE: PCT/US00/22157
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 60/148,680
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-997-003-50

Query Match 100.0%; Score 23; DB 11; Length 22;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCYD 5
Db 6 DQCRD 10

RESULT 67
US-10-300-694A-73
; Sequence 73, Application US/10300694A
; Publication No. US20030185870A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Grinstaff, Mark W.
; APPLICANT: Kenan, Daniel J.
; APPLICANT: Waleh, Elisabeth B.
; APPLICANT: Middleton, Crystan

; TITLE OF INVENTION: INTERFACIAL BIOMATERIALS
; FILE REFERENCE: 180/143/2
; CURRENT APPLICATION NUMBER: US/10/300,694A
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/331,843
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Cell-binding and titanium-binding dual specificity peptide 73
US-10-300-694A-73

Query Match 100.0%; Score 23; DB 14; Length 22;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCYD 5
Db 3 DSCSD 7

RESULT 68
US-09-804-156-25
; Sequence 25, Application US/09804156
; Patent No. US20020086320A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Serine protease Polynucleotides, Polypeptides, and Antibodies
; CURRENT APPLICATION NUMBER: US/09/804,156
; CURRENT FILING DATE: 2001-03-13
; PRIOR FILING DATE: 60/189,025
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-156-25

Query Match 100.0%; Score 23; DB 9; Length 24;
Best Local Similarity 60.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCYD 5
Db 3 DDCAD 7

RESULT 69
US-09-946-633-12
; Sequence 12, Application US/09946633
; Patent No. US20020119925A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: PT005P1
; FILE REFERENCE: Serine proteases
; CURRENT APPLICATION NUMBER: US/09/946,633
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/597,839
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 60/133,239
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/135,163
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 60/147,005
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/152,935

```
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/162,979
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-946-633-12

Query Match
  100.0%; Score 23; DB 9; Length 24;
Best Local Similarity
  60.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DXCXD 5
Db       3 DDCAD 7

RESULT 70
US-09-809-391-737
; Sequence 737, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 737
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-391-737

Query Match
  100.0%; Score 23; DB 10; Length 24;
Best Local Similarity
  60.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DXCXD 5
Db      15 DTCSD 19

RESULT 71
US-09-882-171-737
; Sequence 737, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
```

```
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,598
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,612
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,671
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,674
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,669
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,312
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,313
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,672
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,315
; PRIOR FILING DATE: 1997-04-11
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; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/056,886
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,877
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,889
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,893
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,630
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,878
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,662
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,872
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,882
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,637
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,903
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,888
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,879
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,880
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,894
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,911
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,636
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,874
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,910
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,864
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,631
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,892
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,761
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/047,595
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,588
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,585
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,586
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,590
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576

; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Query Match 100.0%; Score 23; DB 10; Length 24;
Best Local Similarity 60.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 15 DTCS D 19

RESULT 72

US-10-164-861-737
; Sequence 737, Application US/10164861
; Publication No. US2003025248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 737
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-861-737

Query Match 100.0%; Score 23; DB 12; Length 24;
Best Local Similarity 60.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 15 DTCS D 19

RESULT 73

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US-10-125-459-12
; Sequence 12, Application US/10125459
; Publication No. US20020192800A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: PT005P1
; FILE REFERENCE: Serine proteases
; CURRENT APPLICATION NUMBER: US/10/125,459
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US/09/597,839
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 60/133,239
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/135,163
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: 60/147,005
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: 60/152,935
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/162,979
; PRIOR FILING DATE: 1998-11-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-459-12

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```

Query Match      100.0%; Score 23; DB 13; Length 24;
Best Local Similarity 60.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY      1 DXCXD 5
        |:-||
Db       3 DDCAD 7

```

RESULT 74

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US-10-067-761-25
; Sequence 25, Application US/10067761
; Publication No. US20020197701A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Serine protease Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT005P4
; CURRENT APPLICATION NUMBER: US/10/067,761
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 09/804,156
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/189,025
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-761-25

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```

Query Match      100.0%; Score 23; DB 13; Length 24;
Best Local Similarity 60.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 DXCXD 5
        |:-||
Db       3 DDCAD 7

```

RESULT 75

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US-10-319-519-25
; Sequence 25, Application US/10319519
; Publication No. US20030175938A1

```

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; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Serine Protease Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT005P5
; CURRENT APPLICATION NUMBER: US/10/319,519
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 10/125,459
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 09/597,842
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 09/597,843
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 10/067,761
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 09/946,633
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US 09/804,156
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 09/597,839
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/US00/12207
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/189,025
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/162,979
; PRIOR FILING DATE: 1999-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-319-519-25

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Query Match      100.0%; Score 23; DB 14; Length 24;
Best Local Similarity 60.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY      1 DXCXD 5
        |:-||
Db       3 DDCAD 7

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RESULT 76

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US-09-864-761-45896
; Sequence 45896, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664

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;
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45896
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007321.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.98
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.92
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.85
US-09-864-761-45896

Query Match 100.0%; Score 23; DB 9; Length 25;
Best Local Similarity 60.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 12 DKCRD 16

RESULT 77
US-10-339-740-248
; Sequence 248, Application US/10339740
; Publication No. US20030187246A1
; GENERAL INFORMATION:
; APPLICANT: Doberstein, Stephen
; APPLICANT: Reddy, Bindu
; APPLICANT: Platt, Darren
; APPLICANT: Ferguson, Kimberly
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF C. ELEGANS INSULIN-LIKE GENES AND USES THEREOF
; FILE REFERENCE: 7326-069-999
; CURRENT APPLICATION NUMBER: US/10/339,740
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US/09/084,303A
; PRIOR FILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 248
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-339-740-248

Query Match 100.0%; Score 23; DB 14; Length 25;
Best Local Similarity 60.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 12 DACSD 16

RESULT 78
US-09-756-594-40
; Sequence 40, Application US/09756594
; Patent No. US20010014456A1
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: VIII-like Proteins
; FILE REFERENCE: Dyax-008 US Div. 1 sequence listing
; CURRENT APPLICATION NUMBER: US/09/756,594
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: Factor VIII affinity ligand
US-09-756-594-40

Query Match 100.0%; Score 23; DB 9; Length 26;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 14 DHCHD 18

RESULT 79
US-09-731-449-31
; Sequence 31, Application US/09731449
; Patent No. US20020155526A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL SECRETED IMMUNOMODULATORY PROTEINS AND USES THEREOF
; FILE REFERENCE: 07334-320001
; CURRENT APPLICATION NUMBER: US/09/731,449
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/410,350
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/163,523
; PRIOR FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-731-449-31

Query Match 100.0%; Score 23; DB 9; Length 26;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXCXD 5
|:|:
Db 11 DACTD 15


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RESULT 80
US-10-094-401-261
; Sequence 261, Application US/10094401
; Publication No. US20030069395A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Cohen, Edward H.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING MOIETIES
; FILE REFERENCE: DYX-026.2 PCT; DYX-026.2 US
; CURRENT APPLICATION NUMBER: US/10/094,401
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/331,352
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/292,975
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 261
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: albumin binding peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; NAME/KEY: MOD_RES
; LOCATION: (26)..(26)
; OTHER INFORMATION: AMIDATION
US-10-094-401-261

Query Match          100.0%; Score 23; DB 14; Length 26;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DXCXD 5
       |:|:|
Db      4 DGCTD 8

RESULT 81
US-10-254-426-31
; Sequence 31, Application US/10254426
; Publication No. US20030113865A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL SECRETED IMMUNOMODULATORY PROTEINS AND USES THEREOF
; FILE REFERENCE: 07334-320001
; CURRENT APPLICATION NUMBER: US/10/254,426
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/09/731,449
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/410,350
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/163,523
; PRIOR FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-254-426-31

Query Match          100.0%; Score 23; DB 14; Length 26;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DXCXD 5
       |:|:|
Db      4 DGCTD 8

RESULT 82
US-10-272-497-40
; Sequence 40, Application US/10272497
; Publication No. US20030165822A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; FILE REFERENCE: 3421.1004-009
; CURRENT APPLICATION NUMBER: US/10/272,497
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phage Display Sequence
US-10-272-497-40

Query Match          100.0%; Score 23; DB 14; Length 26;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DXCXD 5
       |:|:|
Db      14 DHCHD 18

RESULT 83
US-10-462-262-225
; Sequence 225, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: serum albumin-binding agent
US-10-462-262-225

Query Match          100.0%; Score 23; DB 15; Length 26;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DXCXD 5
       |:|:|
Db      4 DGCTD 8
```

RESULT 84
US-09-864-761-45090
; Sequence 45090, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 4917
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45090
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC013626.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.49
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.53
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.51
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.55
; OTHER INFORMATION: SWISSPROT HIT: Q05471, EVALUATE 5.00e-04
; OTHER INFORMATION: EST_HUMAN HIT: AI935484.1, EVALUATE 7.00e-10
US-09-864-761-45090

Query Match 100.0%; Score 23; DB 9; Length 27;
Best Local Similarity 60.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:

Db 8 DQCFD 12

RESULT 85
US-09-998-042-3
; Sequence 3, Application US/09998042
; Publication No. US20030036632A1
; GENERAL INFORMATION:
; APPLICANT: VISSUM RESEARCH DEVELOPMENT COMPANY OF THE HEBREW
; TITLE OF INVENTION: ACETYLCHOLINESTERASE-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: 7811/WO/99
; CURRENT APPLICATION NUMBER: US/09/998,042
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 27
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-998-042-3

Query Match 100.0%; Score 23; DB 10; Length 27;
Best Local Similarity 60.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:

Db 22 DRCS D 26

RESULT 86
US-09-864-761-39894
; Sequence 39894, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39894
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004686.1 SIGNAL = 9.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 12
; OTHER INFORMATION: EST_HUMAN HIT: BP307002.1, EVALUE 2.00e-08
US-09-864-761-39894

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```

Query Match      100.0%; Score 23; DB 9; Length 28;
Best Local Similarity 60.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DXCXD 5
   |:|:|
Db 21 DYCCKD 25

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RESULT 87

```

US-09-904-380-18
; Sequence 18, Application US/09904380
; Patent No. US2002002229A1
; GENERAL INFORMATION:
; APPLICANT: Jane H. Morse and James A. Knowles
; TITLE OF INVENTION: Role of PPH1 Gene in Pulmonary Hypertension
; FILE REFERENCE: 0575/62430-A/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/904,380
; CURRENT FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-904-380-18

```

```

Query Match      100.0%; Score 23; DB 9; Length 29;
Best Local Similarity 60.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DXCXD 5
   |:|:|
Db 6 DDCWD 10

```

RESULT 88

```

US-09-864-761-45879
; Sequence 45879, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

```

```

; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45879
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010474.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.83
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.79
US-09-864-761-45879

```

```

Query Match      100.0%; Score 23; DB 9; Length 29;
Best Local Similarity 60.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 DXCXD 5
   |:|:|
Db 24 DRCRD 28

```

RESULT 89

```

US-10-291-241-84
; Sequence 84, Application US/10291241
; Publication No. US20030206905A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Aya Jakobovits
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert

```

APPLICANT: Wangmao Ge
APPLICANT: Karen Jane Meyrick Morrison
APPLICANT: Robert Kendall Morrison
APPLICANT: Pia M. Challita-Eid
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
FILE REFERENCE: 51158-20062.20
CURRENT APPLICATION NUMBER: US/10/291,241
PRIORITY FILING DATE: 2003-03-18
PRIORITY APPLICATION NUMBER: US 10/005,480
PRIORITY FILING DATE: 2001-11-07
PRIORITY APPLICATION NUMBER: US 10/062,109
PRIORITY FILING DATE: 2002-01-31
PRIORITY APPLICATION NUMBER: US 60/282,739
PRIORITY FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 103
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 84
LENGTH: 29
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-291-241-84

Query Match 100.0%; Score 23; DB 15; Length 29;
Best Local Similarity 60.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 17 DCCAD 21

RESULT 90
US-09-864-761-42870
Sequence 42870, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 42870
LENGTH: 30
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL109659.17
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
US-09-864-761-42870

Query Match 100.0%; Score 23; DB 9; Length 30;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
Db 5 DDCRD 9

RESULT 91
US-09-813-153-230
Sequence 230, Application US/09813153
Publication No. US20030045459A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 67 Human secreted proteins
FILE REFERENCE: PZ023
CURRENT APPLICATION NUMBER: US/09/813,153
CURRENT FILING DATE: 2001-03-21
PRIORITY APPLICATION NUMBER: US/09/363,044
PRIORITY FILING DATE: 1999-07-29
PRIORITY APPLICATION NUMBER: 60/073,160
PRIORITY FILING DATE: 1998-01-30
PRIORITY APPLICATION NUMBER: 60/073,159
PRIORITY FILING DATE: 1998-01-30
PRIORITY APPLICATION NUMBER: 60/073,165
PRIORITY FILING DATE: 1998-01-30
PRIORITY APPLICATION NUMBER: 60/073,164
PRIORITY FILING DATE: 1998-01-30
PRIORITY APPLICATION NUMBER: 60/073,167
PRIORITY FILING DATE: 1998-01-30
PRIORITY APPLICATION NUMBER: 60/073,162
PRIORITY FILING DATE: 1998-01-30
PRIORITY APPLICATION NUMBER: 60/073,161
PRIORITY FILING DATE: 1998-01-30
PRIORITY APPLICATION NUMBER: 60/073,170
PRIORITY FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 298
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 230
LENGTH: 30
TYPE: PRT
ORGANISM: Homo sapiens
US-09-813-153-230
Query Match 100.0%; Score 23; DB 10; Length 30;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 10 DLCMD 14

RESULT 92

US-10-296-734-944
; Sequence 944, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 944
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: trp-1 segment 3
US-10-296-734-944

Query Match 100.0%; Score 23; DB 12; Length 30;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 14 DICTD 18

RESULT 93

US-10-296-734-1002
; Sequence 1002, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1002
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: tyros segment 16
US-10-296-734-1002

Query Match 100.0%; Score 23; DB 12; Length 30;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 22 DICTD 26

RESULT 94

US-10-296-734-1004

; Sequence 1004, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1004
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: tyros segment 17
US-10-296-734-1004

Query Match 100.0%; Score 23; DB 12; Length 30;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 7 DICTD 11

RESULT 95

US-10-296-734-1074
; Sequence 1074, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1074
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: trp2 segment 17
US-10-296-734-1074

Query Match 100.0%; Score 23; DB 12; Length 30;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 17 DVCTD 21

RESULT 96

US-10-296-734-1076
; Sequence 1076, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04

; PRIOR APPLICATION NUMBER: AU P07761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1076
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: trp2 segment 18
US-10-296-734-1076

Query Match 100.0%; Score 23; DB 12; Length 30;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 2 DVCID 6

RESULT 97
US-10-253-286-525
; Sequence 525, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 525
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Ii-Key/cytosinase non-overlapping hybrid peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)
; OTHER INFORMATION: a-aminovaleric acid
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-253-286-525

Query Match 100.0%; Score 23; DB 12; Length 32;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 11 DICTD 15

RESULT 98
US-10-029-386-31551
; Sequence 31551, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31551
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC022078.12
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.46
US-10-029-386-31551

Query Match 100.0%; Score 23; DB 14; Length 32;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 25 DSCAD 29

RESULT 99
US-10-029-386-31859
; Sequence 31859, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31859
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011358.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.76
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.59
US-10-029-386-31859

Query Match 100.0%; Score 23; DB 14; Length 32;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXCXD 5
|:|:
Db 1 DCCGD 5

RESULT 100
US-10-029-386-33301
; Sequence 33301, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33301

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; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009003.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
US-10-029-386-33301
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Query Match      100.0%; Score 23; DB 14; Length 32;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DXCXD 5
        |:|:|
Db      28 DGCAD 32
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Search completed: May 6, 2004, 10:48:52
Job time : 49 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 13:46:20 ; Search time 35 Seconds
(without alignments)
45.074 Million cell updates/sec

Title: SEQ2
Perfect score: 30
Sequence: 1 dvcqd 5

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 175362

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	30	100.0	81	5 Q8NOM7	Q8NOM7 ctenocephal
2	26	86.7	74	5 Q9UA76	Q9UA76 conus abbre
3	26	86.7	74	5 Q9UA78	Q9UA78 conus abbre
4	26	86.7	74	5 Q9UA77	Q9UA77 conus abbre
5	26	86.7	74	5 Q9UA79	Q9UA79 conus abbre
6	26	86.7	74	5 Q9TVY1	Q9TVY1 conus abbre
7	26	86.7	80	10 Q8LSM1	Q8LSM1 vitis vinif
8	26	86.7	92	2 Q9XAV8	Q9XAV8 pseudomonas
9	26	86.7	92	16 Q8XAP9	Q8XAP9 pseudomonas
10	26	86.7	94	16 Q88IQ9	Q88IQ9 pseudomonas
11	26	86.7	97	16 Q8PEF4	Q8PEF4 xylella fas
12	26	86.7	97	16 Q87EF7	Q87EF7 xylella fas
13	26	86.7	100	12 Q98Z20	Q98Z20 molluscum c
14	25	83.3	46	11 Q8OV51	Q8OV51 mus musculu
15	25	83.3	53	11 Q8RI94	Q8RI94 mus musculu
16	25	83.3	61	16 Q87SC2	Q87SC2 vibrio para

17	25	83.3	66	9 Q8SBL8	Q8SBL8 bacterioph
18	25	83.3	83	16 Q8D9W4	Q8D9W4 vibrio vuln
19	25	83.3	86	2 P94195	P94195 agrobacteri
20	25	83.3	89	10 Q40036	Q40036 hordeum vul
21	25	83.3	89	10 Q43665	Q43665 triticum ae
22	25	83.3	94	16 Q8P2X1	Q8P2X1 streptococ
23	25	83.3	94	16 Q9A1S6	Q9A1S6 streptococ
24	25	83.3	97	16 Q879Q1	Q879Q1 streptococ
25	24	80.0	31	6 O18888	O18888 canis fami
26	24	80.0	38	13 Q9DE17	Q9DE17 gallus gall
27	24	80.0	38	16 Q8DXU1	Q8DXU1 streptococ
28	24	80.0	39	13 Q9DE18	Q9DE18 gallus gall
29	24	80.0	42	16 Q81MR8	Q81MR8 bacillus an
30	24	80.0	42	16 Q819L0	Q819L0 bacillus ce
31	24	80.0	46	4 Q9P0Z7	Q9P0Z7 homo sapien
32	24	80.0	53	10 Q8RYU2	Q8RYU2 oryza sativ
33	24	80.0	54	5 Q9U7K6	Q9U7K6 plasmodium
34	24	80.0	54	16 Q9PDP0	Q9PDP0 xylella fas
35	24	80.0	55	5 Q9BMS4	Q9BMS4 plasmodium
36	24	80.0	55	5 Q9U7G1	Q9U7G1 plasmodium
37	24	80.0	59	5 Q9BJH0	Q9BJH0 plasmodium
38	24	80.0	59	5 Q8WPZ4	Q8WPZ4 plasmodium
39	24	80.0	63	4 Q8N6W4	Q8N6W4 homo sapien
40	24	80.0	68	11 Q8VBV2	Q8VBV2 rattus norv
41	24	80.0	68	16 Q9JWL2	Q9JWL2 neisseria m
42	24	80.0	69	11 Q8K4N2	Q8K4N2 mus musculu
43	24	80.0	70	5 Q9ND04	Q9ND04 plasmodium
44	24	80.0	70	5 Q9ND25	Q9ND25 plasmodium
45	24	80.0	71	5 Q9ND36	Q9ND36 plasmodium

ALIGNMENTS

RESULT 1

Q8NOM7 ID Q8NOM7 PRELIMINARY; PRT; 81 AA.
AC Q8NOM7;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Peritrophin-like protein 3.
OS Ctenocephalides felis (Cat flea).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Siphonaptera; Pulicidae; Pulicinae;
OC Ctenocephalides.
OX NCBI_TaxID=7515;
RN [1]
RP SEQUENCE FROM N.A.
RA Gaines P.J., Wamsley S.J., Brandt K.S., Wisniewski N.;
RT "Cloning of a family of peritrophin-like and mucin-like cDNAs from the cat flea, Ctenocephalides felis, and characterization of two of the encoded proteins";
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF373881; AAM21356.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_PeRA.
DR Pfam; PF01607; CSM_14; 1.
DR SMART; SM00494; ChtBD2; 1.
SQ SEQUENCE 81 AA; 9083 MW; 4B11758B68F3F0C2 CRC64;

Query Match 100.0%; Score 30; DB 5; Length 81;

Best Local Similarity 100.0%; Pred. No. 30; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0;

QY 1 DVCQD 5

Db 23 DVCQD 27

RESULT 2

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Q9UA76
ID Q9UA76 PRELIMINARY; PRT; 74 AA.
AC Q9UA76;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Four-loop conotoxin ABVIA (Fragment).
OS Conus abbreviatus (Abbreviated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=100123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2;
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RL rapid evolution of toxin genes of the venomous gastropod Conus.";
DR EMBL; AF090053; AAD48306.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON TER 1
SQ SEQUENCE 74 AA; 7934 MW; 4B5C6C51E6FE81CA CRC64;

Query Match 86.7%; Score 26; DB 5; Length 74;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 66 DVCQE 70

RESULT 3
Q9UA78
ID Q9UA78 PRELIMINARY; PRT; 74 AA.
AC Q9UA78;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Four-loop conotoxin ABVIA (Fragment).
OS Conus abbreviatus (Abbreviated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=100123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RL rapid evolution of toxin genes of the venomous gastropod Conus.";
DR EMBL; AF090050; AAD48303.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON TER 1
SQ SEQUENCE 74 AA; 7919 MW; 584F66E2F32F21CA CRC64;

Query Match 86.7%; Score 26; DB 5; Length 74;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 66 DVCQE 70

RESULT 3
Q9UA79
ID Q9UA79 PRELIMINARY; PRT; 74 AA.
AC Q9UA79;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Four-loop conotoxin ABVIA (Fragment).
OS Conus abbreviatus (Abbreviated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=100123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RL rapid evolution of toxin genes of the venomous gastropod Conus.";
DR EMBL; AF090050; AAD48303.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON TER 1
SQ SEQUENCE 74 AA; 7935 MW; 4B5C66F1E6F421CA CRC64;

Query Match 86.7%; Score 26; DB 5; Length 74;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 66 DVCQE 70

RESULT 3
Q9UA79
ID Q9UA79 PRELIMINARY; PRT; 74 AA.
AC Q9UA79;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Four-loop conotoxin ABVIA (Fragment).
OS Conus abbreviatus (Abbreviated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=100123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RL rapid evolution of toxin genes of the venomous gastropod Conus.";
DR EMBL; AF090049; AAD48302.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON TER 1
SQ SEQUENCE 74 AA; 7935 MW; 4B5C66F1E6F421CA CRC64;

Query Match 86.7%; Score 26; DB 5; Length 74;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 66 DVCQE 70

RESULT 4
Q9UA77
ID Q9UA77 PRELIMINARY; PRT; 74 AA.
AC Q9UA77;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Four-loop conotoxin ABVIA (Fragment).
OS Conus abbreviatus (Abbreviated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=100123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RL rapid evolution of toxin genes of the venomous gastropod Conus.";
DR EMBL; AF090051; AAD48304.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON TER 1
SQ SEQUENCE 74 AA; 7875 MW; AD4F73F7F5F421D0 CRC64;

Query Match 86.7%; Score 26; DB 5; Length 74;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 66 DVCQE 70

RESULT 5
Q9UA79
ID Q9UA79 PRELIMINARY; PRT; 74 AA.
AC Q9UA79;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Four-loop conotoxin ABVIA (Fragment).
OS Conus abbreviatus (Abbreviated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=100123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RL rapid evolution of toxin genes of the venomous gastropod Conus.";
DR EMBL; AF090049; AAD48302.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON TER 1
SQ SEQUENCE 74 AA; 7935 MW; 4B5C66F1E6F421CA CRC64;

Query Match 86.7%; Score 26; DB 5; Length 74;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 66 DVCQE 70

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Query Match      86.7%; Score 26; DB 5; Length 74;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
DB 66 DVCQE 70

RESULT 6
Q9TVY1 PRELIMINARY; PRT; 74 AA.
AC Q9TVY1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Four-loop conotoxin ABVIA (Fragment).
OS Conus abbreviatus (Abbreviated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=100123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2, and 1;
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RT rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).
DR EMBL; AF090073; AAD48326.1; -
DR EMBL; AF090041; AAD48294.1; -
DR EMBL; AF090042; AAD48295.1; -
DR EMBL; AF090043; AAD48296.1; -
DR EMBL; AF090044; AAD48297.1; -
DR EMBL; AF090045; AAD48298.1; -
DR EMBL; AF090046; AAD48299.1; -
DR EMBL; AF090047; AAD48300.1; -
DR EMBL; AF090048; AAD48301.1; -
DR EMBL; AF090052; AAD48305.1; -
DR EMBL; AF090054; AAD48307.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 74 AA; 7905 MW; 584F66E2F5F421CA CRC64;

Query Match      86.7%; Score 26; DB 5; Length 74;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
DB 66 DVCQE 70

RESULT 7
Q8LSM1 PRELIMINARY; PRT; 80 AA.
AC Q8LSM1;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Resistance gene analog (Fragment).
OS Vitis vinifera (Grape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Vitaceae; Vitis.
OX NCBI_TaxID=29760;
RN [1]
RP SEQUENCE FROM N.A.

Query Match      86.7%; Score 26; DB 5; Length 74;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
DB 66 DVCQE 70

RESULT 8
Q9XAV8 PRELIMINARY; PRT; 92 AA.
AC Q9XAV8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE MOBE.
GN MOBE.
OS Pseudomonas alcaligenes.
OG Plasmid pRA2.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=43263;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIB 9867; TRANSPOSON=Tn5563;
RX MEDLINE=98126538; PubMed=9465390;
RA Kwong S.M., Yeo C.C., Chuah D., Poh C.L.;
RT "Sequence analysis of plasmid pRA2 from Pseudomonas alcaligenes NCIB
RT 9867 (P25X) reveals a novel replication region.";
RL FEMS Microbiol. Lett. 158:159-165(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIB 9867; TRANSPOSON=Tn5563;
RX MEDLINE=98415121; PubMed=9742696;
RA Yeo C.C., Tham J.M., Kwong S.M., Ylin S., Poh C.L.;
RT "Tn5563, a transposon encoding putative mercuric ion transport
RT proteins located on plasmid pRA2 of Pseudomonas alcaligenes.";
RL FEMS Microbiol. Lett. 165:253-260(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIB 9867; TRANSPOSON=Tn5563;
RX MEDLINE=20082846;
RA Kwong S.M., Yeo C.C., Suwanto A., Poh C.L.;
RT "Characterization of the endogenous plasmid from Pseudomonas
RT alcaligenes NCIB 9867: DNA sequence and mechanism of transfer.";
RL J. Bacteriol. 182:81-90(2000).
DR EMBL; U88088; AAD40343.1; -
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
SQ SEQUENCE 92 AA; 10416 MW; B60645FE1237A733 CRC64;

Query Match      86.7%; Score 26; DB 2; Length 92;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
DB 78 DVCRD 82
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RESULT 9
Q88AP9 PRELIMINARY; PRT; 92 AA.
AC Q8GAP9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prevent-host-death family protein.
GN PSTO0337.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
RA Berry K., Utterback T., Van Aken S., Feldblyum T., Winn M.,
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen I.,
RA White O., Fraser C., Collier A.;
RT "Complete sequence of Pseudomonas syringae."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016857; AA053882.1; -.
DR TIGR; PSPT0337; -.
DR InterPro; IPR003756; DUF172.
DR Pfam; PF02604; DUF172; 1.
DR Complete proteome.
KW
SQ SEQUENCE 92 AA; 10237 MW; 70FF62E7376EA96 CRC64;

Query Match 86.7%; Score 26; DB 16; Length 92;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVQCD 5
Db 19 DVCRD 23

RESULT 10
Q88IQ9 PRELIMINARY; PRT; 94 AA.
AC Q88IQ9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Conserved hypothetical protein.
GN P22940.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzapfel E., Scanlan D., Tran K., Moazzez A.,
RA Utterback T., Rizzo W., Lee K., Kosack D., Moesti D., Wedler H.,
RA Lauber J., Stjepandic D., Hohseil J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808 (2002).
DR EMBL; AS016785; AAN68548.1; -.
DR TIGR; P22940; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.

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DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR003756; DUF172.
DR InterPro; IPR001854; Ribosomal_L29.
DR Pfam; PF02604; DUF172; 1.
DR PROSITE; PS00579; RIBOSOMAL_L29; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 94 AA; 10611 MW; E85E051AD9BC4F88 CRC64;

Query Match 86.7%; Score 26; DB 16; Length 94;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVQCD 5
Db 19 DVCRD 23

RESULT 11
Q9PEF4 PRELIMINARY; PRT; 97 AA.
AC Q9PEF4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Xf1074.
GN Xf1074.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5c;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Faciniani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsal S.M., Tshukho M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa."
RL Nature 406:151-159 (2000).
DR EMBL; AE003944; AAF83884.1; -.
DR PIR; G82725; G82725.
DR InterPro; IPR005631; DUF339.
DR Pfam; PF03937; TPR_div1; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 97 AA; 11474 MW; 62D67492F6AF311A CRC64;

Query Match 86.7%; Score 26; DB 16; Length 97;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 DVCQD 5
DB      78 EVCQD 82

RESULT 12
Q87EF7
ID      PRELIMINARY;      PRT;      97 AA.
AC      Q87EF7
DT      01-JUN-2003 (TRENBLrel. 24, Created)
DT      01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE      Conserved hypothetical protein.
GN      PD0354.
OS      Xylella fastidiosa (strain Temeculal / ATCC 700964).
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC      Xanthomonadaceae; Xylella.
OX      NCBI_TaxID=183190;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22421331; PubMed=12533478;
RA      Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
RA      Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
RA      Takita M.A., Lemos E.G.W., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA      Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Tsai S.M.,
RA      Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA      Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
RA      Marino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA      Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
RA      da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA      Leonl S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,
RA      de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
RA      Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA      Kitajima J.P.;
RT      "Comparative analyses of the complete genome sequences of Pierce's
RT      disease and citrus variegated chlorosis strains of Xylella
RT      fastidiosa.";
RL      J. Bacteriol. 185:1018-1026(2003).
DR      EMBL; AE012554; AAO28234.1; -.
DR      InterPro: IPR005631; DUF339.
DR      Pfam; PF03937; TPR div1; 1.
KW      Hypothetical protein; Complete proteome.
SQ      SEQUENCE 97 AA; 11590 MW; F2B072F284862556 CRC64;

Query Match      86.7%; Score 26; DB 16; Length 97;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVCQD 5
DB      78 EVCQD 82

RESULT 13
Q98220
ID      PRELIMINARY;      PRT;      100 AA.
AC      Q98220
DT      01-FEB-1997 (TRENBLrel. 02, Created)
DT      01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT      01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE      Molluscipoxvirus.
GN      MC052R.
OS      Molluscum contagiosum virus subtype 1 (MCV1).
OC      Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC      Molluscipoxvirus.
OX      NCBI_TaxID=10280;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96325459; PubMed=8670425;
RA      Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
RA      Moss B.;
RT      "Genome sequence of a human tumorigenic poxvirus: Prediction of

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RT      specific host response-evasion genes.";
RL      Science 273:813-816(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
RA      Moss B.;
RL      Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U60315; AAC55180.1; -.
DR      PIR; T30654; T30654.
SQ      SEQUENCE 100 AA; 11330 MW; BCFCE74FCA023533 CRC64;

Query Match      86.7%; Score 26; DB 12; Length 100;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVCQD 5
DB      85 EVCQD 89

RESULT 14
Q80V51
ID      PRELIMINARY;      PRT;      46 AA.
AC      Q80V51
DT      01-JUN-2003 (TRENBLrel. 24, Created)
DT      01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE      Ttpa protein.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=FVB/N; TISSUE=Breast tumor;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,
RA      Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      STRAIN=FVB/N; TISSUE=Breast tumor;
RA      Strausberg R.;
RL      Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC043705; AAH43705.1; -.
DR      InterPro: IPR001251; CRAL TRIO C.
SQ      SEQUENCE 46 AA; 5488 MW; 926D19CFC2087456 CRC64;

Query Match      83.3%; Score 25; DB 11; Length 46;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVCQD 5
DB      22 DICQD 26

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RESULT 15
Q8R194
ID Q8R194 PRELIMINARY; PRT; 53-AA.
AC Q8R194;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025010; AAH25010.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 53 AA; 5654 MW; 3CF6B0F82CDFF02C CRC64;

Query Match 83.3%; Score 25; DB 11; Length 53;
Best Local Similarity 80.0%; Pred No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 7 DCCQD 11

Search completed: May 5, 2004, 13:52:18
Job time : 36 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 13:45:45 ; Search time 10 Seconds
(without alignments)
26.035 Million cell updates/sec

Title: SEQ2
Perfect score: 30
Sequence: 1 dvcqd 5

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 15046

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	30	100.0	80	1	SAP_PIG	P81405 sus scrofa
2	27	90.0	74	1	Y777_TREPA	O83756 treponema p
3	26	86.7	78	1	ML20_EUPRA	P39579 bacillus su
4	24	80.0	37	1	DE20_EUPRA	P26888 euplotes ra
5	24	80.0	48	1	R332_MYCGE	Q92b82 mycoplasma
6	24	80.0	48	1	R332_MYCPN	P56850 mycoplasma
7	24	80.0	56	1	IBB1_WHEAT	P09863 triticum ae
8	24	80.0	90	1	YORK_TTV1	P19295 thermoprote
9	24	80.0	91	1	VP22_BPAPS	Q9t1s6 bacterioph
10	24	80.0	99	1	SY08_BOVIN	Q09141 bos taurus
11	23	76.7	20	1	TXV2_PHONI	Q9twr5 phoneutria
12	23	76.7	58	1	RHO_THIFE	P52158 thiobacillu
13	23	76.7	67	1	IBB2_SETIT	P19860 setaria ita
14	23	76.7	67	1	IBB3_SETIT	P22737 setaria ita
15	23	76.7	81	1	NUML_HUMAN	O00483 homo sapien
16	23	76.7	87	1	NUOS_HUMAN	Q9nrx3 homo sapien
17	23	76.7	92	1	SY22_MOUSE	O88430 mus musculu
18	23	76.7	94	1	FIXX_AZOVI	P53658 azotobacter
19	23	76.7	97	1	EOTA_HUMAN	P51671 homo sapien
20	23	76.7	97	1	VE7_HPV55	Q80935 human papil
21	23	76.7	99	1	RS10_HALMA	P23357 halocaulula
22	23	76.7	99	1	RT14_MARPO	P26873 marchantia
23	22	73.3	64	1	IBB1_COILA	P07679 coix lachry
24	22	73.3	76	1	YMZA_BACSU	O31798 bacillus su
25	22	73.3	77	1	FER_BACSC	Q45560 bacillus sc
26	22	73.3	81	1	SAP_CAVPO	P20097 cavia porce
27	22	73.3	88	1	LCSR_YERPE	Q00931 yersinia pe
28	22	73.3	90	1	YT65_CAEEL	Q11081 caenorhabdi
29	22	73.3	94	1	HIS2_PYRAE	O8zy18 pyrobaculum
30	21	70.0	37	1	ME32_EUPRA	P58548 euplotes ra
31	21	70.0	40	1	Y382_TREPA	O83397 treponema p
32	21	70.0	50	1	HUNB_PSYCI	P20032 psychoda ci
33	21	70.0	53	1	IBB2_WHEAT	P09864 triticum ae

RESULT 1

ID	SAP_PIG	STANDARD;	PRT;	80 AA.
AC	P81405;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Saposin B (Cerebroside sulfate activator) (CS-ACT) (Non-specific activator) (Sphingolipid activator protein 1) (SAP-1).			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_taxid=9823;			
RN	[1]			
RP	SEQUENCE OF 1-79.			
RC	TISSUE=Kidney;			
RX	MEDLINE=93229506; PubMed=8471613;			
RA	Stevens R.L., Faull K.F., Conklin K.A., Green B.N., Fluharty A.L.;			
RT	"Porcine cerebroside sulfate activator; further structural characterization and disulfide identification.";			
RL	Biochemistry 32:4051-4059(1993).			
RN	[2]			
RP	SEQUENCE OF 1-64.			
RC	TISSUE=Kidney;			
RX	MEDLINE=9222651; PubMed=1562358;			
RA	Fluharty A.L., Katona Z., Meek W.B., Frei K., Fowler A.V.;			
RT	"The cerebroside sulfate activator from pig kidney: purification and molecular structure.";			
RL	Biochem. Med. Metab. Biol. 47:66-85(1992).			
RN	[3]			
RP	STRUCTURE OF CARBOHYDRATE ON ASN-21.			
RX	MEDLINE=21110404; PubMed=11180632;			
RA	Paull K.F., Johnson J., Kim M.J., To T., Whitelegge J.P.,			
RA	Stevens R.L., Fluharty C.B., Fluharty A.L.;			
RT	"Structure of the asparagine-linked sugar chains of porcine kidney and human urine cerebroside sulfate activator protein.";			
RL	J. Mass Spectrom. 35:1416-1424(2000).			
RN	[4]			
RP	MASS SPECTROMETRY.			
RC	TISSUE=Kidney;			
RX	MEDLINE=99441404; PubMed=10510427;			
RA	Paull K.F., Whitelegge J.P., Higginson J., To T., Johnson J.,			
RA	Krutchinsky A., Standing K.G., Waring A.J., Stevens R.L.,			
RT	"Cerebroside sulfate activator protein (Saposin B): chromatographic and electrospray mass spectrometric properties.";			
RL	J. Mass Spectrom. 34:1040-1054(1999).			
CC	-!- FUNCTION: Saposin B stimulates the hydrolysis of galacto-			
CC	cerebroside sulfate by arylsulfatase A (EC 3.1.6.8), GM1			
CC	gangliosides by beta-galactosidase A (EC 3.2.1.23) and			
CC	globotriaosylceramide by alpha-galactosidase A (EC 3.2.1.22).			
CC	Saposin B forms a solubilizing complex with the substrates of the			
CC	sphingolipid hydrolases.			
CC	-!- SUBUNIT: Saposin B is a homodimer (By similarity).			
CC	-!- PTM: The one residue extended Saposin B-Val is only found in a			
CC	minority of the chains.			

ALIGNMENTS

-1- SIMILARITY: Contains 1 saposin B-type domain.

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CC GlycoSuiteDB; P01405; -.
DR InterPro; IPR007856; SapB_1.
DR InterPro; IPR008138; SapB_2.
DR InterPro; IPR008373; Saposin.
DR InterPro; IPR008139; SaposinB.
DR Pfam; PF05184; SapB_1; 1.
DR Pfam; PF03489; SapB_2; 1.
DR PRINTS; PR01797; SAPOSIN.
DR SMART; SM01118; SAPB; 1.
KW Glycoprotein; Sphingolipid metabolism.
FT CHAIN 1 79
FT DOMAIN 1 80
FT SAPOSIN B-VAL.
FT SAPOSIN-LIKE TYPE B.
FT DISULFID 4 77
FT DISULFID 7 71
FT DISULFID 36 47
FT CARBOHYD 21 21
SQ SEQUENCE 80 AA; 8949 MW; EF7BA249B63E789C CRC64;

Query Match 100.0%; Score 30; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
DB 2 DVCQD 6

RESULT 2
Y777-TREPA STANDARD; PRT; 74 AA.
AC O83756;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Hypothetical protein TP0777.
GN TP0777.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.;
RA "Complete genome sequence of Treponema pallidum, the syphilis agent."
RT spirochete.
RL Science 281:375-388(1998).
CC

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CC
CC EMBL; AE001249; AAC65750.1; -.
DR PIR; B71282; B71282.
DR TIGR; TP0777; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 74 AA; 9018 MW; 299EB9E2CEC32D5 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 74;
Best Local Similarity 80.0%; Pred. No. 29;

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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
DB 29 DVCED 33

RESULT 3
DLTC_BACSU STANDARD; PRT; 78 AA.
ID DLTC_BACSU
AC F39579;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE D-alanine--poly(phosphoribitol)ligase subunit 2 (EC 6.1.1.13) (D-alanyl carrier protein) (DCP).
DE DLTC OR IPA-3R OR BSU38520.
GN Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=95020537; PubMed=7934828;
RA Glaser P., Kunst P., Arnaud M., Coudart M.P., Gonzales W., Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I., Presecan E., Santana M., Schneider E., Schweizer J., Vertes A., Rapoport G., Danchin A.;
RT "Bacillus subtilis genome project: cloning and sequencing of the 97 kb region from 325 degrees to 333 degrees."
RL Mol. Microbiol. 10:371-384(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G., Guiseppi H., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Maubel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche R., Rose M., Sadate Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Sertor P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Toato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T., Winters P., Wiput A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis."
RL Nature 390:249-256(1997).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=95318144; PubMed=7797557;
RA Perego M., Glaser P., Minutello A., Strauch M.A., Leopold K., Fischer W.;
RT "Incorporation of D-alanine into lipoteichoic acid and wall teichoic acid in Bacillus subtilis. Identification of genes and regulation."

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RL J. Biol. Chem. 270:15598-15606(1995).
CC -!- FUNCTION: Involved in the biosynthesis of D-alanyl-lipoteichoic
CC acid (LTA). Activated D-alanyl-Dcp donates its D-alanyl
CC substituent to membrane-associated LTA.
CC -!- CATALYTIC ACTIVITY: ATP + D-alanine + poly(ribitol phosphate) =
CC AMP + diphosphate + O-D-alanyl-poly(ribitol phosphate).
CC -!- PATHWAY: D-alanyl-lipoteichoic acid biosynthesis.
CC -!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-DCP (By similarity).
CC -!- SIMILARITY: Contains 1 acyl carrier domain.
CC -----
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CC -----
DR EMBL; X73124; CAA51559.1; -.
DR EMBL; Z99123; CAB15878.1; -.
DR PIR; S39658; S39658.
DR Subtilist; BG10549; dlctc.
DR HAMAP; MF_00565; -. 1.
DR InterPro; IPR003230; D-ala_carrier.
DR InterPro; IPR006163; Pp_bind.
DR ProDom; PD015103; D-ala_carrier; 1.
DR PROSITE; PS00075; ACP DOMAIN; FALSE NEG.
KW Ligase; Cell wall; Phosphopantetheine; Complete proteome.
FT BINDING 36 36 PHOSPHOPANTHETHEINE (PROBABLE).
SQ SEQUENCE 78 AA; 9009 MW; 4A3F51C4A4CE8F6 CRC64;

Query Match 86.7%; Score 26; DB 1; Length 78;
Best Local Similarity 80.0%; Pred. No. 48;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 13 EVCQD 17

RESULT 4
ME20 EUPRA STANDARD; PRT; 37 AA.
AC P26888;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mating pheromone Br-20 (Euplome R20) (Fragment).
GN MAT20.
OS Euplotes raikovi.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euplotida; Euplotidae; Euplotes.
OX NCBI_TaxID=5938;
RN [1]
RP SEQUENCE.
RC STRAIN=GA-4;
RX MEDLINE=92196059; PubMed=1549567;
RA Raffioni S., Miceli C., Vallesi A., Chowdhury S.K., Chait B.T.,
RA Luporini P., Bradshaw R.A.;
RT "Primary structure of Euplotes raikovi pheromones: comparison of five
RT sequences of pheromones from cells with variable mating
RT interactions."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2071-2075(1992).
CC -!- FUNCTION: Mating ciliate pheromones (or gamones) are diffusible
CC extra-cellular communication signals that distinguish different
CC intraspecific classes of cells commonly referred to as "mating
CC types". They prepare the latter for conjugation by changing their
CC cell surface properties.
CC -!- SUBUNIT: Homodimer (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; C41933; C41933.
DR HSP; P26887; 1ERY.

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KW Pheromone. 3 18 BY SIMILARITY.
FT DISULFID 10 32 BY SIMILARITY.
FT DISULFID 15 24 BY SIMILARITY.
FT NON_TER 37 37
SQ SEQUENCE 37 AA; 4002 MW; DD8C85FD78F704CF CRC64;

Query Match 80.0%; Score 24; DB 1; Length 37;
Best Local Similarity 60.0%; Pred. No. 58;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 1 DICDD 5

RESULT 5
R332 MYCGE STANDARD; PRT; 48 AA.
AC Q9ZB82;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S0S ribosomal protein L33 type 2.
GN RPMG2 OR MG055.1.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A. / G-37;
RC STRAIN=ATCC 33530 / G-37; PubMed=7569993;
RX MEDLINE=96026346;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RA "The minimal gene complement of Mycoplasma genitalium."
RT Science 270:397-403(1995).
RL [2]
RN IDENTIFICATION.
RP Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RA Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RL -!- SIMILARITY: Belongs to the L33p family of ribosomal proteins.
CC -----
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CC -----
DR EMBL; U39684; AAC71272.1; -.
DR TIGR; MG055.1; -.
DR HAMAP; MF_00294; -. 1.
DR InterPro; IPR001705; Ribosomal L33.
DR ProDom; PD002595; Ribosomal L33; 1.
DR TIGRFAMs; TIGR01023; xpmg_bact; 1.
DR PROSITE; PS00382; RIBOSOMAL_L33; FALSE_NEG.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 48 AA; 5946 MW; 33C7A47A3B98B65F CRC64;

Query Match 80.0%; Score 24; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 VCQD 5
Db      8 VCQD 11

RESULT 6
R332_MYCPN          STANDARD;          PRT;          48 AA.
ID   P56850;
AC   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DE   28-FEB-2003 (Rel. 41, Last annotation update)
GN   50S ribosomal protein L33 type 2.
OS   Mycoplasma pneumoniae.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2104;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 29342 / M129;
RX   MEDLINE=97105885; PubMed=9948633;
RA   Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RT   Herrmann R.;
RL   "Complete sequence analysis of the genome of the bacterium Mycoplasma
CC   pneumoniae.";
CC   -!- SIMILARITY: Belongs to the L33P family of ribosomal proteins.
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CC   -----
DR   EMBL; AE000010; AAC34736.1; -
DR   HAMAP; MF 00294; -; 1.
DR   InterPro; IPR001705; Ribosomal_L33.
DR   ProDom; PD002595; Ribosomal_L33; 1.
DR   TIGRFAMs; TIGR01023; rplM3 bact; 1.
DR   PROSITE; PS00582; RIBOSOMAL_L33; FALSE_NEG.
KW   Ribosomal protein; Complete proteome.
SQ   SEQUENCE 48 AA; 5863 MW; 93A1A3157098ABED CRC64;

Query Match          80.0%; Score 24; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VCQD 5
Db      8 VCQD 11

RESULT 7
IBBI_WHEAT
ID   IBBI_WHEAT          STANDARD;          PRT;          56 AA.
AC   P09863;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Bowman-Birk type proteinase inhibitor I-2B (Fragment).
OS   Triticum aestivum (Wheat).
OC   Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Triticeae; Triticum.
OX   NCBI_TaxID=4565;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=87137364; PubMed=3818572;
RA   Odani S., Koide T., Ono T.;
RT   "Wheat germ trypsin inhibitors. Isolation and structural
RT   characterization of single-headed and double-headed inhibitors of the

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RT      Bowman-Birk type";
RL      J. Biochem. 100:975-983 (1986).
CC      -!- SIMILARITY: Belongs to the Bowman-Birk serine protease inhibitor
CC      family.
DR      PIR; A25507; A25507.
DR      HSSP; P01064; 1P12.
DR      InterPro; IPR000877; Bowman-Birk leg.
DR      Pfam; PF00228; Bowman-Birk leg; 2.
DR      ProDom; PD002168; Bowman-Birk leg; 1.
DR      SMART; SM00269; BowB; 1.
DR      PROSITE; PS00281; BOWMAN BIRK; 1.
KW      Serine protease inhibitor.
FT      NON_TER 1
FT      ACT_SITE 17 18 REACTIVE BOND (BY SIMILARITY).
FT      ACT_SITE 43 44 REACTIVE BOND (BY SIMILARITY).
FT      NON_TER 56 56
SQ      SEQUENCE 56 AA; 6223 MW; 9821FD0C45420B09 CRC64;

Query Match          80.0%; Score 24; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VCQD 5
Db      50 VCQD 53

RESULT 8
YORK_TTV1
ID   YORK_TTV1          STANDARD;          PRT;          90 AA.
AC   P19295;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   01-NOV-1990 (Rel. 16, Last annotation update)
DE   Hypothetical 10.5 kDa protein.
OS   Thermoproteus tenax virus 1 (strain KRAL) (TTV1).
OC   Viruses; dsDNA viruses, no RNA stage; Lipothrirkviridae;
OC   Lipothrirkvirus.
OX   NCBI_TaxID=10480;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Neumann H.;
RL   Submitted (MAR-1989) to the EMBL/GenBank/DBJ databases.
CC   -----
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CC   -----
DR   EMBL; X14855; CAA32991.1; -
KW   Hypothetical protein.
SQ      SEQUENCE 90 AA; 10547 MW; 81D70159EB62911 CRC64;

Query Match          80.0%; Score 24; DB 1; Length 90;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 DVCQD 5
Db      40 DVCQD 44

RESULT 9
VP22_BPAPS
ID   VP22_BPAPS          STANDARD;          PRT;          91 AA.
AC   Q9T1S6;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Putative protein P22.

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GN 22.
OS Bacteriophage APSE-1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OX NCBI_TaxID=106199;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99420383; PubMed=10489345;
RA van der Wilk F., Dulleman A.M., Verbeek M., van den Heuvel J.F.J.M.;
RT "Isolation and characterization of APSE-1, a bacteriophage infecting
RL the secondary endosymbiont of acyrthosiphon pisum.";
RL Virology 262:104-113 (1999).
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CC -----
DR EMBL; AF157835; AAF03965.1; -.
KW Hypothetical protein.
SQ SEQUENCE 91 AA; 10457 MW; D88C337C17B11B49 CRC64;

Query Match 80.0%; Score 24; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQ 4
DB 37 DVCQ 40

RESULT 10
SY08_BOVIN
ID SY08_BOVIN STANDARD; PRT; 99 AA.
AC Q09141;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemoattract
DE protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
GN CCL8 OR SCV48 OR MCP2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94114084; PubMed=8286035;
RA Wempe F., Hanes J., Scheit K.H.;
RT "Cloning of the gene for bovine monocyte chemoattractant protein-2.";
RL DNA Cell Biol. 13:1-8 (1994).
CC -!- FUNCTION: Chemoattractant factor that attracts monocytes. This protein
CC can bind heparin.
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SIMILARITY: Belongs to the interleukin 6 (chemokine CC) family.
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CC -----
DR EMBL; S67954; AAD14005.1; -.
DR EMBL; S67956; AAB29750.1; -.
DR HSSP; P51671; 1E0T.
DR InterPro; IPR000827; CC_chemokine sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.

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DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.
KW Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response;
KW Pyroglutamate carboxylic acid.
FT SIGNAL 1 23
FT CHAIN 24 99
FT MOD_RES 24 24
FT PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT DISULFID 34 59
FT DISULFID 35 75
FT BY SIMILARITY.
SQ SEQUENCE 99 AA; 10900 MW; 01974CDB3FF9119B CRC64;

Query Match 80.0%; Score 24; DB 1; Length 99;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVCQ 5
DB 73 DVCQ 77

RESULT 11
TXV2_PHONI
ID TXV2_PHONI STANDARD; PRT; 20 AA.
AC Q9TWR5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Toxin PnV2 (Fragment).
OS Phoneutria nigriventer (Brazilian armed spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX NCBI_TaxID=6918;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94030062; PubMed=8216354;
RA Bento A.C., Novello J.C., Marangoni S., Antunes E., Giglio J.R.,
RA Oliveira B., de Nucci G.;
RT "Identification of a new vascular smooth muscle contracting
RT polypeptide in Phoneutria nigriventer spider venom.";
RL Biochem. Pharmacol. 46:1092-1095 (1993).
CC -!- FUNCTION: Has a vascular smooth muscle contracting activity.
CC Causes short-lived contractions of both arterial and venous rabbit
CC vessels.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- PTM: Contains four disulfide bonds (Probable).
KW Toxin.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2176 MW; F28C3D81D983BCA5 CRC64;

Query Match 76.7%; Score 23; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQ 4
DB 6 DVCQ 9

RESULT 12
RHO_THIFE
ID RHO_THIFE STANDARD; PRT; 58 AA.
AC P52I58;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transcription termination factor rho (Fragment).
GN RHO.
OS Thiobacillus ferrooxidans.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales;
OC Acidithiobacillaceae; Acidithiobacillus.

```

```

OX  NCBI_TaxID=920;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 33020;
RX  MEDLINE=96118698; PubMed=7496529;
RA  Powles R.E., Deane S.M., Rawlings D.E.;
RT  "Molecular genetic analysis of a thioredoxin gene from Thiobacillus
RL  ferrooxidans.";
CC  Microbiology 141:2175-2181(1995).
CC  -1- FUNCTION: Facilitates transcription termination by a mechanism
CC  that involves Rho binding to the nascent RNA, activation of Rho's
CC  RNA-dependent ATPase activity, and release of the mRNA from the
CC  DNA template (By similarity).
CC  -1- SUBUNIT: Homohexamer (By similarity).
CC  -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  use by non-profit institutions as long as its content is in no way
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; U20361; AAA88940.1; -
DR  HSP; P03002; IABV.
KW  Transcription termination; Helicase; ATP-binding; RNA-binding.
FT  DOMAIN 21 25 RNA-BINDING (RNP2) (BY SIMILARITY).
FT  NON TER 58
SQ  SEQUENCE 58 AA; 6436 MW; 5F11D1CD9324545E CRC64;

Query Match 76.7%; Score 23; DB 1; Length 58;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VCQD 5
Db [1]
17 ICQD 20

RESULT 13
ID IBB2_SETIT STANDARD; PRT; 67 AA.
AC P19850;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE Bowman-Birk type major trypsin inhibitor (FMTI-II).
OS Setaria italica (Foxtail millet).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Paniceae; Setaria.
OX NCBI_TaxID=4555;
RN [1]
RP SEQUENCE.
RX MEDLINE=91154179; PubMed=2292595;
RA Tashiro M., Asao T., Hirata C., Takahashi K., Kanamori M.;
RT "The complete amino acid sequence of a major trypsin inhibitor from
RT seeds of foxtail millet (Setaria italica).";
RL J. Biochem. 108:669-672(1990).
CC -1- SIMILARITY: Belongs to the Bowman-Birk serine protease inhibitor
CC family.
DR PIR; JX0136; TIIIP2.
DR HSSP; P56679; IPBI.
DR InterPro; IPR000877; Bowman-Birk_leg.
DR Pfam; PF00228; Bowman-Birk_leg; 2.
DR ProDom; PD002168; Bowman-Birk_leg; 1.
DR SMART; SM00269; BowB; 1.
DR PROSITE; PS00281; BOWMAN_BIRK; 1.
KW Serine protease inhibitor.
FT ACT SITE 16 17 INTERACTION WITH TRYPSIN (BY SIMILARITY).
FT DISULFID 8 63 BY SIMILARITY.
FT DISULFID 9 24 BY SIMILARITY.
FT DISULFID 14 22 BY SIMILARITY.
FT DISULFID 31 38 BY SIMILARITY.
FT DISULFID 35 51 BY SIMILARITY.
SQ SEQUENCE 67 AA; 7680 MW; 0D5AF30F33248949 CRC64;

Query Match 76.7%; Score 23; DB 1; Length 67;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VCQD 5
Db [1]
50 ICQD 53

RESULT 14
ID IBB3_SETIT STANDARD; PRT; 67 AA.
AC P22737;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE Bowman-Birk type trypsin inhibitor III (FMTI-III).
OS Setaria italica (Foxtail millet).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Paniceae; Setaria.
OX NCBI_TaxID=4555;
RN [1]
RP SEQUENCE.
RX MEDLINE=91299279; PubMed=1368693;
RA Tashiro M., Asao T., Hirata C., Takahashi K.;
RT "Purification, characterization, and amino acid sequence of foxtail
RT millet trypsin inhibitor III.";
RL Agric. Biol. Chem. 55:419-426(1991).
CC -1- SIMILARITY: Belongs to the Bowman-Birk serine protease inhibitor
CC family.
DR PIR; JG0013; TIIIP3.
DR HSSP; P56679; IPBI.
DR InterPro; IPR000877; Bowman-Birk_leg.
DR Pfam; PF00228; Bowman-Birk_leg; 2.
DR ProDom; PD002168; Bowman-Birk_leg; 1.
DR SMART; SM00269; BowB; 1.
DR PROSITE; PS00281; BOWMAN_BIRK; 1.
KW Serine protease inhibitor.
FT ACT SITE 16 17 INTERACTION WITH TRYPSIN (BY SIMILARITY).
FT DISULFID 8 63 BY SIMILARITY.
FT DISULFID 9 24 BY SIMILARITY.
FT DISULFID 14 22 BY SIMILARITY.
FT DISULFID 31 38 BY SIMILARITY.
FT DISULFID 35 51 BY SIMILARITY.
SQ SEQUENCE 67 AA; 7680 MW; 0D5AF30F33248949 CRC64;

Query Match 76.7%; Score 23; DB 1; Length 67;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VCQD 5
Db [1]
50 ICQD 53

RESULT 15
ID NUML_HUMAN STANDARD; PRT; 81 AA.
AC C00483;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE NADH-ubiquinone oxidoreductase MLRQ subunit (EC 1.6.5.3) (EC 1.6.99.3)
DE (Complex I-MLRQ) (CI-MLRQ).
GN NDUF44.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

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FT DISULFID 14 22 BY SIMILARITY.
FT DISULFID 31 38 BY SIMILARITY.
FT DISULFID 35 51 BY SIMILARITY.
SQ SEQUENCE 67 AA; 7679 MW; 109AF30F33248949 CRC64;

Query Match 76.7%; Score 23; DB 1; Length 67;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VCQD 5
Db [1]
50 ICQD 53

RESULT 14
ID IBB3_SETIT STANDARD; PRT; 67 AA.
AC P22737;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE Bowman-Birk type trypsin inhibitor III (FMTI-III).
OS Setaria italica (Foxtail millet).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Paniceae; Setaria.
OX NCBI_TaxID=4555;
RN [1]
RP SEQUENCE.
RX MEDLINE=91299279; PubMed=1368693;
RA Tashiro M., Asao T., Hirata C., Takahashi K.;
RT "Purification, characterization, and amino acid sequence of foxtail
RT millet trypsin inhibitor III.";
RL Agric. Biol. Chem. 55:419-426(1991).
CC -1- SIMILARITY: Belongs to the Bowman-Birk serine protease inhibitor
CC family.
DR PIR; JG0013; TIIIP3.
DR HSSP; P56679; IPBI.
DR InterPro; IPR000877; Bowman-Birk_leg.
DR Pfam; PF00228; Bowman-Birk_leg; 2.
DR ProDom; PD002168; Bowman-Birk_leg; 1.
DR SMART; SM00269; BowB; 1.
DR PROSITE; PS00281; BOWMAN_BIRK; 1.
KW Serine protease inhibitor.
FT ACT SITE 16 17 INTERACTION WITH TRYPSIN (BY SIMILARITY).
FT DISULFID 8 63 BY SIMILARITY.
FT DISULFID 9 24 BY SIMILARITY.
FT DISULFID 14 22 BY SIMILARITY.
FT DISULFID 31 38 BY SIMILARITY.
FT DISULFID 35 51 BY SIMILARITY.
SQ SEQUENCE 67 AA; 7680 MW; 0D5AF30F33248949 CRC64;

Query Match 76.7%; Score 23; DB 1; Length 67;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VCQD 5
Db [1]
50 ICQD 53

RESULT 15
ID NUML_HUMAN STANDARD; PRT; 81 AA.
AC C00483;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE NADH-ubiquinone oxidoreductase MLRQ subunit (EC 1.6.5.3) (EC 1.6.99.3)
DE (Complex I-MLRQ) (CI-MLRQ).
GN NDUF44.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=9601339; PubMed=9352085;
RA Kim J.W., Lee Y., Kang H.B., Chose Y.K., Chung T.W., Chang S.Y.,
RA Lee K.S., Choe I.S.;
RT "Cloning of the human cDNA sequence encoding the NADH:ubiquinone
RT oxidoreductase MLRQ subunit.";
RL Biochem. Mol. Biol. Int. 43:669-675(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Kanagarajah D., Raha S., Scherer S., Robinson B.H.;
RT "Genomic sequence, cDNA sequence and chromosomal localization of the
RT NDUF44 human gene coding for the MLRQ subunit of NADH:ubiquinone
RT oxidoreductase and its pseudogene.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Transfer of electrons from NADH to the respiratory
CC chain. The immediate electron acceptor for the enzyme is believed
CC to be ubiquinone.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane; matrix side.
CC -!- SIMILARITY: Belongs to the complex I NDUF44 subunit family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U94586; AAB52726.1; -.
DR EMBL; AF201077; AAF09253.1; -.
DR GenBank; HGNC:7687; NDUF44.
DR MIM; 603833; -.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; TAS.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 81 AA; 9370 MW; 2FAD115EDE24C7 CRC64;

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Query Match 76.7%; Score 23; DB 1; Length 81;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 42 DVCWD 46

Search completed: May 5, 2004, 13:50:54
Job time : 10 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 13:47:50 ; Search time 13.5 Seconds
(without alignments)
35.626 Million cell updates/sec

Title: S902

Perfect score: 30

Sequence: 1 dvcqd 5

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 37674

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	79	2 A49475	cerebroside sulfat
2	27	90.0	74	2 B71282	hypothetical prote
3	26	86.7	78	2 S39658	D-alanine carrier
4	26	86.7	97	2 G82725	conserved hypothet
5	26	86.7	100	2 T30654	hypothetical prote
6	25	83.3	89	2 S71555	proteinase inhibit
7	25	83.3	89	2 JQ2361	wheat aluminum ind
8	24	80.0	37	2 C41933	mating pheromone E
9	24	80.0	54	2 H82693	hypothetical prote
10	24	80.0	56	2 A25507	proteinase inhibit
11	24	80.0	68	2 D82027	hypothetical prote
12	24	80.0	100	2 T16810	hypothetical prote
13	23	76.7	18	2 B61110	68K collagen-bind
14	23	76.7	43	2 A70231	hypothetical prote
15	23	76.7	61	2 AD2033	hypothetical prote
16	23	76.7	67	1 T11LF2	trypsin inhibitor
17	23	76.7	67	1 T11LF3	trypsin inhibitor
18	23	76.7	77	2 AD2086	hypothetical prote
19	23	76.7	84	2 AD2554	hypothetical prote
20	23	76.7	94	2 S43190	ferredoxin [4Fe-4S
21	23	76.7	96	2 S07627	T-cell receptor be
22	23	76.7	97	2 JC4912	eotaxin precursor
23	23	76.7	99	2 S25947	ribosomal protein
24	22	73.3	64	1 T1OAB	trypsin inhibitor
25	22	73.3	76	2 G69886	hypothetical prote
26	22	73.3	78	2 JC2496	ferredoxin [3Fe-4S
27	22	73.3	81	2 A32026	glucosylceramide b
28	22	73.3	87	2 E81063	hypothetical prote
29	22	73.3	88	2 T43562	probable IS elemen

ALIGNMENTS

RESULT 1

A49475

cerebroside sulfate activator - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 17-May-1996

C:Accession: A49475

R:Stevens, R.L.; Faull, K.F.; Conklin, K.A.; Green, B.N.; Fluharty, A.L.

Biochemistry 32, 4051-4059, 1993

A:Title: Porcine cerebroside sulfate activator: further structural characterization and

A:Reference number: A49475; MUID:93229506; PMID:8471613

A:Accession: A49475

A>Status: preliminary

A:Molecule type: Protein

A:Residues: 1-79 <STE>

A:Experimental source: kidney

A:Note: sequence extracted from NCBI backbone (NCBIP:129597)

C:Superfamily: saposin; saposin repeat homology

F:1-79/Domain: saposin repeat homology <SAP>

Query Match 100.0%; Score 30; DB 2; Length 79;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCOD 5

Db 2 DVCQD 6

RESULT 2

B71282

hypothetical protein TP0777 - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 03-Nov-1999

C:Accession: B71282

R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin

rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770; PMID:9665876

A:Accession: B71282

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-74 <COL>

A:Cross-references: GB:AS001249; GB:AE000520; NID:G3323083; PIDN:AAC65750.1; PID:G3323091

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0777

Query Match

Best Local Similarity 90.0%; Score 27; DB 2; Length 74;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
 |||||
 Db 29 DVCED 33

RESULT 3

S39658
 D-alanine carrier protein dltC - Bacillus subtilis
 N:Alternate names: protein ipa-3r
 C:Species: Bacillus subtilis
 C>Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 26-May-2000
 C:Accession: S39658; E69616
 R:Glaser, P.; Kunst, F.; Danchin, A.
 A.; Rapoport, G.; Farnham, A.
 Mol. Microbiol. 10, 371-384, 1993
 A>Title: Bacillus subtilis genome project: cloning and sequencing of the 97 kb region fr
 A:Reference number: S39655; MUID:95020537; PMID:7934828
 A:Accession: S39658
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-78 <GLA>

A:Cross-references: EMBL:X73124; NID:g413923; PIDN:CAA51559.1; PID:g413927
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993
 R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertoni
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tsubota, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumsstein, E.; Yoshikawa, H.; Danchin, A.
 A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: E69616
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
 A:Residues: 1-78 <KUN>

A:Cross-references: GB:Z99123; GB:AL009126; NID:g2636240; PIDN:CAB15878.1; PID:el186351;
 A:Experimental source: strain 168

C:Genetics:
 A:Gene: dltC

C:Superfamily: acyl carrier protein homology

C:Keywords: carrier protein

F:1-70/Domain: acyl carrier protein homology <ACP>

Query Match 86.7%; Score 26; DB 2; Length 78;
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
 |||||
 Db 13 EVCQD 17

RESULT 4

G82725
 conserved hypothetical protein XF1074 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: G82725

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000

A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A>Note: for a complete list of authors see reference number A59328 below

A:Accession: G82725

A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-97 <SIM>

A:Cross-references: GB:AE003944; GB:AE003849; NID:g9106023; PIDN:AAF83884.1; GSPDB:GN0012

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohne

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

. F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Teshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1074

Query Match 86.7%; Score 26; DB 2; Length 97;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5

|||||

Db 78 EVCQD 82

RESULT 5

T30654
 hypothetical protein 52R - Molluscum contagiosum virus 1

N:Alternate names: MC052R

C:Species: Molluscum contagiosum virus 1

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 16-Feb-2001

R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.

Science 273, 813-816, 1996

A>Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host res

A:Reference number: Z20876; MUID:96325459; PMID:8670425

A:Accession: T30654

A>Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-100 <SEN>

A:Cross-references: EMBL:U60315; NID:gl491943; PIDN:AAC55180.1; PID:gl491995

C:Genetics:

A>Note: MC052R

C:Superfamily: Molluscum contagiosum virus 1 hypothetical protein 52R

Query Match 86.7%; Score 26; DB 2; Length 100;

Best Local Similarity 80.0%; Pred. No. 1.9e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5

|||||

Db 85 EVCQD 89

RESULT 6

S71555

proteinase inhibitor-related protein bsII precursor - barley

C:Species: Hordeum vulgare (barley)

C>Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 21-Jul-2000

C:Accession: S71555; S53102

R:Stevens, C.; Titarenko, B.; Hargreaves, J.A.; Gurr, S.J.

Plant Mol. Biol. 31, 741-749, 1996

A>Title: Defence-related gene activation during an incompatible interaction between Stago

A:Reference number: S71554; MUID:96400029; PMID:8806405

A:Accession: S71555

A:Molecule type: DNA

A:Residues: 1-89 <STB>

A;Cross-references: EMBL:Z48729; NID:g732808; PIDN:CAA88619.1; PID:g732809
C;Genetics:
A;Gene: bsII
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-89/Product: proteinase inhibitor-related protein bsII #status predicted <MAT>

Query Match 83.3%; Score 25; DB 2; Length 89;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVCQD 5
|||
Db 43 DVCDD 47

RESULT 7
JQ2361
wheat aluminum induced protein wali 5 - wheat
C;Species: Triticum aestivum (common wheat)
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 29-Oct-1999
C;Accession: JQ2361
R;Snowden, K.C.; Gardner, R.C.
Plant Physiol. 103, 855-861, 1993
A;Title: Five genes induced by aluminum in wheat (Triticum aestivum L.) roots.
A;Reference number: JQ2358; MUID:94294563; PMID:8022939
A;Accession: JQ2361
A;Molecule type: mRNA
A;Residues: 1-89 <SNO>
A;Cross-references: GB:L11882; NID:gl70794; PIDN:AAA50850.1; PID:gl70795
A;Experimental source: root, cv. Warigal
C;Keywords: metal binding

Query Match 83.3%; Score 25; DB 2; Length 89;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVCQD 5
|||
Db 43 DVCDD 47

RESULT 8
C41933
mating pheromone Er-20 - Euplotes raikovi
N;Alternate names: euplomone
C;Species: Euplotes raikovi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 07-Dec-1999
C;Accession: C41933
R;Raffioni, S.; Miceli, C.; Vallesi, A.; Chowdhury, S.K.; Chait, B.T.; Luporini, P.; Bra
Proc. Natl. Acad. Sci. U.S.A. 89, 2071-2075, 1992
A;Title: Primary structure of Euplotes raikovi pheromones: comparison of five sequences
A;Reference number: A41933; MUID:92196059; PMID:1549567
A;Accession: C41933
A;Molecule type: protein
A;Residues: 1-37 <RAF>
A;Cross-references: PIDN:AA821809.1; PID:g247247
A;Note: sequence extracted from NCBI backbone (NCBIP:104633)
C;Genetics:
A;Genetic code: SGC9
A;Keywords: pheromone
F;3-18,10-32,15-24/Disulfide bonds: #status predicted

Query Match 80.0%; Score 24; DB 2; Length 37;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVCQD 5
|:
Db 1 DICDD 5

RESULT 9
H82693

hypothetical protein XF1339 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: H82693
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: H82693
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-54 <SIM>
A;Cross-references: GB:AF003966; GB:AE003849; NID:g9106327; PIDN:AAF84148.1; GSPDB:GN0011
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorzy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matekuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1339

Query Match 80.0%; Score 24; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQ 4
|||
Db 13 DVCQ 16

RESULT 10
A25507
proteinase inhibitor (Bowman-Birk) I-2b - wheat (fragment)
C;Species: Triticum aestivum (common wheat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 13-Jan-1995
C;Accession: A25507
R;Odani, S.; Koide, T.; Ono, T.
J. Biochem. 100, 975-983, 1986
A;Title: Wheat germ trypsin inhibitors. Isolation and structural characterization of sing
A;Reference number: A91908; MUID:87137364; PMID:3818572
A;Accession: A25507
A;Molecule type: protein
A;Residues: 1-56 <ODA>
C;Superfamily: barley rootlet proteinase inhibitor; Bowman-Birk inhibitor repeat homology <BB1>
F;10-35/Domain: Bowman-Birk inhibitor repeat homology <BB1>

Query Match 80.0%; Score 24; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VCQD 5
|||
Db 50 VCQD 53

RESULT 11
D82027
hypothetical protein NMA0318 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: D82027
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
 A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
 A;Reference number: AB1775; MUID:20222556; PMID:10761919
 A;Accession: D82027
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-68 <PAR>
 A;Cross-references: GB:AL162752; GB:AL157959; NID:G7378778; PIDN:CAB83623.1; PID:G737907
 A;Experimental source: serogroup A, strain Z2491
 C;Genetics:
 A;Genome: NMA0318

Query Match 80.0%; Score 24; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQ 4
 ||||
 Db 33 DVCQ 36

RESULT 12

T16810

hypothetical protein T05C1.5 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

A;Accession: T16810

R;Geisel, C.

submitted to the EMBL Data Library, June 1995

A;Description: The sequence of *C. elegans* cosmid T05C1.

A;Reference number: Z18581

A;Accession: T16810

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-100 <GFI>

A;Cross-references: EMBL:U28992; NID:G861370; PID:G861374; PIDN:AAA68392.1; CESP:T05C1.5

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:T05C1.5

A;Introns: 42/1; 88/1

Query Match 80.0%; Score 24; DB 2; Length 100;

Best Local Similarity 60.0%; Pred. No. 4.7e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
 ||||
 Db 50 DLCD 54

RESULT 13

B61110

68K collagen-binding protein, light form - chicken (fragments)

C;Species: *Gallus gallus* (chicken)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Oct-1994

A;Accession: B61110

R;Tidball, J.G.

J. Biol. Chem. 267, 21211-21219, 1992

A;Title: Identification and distribution of a novel, collagen-binding protein in the dev

A;Reference number: A61110; MUID:93016046; PMID:1328225

A;Accession: B61110

A;Molecule type: protein

A;Residues: 1-18 <IID>

C;Keywords: collagen binding

Query Match 76.7%; Score 23; DB 2; Length 18;

Best Local Similarity 80.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVCQD 5
 ||||
 Db 1 DVCLD 5

RESULT 14

A70231

hypothetical protein BBF28 - Lyme disease spirochete plasmid F/1p28-1

C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999

A;Accession: A70231

R;Fraser, C.M.; Carjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horat, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.

A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: A70231

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-43 <MLE>

A;Cross-references: GB:AE000794; NID:G2689981; PIDN:AAC66389.1; PID:G2690006; TIGR:BBF28

A;Experimental source: strain B31

C;Genetics:

A;Genome: plasmid

Query Match 76.7%; Score 23; DB 2; Length 43;

Best Local Similarity 60.0%; Pred. No. 3.5e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
 ||||
 Db 20 DMCD 24

RESULT 15

AD2033

hypothetical protein asr1818 [imported] - *Nostoc* sp. (strain PCC 7120)

C;Species: *Nostoc* sp. PCC 7120

A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

A;Accession: AD2033

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AD2033

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-61 <KUR>

A;Cross-references: GB:BA000019; PIDN:BAF73517.1; PID:gl7130908; GSPDB:GN00179

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: asr1818

Query Match 76.7%; Score 23; DB 2; Length 61;

Best Local Similarity 60.0%; Pred. No. 4.7e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
 ||||
 Db 38 DVCEE 42

Search completed: May 5, 2004, 13:52:58

Job time : 13.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 13:50:26 ; Search time 37.5 Seconds
(without alignments)
36.959 Million cell updates/sec

Title: SEQ2

Perfect score: 30

Sequence: 1 dvcqd 5

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 472710

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	81	10	US-09-991-936-1888
2	30	100.0	81	15	US-10-401-324-17
3	30	100.0	83	12	US-10-424-599-162856
4	27	90.0	40	14	US-10-153-344-27
5	27	90.0	48	10	US-09-774-639-204
6	27	90.0	48	10	US-09-969-730-206
7	27	90.0	48	16	US-10-621-363-206
8	27	90.0	55	9	US-09-864-761-37337
9	27	90.0	61	12	US-10-424-599-247518
10	27	90.0	66	12	US-10-424-599-204388
11	27	90.0	79	12	US-10-424-599-180557
12	27	90.0	83	10	US-09-498-272-52
13	26	86.7	47	9	US-09-864-761-33503
14	26	86.7	72	12	US-10-424-599-152024
15	26	86.7	77	12	US-10-424-599-245254

16	26	86.7	86	10	US-09-498-272-45	Sequence 45, Appl
17	26	86.7	86	10	US-09-498-272-46	Sequence 46, Appl
18	26	86.7	87	10	US-09-498-272-44	Sequence 44, Appl
19	26	86.7	88	10	US-09-498-272-43	Sequence 43, Appl
20	26	86.7	91	12	US-10-424-599-216669	Sequence 216669,
21	26	86.7	93	12	US-10-424-599-273210	Sequence 273210,
22	26	86.7	94	9	US-09-864-761-38043	Sequence 38043, A
23	26	86.7	100	12	US-10-424-599-258943	Sequence 258943,
24	25	83.3	36	10	US-09-892-877-283	Sequence 283, App
25	25	83.3	36	10	US-09-948-783-295	Sequence 295, App
26	25	83.3	42	12	US-10-424-599-199151	Sequence 199151,
27	25	83.3	49	14	US-10-029-386-34119	Sequence 34119, A
28	25	83.3	50	12	US-10-424-599-206216	Sequence 206216,
29	25	83.3	52	9	US-09-796-692-787	Sequence 787, App
30	25	83.3	52	9	US-09-796-692-1428	Sequence 1428, Ap
31	25	83.3	52	9	US-09-796-692-1892	Sequence 1892, Ap
32	25	83.3	52	12	US-10-424-599-222152	Sequence 222152,
33	25	83.3	52	14	US-10-040-862-787	Sequence 787, App
34	25	83.3	52	14	US-10-040-862-1428	Sequence 1428, Ap
35	25	83.3	52	14	US-10-040-862-1892	Sequence 1892, Ap
36	25	83.3	52	15	US-10-057-475B-787	Sequence 787, App
37	25	83.3	52	15	US-10-057-475B-1428	Sequence 1428, Ap
38	25	83.3	52	15	US-10-057-475B-1892	Sequence 1892, Ap
39	25	83.3	52	15	US-10-154-884B-787	Sequence 787, App
40	25	83.3	52	15	US-10-154-884B-1428	Sequence 1428, Ap
41	25	83.3	52	15	US-10-154-884B-1892	Sequence 1892, Ap
42	25	83.3	59	12	US-10-424-599-173624	Sequence 173624,
43	25	83.3	62	12	US-10-424-599-245290	Sequence 245290,
44	25	83.3	64	12	US-10-424-599-257942	Sequence 257942,
45	25	83.3	90	9	US-09-796-692-1334	Sequence 1334, Ap

ALIGNMENTS

RESULT 1

US-09-991-936-1888
; Sequence 1888, Application US/09991936
; Publication No. US20030073827A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; FILE REFERENCE: FC-6-CI
; CURRENT APPLICATION NUMBER: US/09/991,936
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US/09/543,668
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,704
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1959
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1888
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Ctenocephalides felis
US-09-991-936-1888

Query Match 100.0%; Score 30; DB 10; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
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Db 23 DVCQD 27

RESULT 2

US-10-401-324-17
; Sequence 17, Application US/10401324

```
; Publication No. US20030220487A1
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: FLEA PERITROPHIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; FILE REFERENCE: FC-6-C2
; CURRENT APPLICATION NUMBER: US/10/401,324
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US/09/686,583B
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 09/543,668
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,704
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Ctenocephalides felis
US-10-401-324-17

Query Match          100.0%; Score 30; DB 15; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 23 DVCQD 27

RESULT 3
US-10-424-599-162856
; Sequence 162856, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 162856
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT MRT3847_118077C.1.pep
US-10-424-599-162856

Query Match          100.0%; Score 30; DB 12; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 42 DVCQD 46

RESULT 4
US-10-153-344-27
; Sequence 27, Application US/10153344
; Publication No. US20030004124A1
; GENERAL INFORMATION:
; APPLICANT: ROTHMAN, JOEL
; APPLICANT: BLOSS, TIM
; APPLICANT: WITZE, ERIC
; TITLE OF INVENTION: BTF3: AN INHIBITOR OF APOPTOSIS
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; FILE REFERENCE: 407T-300410US
; CURRENT APPLICATION NUMBER: US/10/153,344
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/292,559
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: X is any amino acid.
US-10-153-344-27

Query Match          90.0%; Score 27; DB 14; Length 40;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 12 DVCQD 16

RESULT 5
US-09-774-639-204
; Sequence 204, Application US/09774639
; Publication No. US20030003555A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 204
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-639-204

Query Match          90.0%; Score 27; DB 10; Length 48;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 28 DVCQD 32

RESULT 6
US-09-969-730-206
; Sequence 206, Application US/09969730
; Publication No. US20030054443A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P2
; CURRENT APPLICATION NUMBER: US/09/969,730
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
```

PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,366
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,370
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,367
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,365
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,731
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,557
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,563
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/055,970
PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,986
PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,311
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,808
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,803
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,804
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,809
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,806
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,310
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,798
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,309
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,312
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,807
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,386
PRIOR FILING DATE: 1997-08-05
NUMBER OF SEQ ID NOS: 373
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 206
LENGTH: 48
TYPE: PRT
ORGANISM: Homo sapiens
US-09-969-730-206

Query Match 90.0%; Score 27; DB 10; Length 48;
Best Local Similarity 80.0%; Pred.No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
|:|
Db 28 DLQCD 32

RESULT 7
US-10-621-363-206
Sequence 206, Application US/10621363
Publication No. US20040023283A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P2C1

CURRENT APPLICATION NUMBER: US/10/621,363
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: PCT/US98/16235
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,366
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,370
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 373
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 206
LENGTH: 48
TYPE: PRT
ORGANISM: Homo sapiens
US-10-621-363-206

Query Match 90.0%; Score 27; DB 16; Length 48;
Best Local Similarity 80.0%; Pred.No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
|:|
Db 28 DLQCD 32

RESULT 8
US-09-864-761-37337
Sequence 37337, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/532,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 37337
LENGTH: 55
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC009721.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.7
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 9.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.3
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 9.6
OTHER INFORMATION: EST HUMAN HIT: BES41441.1, EVALU6 3.00e-26
OTHER INFORMATION: SWISSPROT HIT: P25167, EVALU6 2.00e-18
US-09-864-761-37337

Query Match 90.0%; Score 27; DB 9; Length 55;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 32 DVCED 36

RESULT 9
US-10-424-599-247518
; Sequence 247518, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 247518
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(61)
; OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65538C.1.pap

US-10-424-599-247518

Query Match 90.0%; Score 27; DB 12; Length 61;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 40 DMCQD 44

RESULT 10
US-10-424-599-204388
; Sequence 204388, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 204388
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_2658C.1.pap
US-10-424-599-204388

Query Match 90.0%; Score 27; DB 12; Length 66;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 42 DLQCD 46

RESULT 11
US-10-424-599-180557
; Sequence 180557, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 180557
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_134057C.1.pap
US-10-424-599-180557

Query Match 90.0%; Score 27; DB 12; Length 79;
Best Local Similarity 80.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
Db 51 DVCED 55

RESULT 12

US-09-498-272-52
; Sequence 52, Application US/09498272
; Publication No. US20030113890A1

GENERAL INFORMATION:

APPLICANT: Vlasuk, George Phillip
; Stanssens, Patrick Eric Hugo
; Messens, Joris Hilda Lieven
; Lauwereys, Marc Josef
; Laroche, Yves Rene
; Jaspers, Laurent Stephane
; Ganssemans, Yannick Georges Jozef
; Moyle, Matthew
; Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT

PROTEIN

NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
; Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER READABLE FORM:

Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:
LENGTH: 83 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:

ORGANISM: Ancylostoma duodenale
SEQUENCE DESCRIPTION: SEQ ID NO: 52:

US-09-498-272-52

Query Match 90.0%; Score 27; DB 10; Length 83;
Best Local Similarity 80.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCOD 5
DB 68 DVCED 72

RESULT 13

US-09-864-761-33503
; Sequence 33503, Application US/09864761
; Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aemica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/006666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/006667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/006664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/006669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/006665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/006668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/006663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/006662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/006661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/006670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 33503

LENGTH: 47

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AL035681.13
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.8

; OTHER INFORMATION: EST_HUMAN HIT: AL120419.1, EVALUE 3.00e-23
; OTHER INFORMATION: EST_HUMAN HIT: AL120211.1, EVALUE 2.00e-23
; OTHER INFORMATION: SWISSPROT HIT: P54725, EVALUE 2.70e+00
US-09-864-761-33503

Query Match 86.7%; Score 26; DB 9; Length 47;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVCQD 5
| | | |
Db 22 DTCQD 26

RESULT 14

US-10-424-599-152024
; Sequence 152024, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 152024
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_108300C.1.pap
US-10-424-599-152024

Query Match 86.7%; Score 26; DB 12; Length 72;
Best Local Similarity 80.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
| | | |
Db 29 DVCRD 33

RESULT 15

US-10-424-599-245254
; Sequence 245254, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 245254
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_63496C.1.pap
US-10-424-599-245254

Query Match 86.7%; Score 26; DB 12; Length 77;
Best Local Similarity 60.0%; Pred. No. 8.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVCQD 5
| | | |
Db 29 DICED 33

Search completed: May 5, 2004, 13:55:08
Job time : 37.5 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2004, 10:37:15 ; Search time 54 Seconds
(without alignments)
26.162 Million cell updates/sec

Title: SEQ2

Perfect score: 30

Sequence: 1 dvcqd 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 891005

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_29Jan04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003bs:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	5	3	AAV58700 Antiangio
2	30	100.0	6	3	AAV58699 Antiangio
3	30	100.0	7	3	AAV58698 Antiangio
4	30	100.0	8	3	AAV58697 Antiangio
5	30	100.0	9	3	AAV58696 Antiangio
6	30	100.0	10	3	AAV58693 Antiangio
7	30	100.0	11	3	AAV58705 Antiangio
8	30	100.0	11	3	AAV58691 Antiangio
9	30	100.0	15	2	AAW18587 Universal
10	30	100.0	15	3	AAV58685 Antiangio
11	30	100.0	19	2	AAW18588 Universal
12	30	100.0	81	3	AAE29624 Cat flea
13	30	100.0	81	5	AAE24070 Flea peri
14	30	100.0	83	4	AAAB31929 Amino aci
15	30	100.0	84	4	AAAB6358 Human eSA
16	30	100.0	85	4	AAAB31912 Amino aci
17	29	96.7	5	3	AAV58708 Antiangio
18	27	90.0	5	3	AAV58709 Antiangio
19	27	90.0	5	3	AAV58711 Antiangio
20	27	90.0	40	6	ABP71131 E10 CARD
21	27	90.0	48	7	ADB47923 Novel hum
22	27	90.0	55	4	AAW17684 Peptide #
23	27	90.0	55	4	ABB36706 Peptide #
24	27	90.0	55	4	AAW30198 Peptide #
25	27	90.0	55	4	ABB31493 Peptide #

ALIGNMENTS

RESULT 1

AAV58700
ID AAV58700 standard; peptide; 5 AA.

XX AAV58700;

XX AC AAV58700;

XX 25-APR-2000 (first entry)

DE Antiangiogenic peptide derived from saposin B.

XX Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
KW antimitigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.

XX Homo sapiens.

XX WO200002902-A1.

XX PN

XX 20-JAN-2000.

26	27	90.0	55	4	ABB22039	Abb22039 Protein #
27	27	90.0	55	4	AAW69858	AAW69858 Human bon
28	27	90.0	55	4	AAW57463	AAW57463 Human bra
29	27	90.0	55	4	ABG51557	ABG51557 Human liv
30	27	90.0	55	4	AAW05345	AAW05345 Peptide #
31	27	90.0	55	5	ABG39490	ABG39490 Human pep
32	27	90.0	83	2	AAV30425	AAV30425 Mature ne
33	26	86.7	5	3	AAV58707	AAV58707 Antiangio
34	26	86.7	47	4	AAW13785	AAW13785 Peptide #
35	26	86.7	47	4	ABB32719	ABB32719 Peptide #
36	26	86.7	47	4	AAW26183	AAW26183 Peptide #
37	26	86.7	47	4	ABB27560	ABB27560 Human pep
38	26	86.7	47	4	ABW18205	ABW18205 Protein #
39	26	86.7	47	4	AAW65918	AAW65918 Human bon
40	26	86.7	47	4	AAW53537	AAW53537 Human bra
41	26	86.7	47	4	ABG47574	ABG47574 Human liv
42	26	86.7	47	4	AAW01530	AAW01530 Peptide #
43	26	86.7	47	5	ABG35554	ABG35554 Human pep
44	26	86.7	54	3	AAV83246	AAV83246 Delta 6 d
45	26	86.7	86	2	AAV30419	AAV30419 Mature ne
46	26	86.7	86	2	AAV30418	AAV30418 Mature ne
47	26	86.7	86	3	AAW15304	AAW15304 A. caninu
48	26	86.7	86	3	AAW15303	AAW15303 A. caninu
49	26	86.7	87	2	AAV30417	AAV30417 Mature ne
50	26	86.7	87	3	AAW15302	AAW15302 A. caninu
51	26	86.7	88	2	AAV30416	AAV30416 Mature ne
52	26	86.7	88	3	AAW15301	AAW15301 A. caninu
53	26	86.7	94	4	ABB37452	ABB37452 Peptide #
54	26	86.7	94	4	ABB32200	ABB32200 Peptide #
55	26	86.7	94	4	ABB22745	ABB22745 Protein #
56	26	86.7	94	4	AAW58127	AAW58127 Human bra
57	26	86.7	94	5	ABG40237	ABG40237 Human pep
58	25	83.3	5	3	AAV58710	AAV58710 Antiangio
59	25	83.3	5	3	AAV58712	AAV58712 Antiangio
60	25	83.3	14	1	AAW60041	AAW60041 Sequence
61	25	83.3	14	1	AAW60041	AAW60041 Junction
62	25	83.3	21	4	AAW66970	AAW66970 Mutant pr
63	25	83.3	29	4	AAW66979	AAW66979 Mutant pr
64	25	83.3	29	4	AAW66968	AAW66968 Mutant pr
65	25	83.3	29	4	AAW66967	AAW66967 Castor oi
66	25	83.3	36	3	AAV76281	AAV76281 Fragment
67	25	83.3	36	7	ADE11923	ADE11923 Human sec
68	25	83.3	52	4	AAW80423	AAW80423 Human hae
69	25	83.3	52	4	AAW81064	AAW81064 Human hae
70	25	83.3	52	4	AAW81528	AAW81528 Human hae
71	25	83.3	56	4	AAU51158	AAU51158 Propionib
72	25	83.3	56	6	ABW47677	ABW47677 Propionib
73	25	83.3	63	4	ABG10437	ABG10437 Novel hum
74	25	83.3	81	3	AAW15258	AAW15258 Arabidops
75	25	83.3	89	6	ABR40904	ABR40904 Deduced a

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XX PF 12-JUL-1999; 99WO-US015772.
XX PR 13-JUL-1998; 98US-0092647P.
XX PA (GILL/) GILL P S.
XX PI Gill PS;
XX DR WPI; 2000-171128/15.
XX PT Saposin B derived peptides, useful as inhibitors of angiogenesis and
XX PT tumor growth.
XX PS Claim 4; Page 57; 78pp; English.
XX CC The present sequence is that of a claimed peptide, derived from human
XX CC saposin B, that has antiangiogenic activity. The invention is based on
XX CC the discovery that saposin B (see AAY58716), previously known to be
XX CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
XX CC and antitumor activity, and also has antiproliferative and antimigratory
XX CC activity against endothelial cells. This activity is conserved in cryptic
XX CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
XX CC synthetically prepared and used in vitro or in vivo for the treatment of
XX CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
XX CC (claimed). The polypeptides can also be used in conjunction with
XX CC cytotoxic moieties to selectively kill certain cell types, e.g. for
XX CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
XX CC malformation, nonunion fracture, arthritis and other connective tissue
XX CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
XX CC corneal graft neovascularization, pyogenic granuloma, retrolental
XX CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
XX CC vascular adhesions and hypertrophic scars
XX SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
DB 1 DVCQD 5

RESULT 2
AAY58699
ID AAY58699 standard; peptide; 6 AA.
XX AC AAY58699;
XX DT 25-APR-2000 (first entry)
XX DE Antiangiogenic peptide derived from saposin B.
XX KW Antiangiogenic; angiogenesis inhibitor; antitumor; antiproliferative;
XX KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
XX OS Homo sapiens.
XX PN WO200002902-A1.
XX PD 20-JAN-2000.
XX PF 12-JUL-1999; 99WO-US015772.
XX PR 13-JUL-1998; 98US-0092647P.
XX PA (GILL/) GILL P S.
XX PI Gill PS;
XX DR WPI; 2000-171128/15.
XX PT Saposin B derived peptides, useful as inhibitors of angiogenesis and
XX PT tumor growth.
XX PS Disclosure; Page 19; 78pp; English.
XX CC The present sequence is that of a novel peptide, derived from human
XX CC saposin B, that has antiangiogenic activity. The invention is based on
XX CC the discovery that saposin B (see AAY58716), previously known to be
XX CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
XX CC activity against endothelial cells. This activity is conserved in cryptic
XX CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
XX CC synthetically prepared and used in vitro or in vivo for the treatment of
XX CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
XX CC (claimed). The polypeptides can also be used in conjunction with
XX CC cytotoxic moieties to selectively kill certain cell types, e.g. for
XX CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
XX CC malformation, nonunion fracture, arthritis and other connective tissue
XX CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
XX CC corneal graft neovascularization, pyogenic granuloma, retrolental
XX CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
XX CC vascular adhesions and hypertrophic scars
XX SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
DB 1 DVCQD 5

RESULT 3
AAY58698
ID AAY58698 standard; peptide; 7 AA.
XX AC AAY58698;
XX DT 25-APR-2000 (first entry)
XX DE Antiangiogenic peptide derived from saposin B.
XX KW Antiangiogenic; angiogenesis inhibitor; antitumor; antiproliferative;
XX KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
XX OS Homo sapiens.
XX PN WO200002902-A1.
XX PD 20-JAN-2000.
XX PF 12-JUL-1999; 99WO-US015772.
XX PR 13-JUL-1998; 98US-0092647P.
XX PA (GILL/) GILL P S.
XX PI Gill PS;
XX DR WPI; 2000-171128/15.
XX PT Saposin B derived peptides, useful as inhibitors of angiogenesis and
XX PT tumor growth.
XX PS Disclosure; Page 19; 78pp; English.
XX CC The present sequence is that of a novel peptide, derived from human
XX CC saposin B, that has antiangiogenic activity. The invention is based on
XX CC the discovery that saposin B (see AAY58716), previously known to be
XX CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic

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XX PT Saposin B derived peptides, useful as inhibitors of angiogenesis and
XX PT tumor growth.
XX PS Disclosure; Page 19; 78pp; English.
XX CC The present sequence is that of a novel peptide, derived from human
XX CC saposin B, that has antiangiogenic activity. The invention is based on
XX CC the discovery that saposin B (see AAY58716), previously known to be
XX CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
XX CC and antitumor activity, and also has antiproliferative and antimigratory
XX CC activity against endothelial cells. This activity is conserved in cryptic
XX CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
XX CC synthetically prepared and used in vitro or in vivo for the treatment of
XX CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
XX CC (claimed). The polypeptides can also be used in conjunction with
XX CC cytotoxic moieties to selectively kill certain cell types, e.g. for
XX CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
XX CC malformation, nonunion fracture, arthritis and other connective tissue
XX CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
XX CC corneal graft neovascularization, pyogenic granuloma, retrolental
XX CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
XX CC vascular adhesions and hypertrophic scars
XX SQ Sequence 6 AA;

Query Match 100.0%; Score 30; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
DB 1 DVCQD 5

RESULT 3
AAY58698
ID AAY58698 standard; peptide; 7 AA.
XX AC AAY58698;
XX DT 25-APR-2000 (first entry)
XX DE Antiangiogenic peptide derived from saposin B.
XX KW Antiangiogenic; angiogenesis inhibitor; antitumor; antiproliferative;
XX KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
XX OS Homo sapiens.
XX PN WO200002902-A1.
XX PD 20-JAN-2000.
XX PF 12-JUL-1999; 99WO-US015772.
XX PR 13-JUL-1998; 98US-0092647P.
XX PA (GILL/) GILL P S.
XX PI Gill PS;
XX DR WPI; 2000-171128/15.
XX PT Saposin B derived peptides, useful as inhibitors of angiogenesis and
XX PT tumor growth.
XX PS Disclosure; Page 19; 78pp; English.
XX CC The present sequence is that of a novel peptide, derived from human
XX CC saposin B, that has antiangiogenic activity. The invention is based on
XX CC the discovery that saposin B (see AAY58716), previously known to be
XX CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic

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CC and antitumour activity, and also has antiproliferative and antimigratory
 CC activity against endothelial cells. This activity is conserved in cryptic
 CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
 CC synthetically prepared and used in vitro or in vivo for the treatment of
 CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
 CC (claimed). The polypeptides can also be used in conjunction with
 CC cytotoxic moieties to selectively kill certain cell types, e.g. for
 CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
 CC malformation, nonunion fracture, arthritis and other connective tissue
 CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
 CC corneal graft neovascularization, pyogenic granuloma, retrolental
 CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
 CC vascular adhesions and hypertrophic scars
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 30; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVCQD 5
 |||||
 Db 1 DVCQD 5
 RESULT 4
 AAY58697
 ID AAY58697 standard; peptide; 8 AA.
 AC AAY58697;
 XX
 XX 25-APR-2000 (first entry)
 DT
 DE Antiangiogenic peptide derived from saposin B.
 XX
 XX Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
 KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX
 XX Homo sapiens.
 OS
 XX WO200002902-A1.
 PN
 XX 20-JAN-2000.
 PD
 XX 12-JUL-1999; 99WO-US015772.
 PF
 XX 13-JUL-1998; 98US-0092647P.
 PR
 XX (GILL/) GILL P S.
 PA
 XX Gill PS;
 PI
 XX WPI; 2000-171128/15.
 PD
 XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
 PT tumor growth.
 PS Disclosure; Page 19; 78pp; English.
 XX
 XX The present sequence is that of a novel peptide, derived from human
 CC saposin B, that has antiangiogenic activity. The invention is based on
 CC the discovery that saposin B (see AAY58716), previously known to be
 CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
 CC and antitumour activity, and also has antiproliferative and antimigratory
 CC activity against endothelial cells. This activity is conserved in cryptic
 CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
 CC synthetically prepared and used in vitro or in vivo for the treatment of
 CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
 CC (claimed). The polypeptides can also be used in conjunction with
 CC cytotoxic moieties to selectively kill certain cell types, e.g. for
 CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
 CC malformation, nonunion fracture, arthritis and other connective tissue
 CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
 CC corneal graft neovascularization, pyogenic granuloma, retrolental
 CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
 CC vascular adhesions and hypertrophic scars

CC corneal graft neovascularization, pyogenic granuloma, retrolental
 CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
 CC vascular adhesions and hypertrophic scars
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 30; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVCQD 5
 |||||
 Db 1 DVCQD 5
 RESULT 5
 AAY58696
 ID AAY58696 standard; peptide; 9 AA.
 XX
 AC AAY58696;
 XX
 XX 25-APR-2000 (first entry)
 DT
 DE Antiangiogenic peptide derived from saposin B.
 XX
 XX Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
 KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX
 XX Homo sapiens.
 OS
 XX WO200002902-A1.
 PN
 XX 20-JAN-2000.
 PD
 XX 12-JUL-1999; 99WO-US015772.
 PF
 XX 13-JUL-1998; 98US-0092647P.
 PR
 XX (GILL/) GILL P S.
 PA
 XX Gill PS;
 PI
 XX WPI; 2000-171128/15.
 PD
 XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
 PT tumor growth.
 PS Disclosure; Page 19; 78pp; English.
 XX
 XX The present sequence is that of a novel peptide, derived from human
 CC saposin B, that has antiangiogenic activity. The invention is based on
 CC the discovery that saposin B (see AAY58716), previously known to be
 CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
 CC and antitumour activity, and also has antiproliferative and antimigratory
 CC activity against endothelial cells. This activity is conserved in cryptic
 CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
 CC synthetically prepared and used in vitro or in vivo for the treatment of
 CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
 CC (claimed). The polypeptides can also be used in conjunction with
 CC cytotoxic moieties to selectively kill certain cell types, e.g. for
 CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
 CC malformation, nonunion fracture, arthritis and other connective tissue
 CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
 CC corneal graft neovascularization, pyogenic granuloma, retrolental
 CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
 CC vascular adhesions and hypertrophic scars
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 30; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX PN WO200002902-A1.
 XX PD 20-JAN-2000.
 XX PF 12-JUL-1999; 99WO-US015772.
 XX PR 13-JUL-1999; 98US-0092647P.
 XX PA (GILL/) GILL P S.
 XX PI Gill PS;
 XX DR WPI; 2000-171128/15.
 XX PT Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.
 XX PS Claim 23; Page 59; 78pp; English.
 XX CC The present sequence is that of a claimed peptide, derived from human saposin B, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumor activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, CC vascular adhesions and hypertrophic scars
 XX SQ
 XX Sequence 11 AA;
 Query Match 100.0%; Score 30; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVCQD 5
 Db |||||
 2 DVCQD 6
 RESULT 9
 AA018587
 ID AA018587 standard; peptide; 15 AA.
 XX AC AA018587;
 XX DT 01-FEB-1998 (first entry)
 XX DE Universal primary sperm-egg binding protein inactive fragment.
 XX KW Universal primary sperm-egg binding protein; UPSEBP; fertility; contraceptive.
 XX OS Synthetic.
 XX PN WO9725620-A1.
 XX PD 17-JUL-1997.
 XX PF 06-JAN-1997; 97WO-US000105.
 XX PR 11-JAN-1996; 96US-00584671.
 XX PA (PENN-) PENN STATE RES FOUND.

XX PI Hammerstedt RH, Cramer PG, Barbato GF;
 XX DR WPI; 1997-373003/34.
 XX PT Protein providing for initial binding of sperm to oocyte investment(s) - used for enhancing sperm binding, contraception and determining the number of sperm binding sites on an oocyte investment.
 XX PS Disclosure; Page 29; 46pp; English.
 XX CC A synthetic peptide (see AAW18581) provides sperm binding capability similar to that of universal primary sperm-egg binding protein (UPSEBP). UPSEBP was originally isolated from rooster sperm. It provides for initial bonding of sperm to oocyte investments and has biological activity in a variety of avian and mammalian species. A shorter amino acid sequence (AAW18586) of the synthetic peptide is devoid of binding capability, and addition of amino acids distal to the N-terminal Asn residue of this short peptide (AAW18587 and AAW18588) did not substantially alter biological activity. Native or synthetic UPSEBPs can be used in claimed methods for enhancing sperm-egg binding, particularly of thawed cryopreserved sperm, for determining the fertilisation potential of sperm, and for determining the number of sperm binding binding sites on an egg investment. Analogues of the polypeptides that bind sperm but not oocytes can be used as contraceptives
 XX SQ
 XX Sequence 15 AA;
 Query Match 100.0%; Score 30; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVCQD 5
 Db |||||
 9 DVCQD 13
 RESULT 10
 AA058685
 ID AA058685 standard; peptide; 15 AA.
 XX AC AA058685;
 XX DT 25-APR-2000 (first entry)
 XX DE Antiangiogenic peptide derived from saposin B.
 XX KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative; antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN WO200002902-A1.
 XX PD 20-JAN-2000.
 XX PF 12-JUL-1999; 99WO-US015772.
 XX PR 13-JUL-1999; 98US-0092647P.
 XX PA (GILL/) GILL P S.
 XX PI Gill PS;
 XX DR WPI; 2000-171128/15.
 XX PT Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.
 XX PS Disclosure; Page 19; 78pp; English.
 XX CC The present sequence is that of a novel peptide, based on a human saposin

CC B derived peptide, that has antiangiogenic activity. The invention is
 CC based on the discovery that saposin B (see AAV58716), previously known to
 CC be involved in the hydrolysis of sphingolipids, has potent antiangiogenic
 CC and antitumor activity, and also has antiproliferative and antimigratory
 CC activity against endothelial cells. This activity is conserved in cryptic
 CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
 CC synthetically prepared and used in vitro or in vivo for the treatment of
 CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
 CC (claimed). The polypeptides can also be used in conjunction with
 CC cytotoxic moieties to selectively kill certain cell types, e.g. for
 CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
 CC malformation, nonunion fracture, arthritis and other connective tissue
 CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
 CC corneal graft neovascularization, pyogenic granuloma, retrolental
 CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
 CC vascular adhesions and hypertrophic scars

XX Sequence 15 AA;

Query Match 100.0%; Score 30; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
 | | | | |
 Db 7 DVCQD 11

RESULT 11

AAW18588
 ID AAW18588 standard; peptide; 19 AA.

AC AAW18588;

XX 01-FEB-1998 (first entry)

XX Universal primary sperm-egg binding protein inactive fragment.

XX Universal primary sperm-egg binding protein; UPSEBP; fertility;
 KW contraceptive.

XX Synthetic.

XX WO9725620-A1.

XX 17-JUL-1997.

XX 06-JAN-1997; 97WO-US000105.

XX 11-JAN-1996; 96US-00584671.

XX (PENN-) PENN STATE RES FOUND.

XX Hammerstedt RH, Cramer PG, Barbato GF;

XX WPI; 1997-373003/34.

XX Protein providing for initial binding of sperm to oocyte investment (s) -
 PT used for enhancing sperm binding, contraception and determining the
 PT number of sperm binding sites on an oocyte investment.

XX Disclosure; Page 29; 46pp; English.

XX A synthetic peptide (see AAW18581) provides sperm binding capability
 CC similar to that of universal primary sperm-egg binding protein (UPSEBP).
 CC UPSEBP was originally isolated from rooster sperm. It provides for
 CC initial bonding of sperm to oocyte investments and has biological
 CC activity in a variety of avian and mammalian species. A shorter amino
 CC acid sequence (AAW18586) of the synthetic peptide is devoid of binding
 CC capability, and addition of amino acids distal to the N-terminal Asn
 CC residue of this short peptide (AAW18587 and AAW18588) did not
 CC substantially alter biological activity. Native or synthetic UPSEBPs can
 CC be used in claimed methods for enhancing sperm-egg binding, particularly

CC of thawed cryopreserved sperm, for determining the fertilisation
 CC potential of sperm, and for determining the number of sperm binding
 CC binding sites on an egg investment. Analogues of the polypeptides that
 CC bind sperm but not oocytes can be used as contraceptives

XX Sequence 19 AA;

Query Match 100.0%; Score 30; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
 | | | | |
 Db 8 DVCQD 12

RESULT 12

AAE29624

ID AAB29624 standard; protein; 81 AA.

AC AAB29624;

XX 19-FEB-2001 (first entry)

XX Cat flea HMT peritrophin-like protein PL3, SEQ ID NO:1888.

XX Cat flea; hindgut and Malpighian tubule protein; HMT; flea infestation;
 KW vaccine; antiparasitic; therapeutic target; diagnosis; detection.

XX Ctenocephalides felis.

XX WO200061621-A2.

XX 19-OCT-2000.

XX 07-APR-2000; 2000WO-US009437.

XX 09-APR-1999; 99US-0128704P.

XX (HESK-) HESKA CORP.

XX Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;

XX WPI; 2000-656323/63.

XX N-PSDB; AAC95387, AAC95388, AAC95389, AAC95390.

XX Flea Malpighian tubule and head and nerve cord tissue derived nucleic
 PT acids useful for the prevention, diagnosis and treatment of flea
 PT infestations.

XX Claim 10; Page 911-912; 964pp; English.

XX The invention relates to novel cat flea (Ctenocephalides felis) nucleic
 CC acids which are expressed in hindgut and Malpighian tubule (HMT) tissue
 CC or head and nerve cord (HNC) tissue. The invention also relates to the
 CC encoded proteins. The invention additionally encompasses expression
 CC constructs, recombinant viruses and recombinant cells comprising the
 CC nucleic acids of the invention, recombinant production of the proteins,
 CC antibodies against the proteins, a method of identifying inhibitors of
 CC the proteins and compositions comprising the inhibitors for
 CC administration to an animal. The nucleic acids, and the proteins they
 CC encode may be used in the prevention, treatment and diagnosis of diseases
 CC associated with flea infestations. For example, the nucleic acids may be
 CC used to produce an HMT or HNC protein according to standard recombinant
 CC DNA methodology by inserting the nucleic acids into a host cell and
 CC culturing the cell to express the protein. The HMT and HNC nucleic acids
 CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect
 CC and quantitate the presence of cat flea or other homologous nucleic acid
 CC sequences in samples. They may also be used to study the expression and
 CC function of the proteins and their role in metabolism. The HMT and HNC
 CC proteins may be used as antigens in the production of specific
 CC antibodies, and in assays to identify modulators (agonists and
 CC antagonists) of HMT and/or HNC protein expression and activity. The anti-

CC HMT/HNC protein antibodies and antagonists may also be used to
 CC downregulate protein expression and activity. The antibodies may also be
 CC used as diagnostic agents for detecting the presence of flea polypeptides
 CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The
 CC present sequence represents a cat flea HMT protein of the invention
 XX
 XX Sequence 81 AA;
 SQ

Query Match 100.0%; Score 30; DB 3; Length 81;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
 DB 23 DVCQD 27

RESULT 13
 AAE24070
 ID AAE24070 standard; protein; 81 AA.
 XX
 AC AAE24070;
 XX
 DT 23-SEP-2002 (first entry)
 XX
 DE Flea peritrophin 3 protein, PCFPL381.
 XX
 KW Flea; peritrophin; PL protein; chitin-binding protein; infestation;
 KW vaccine; antiparasitic.
 XX
 OS Ctenocephalides felis.
 XX
 PN WO200231180-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 11-OCT-2001; 2001WO-US031959.
 XX
 PR 11-OCT-2000; 2000US-00686583.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Gaines PJ, Wisniewski N;
 XX
 DR WPI; 2002-394468/42.
 DR N-PSDB; AAD39061.
 XX
 PT New flea peritrophin proteins and nucleic acids useful as vaccines for
 PT protecting animals from flea infestation.
 XX
 PS Claim 15, Page 92; 121pp; English.
 XX
 CC The present invention relates to novel flea peritrophin proteins (also
 CC referred as PL proteins) and polynucleotides encoding such proteins. Flea
 CC peritrophins are putative chitin-binding proteins. Sequences of the
 CC invention are useful as vaccines for protecting animals from flea
 CC infestation. The present sequence is flea peritrophin 3 protein, PCFPL381
 XX
 SQ Sequence 81 AA;

Query Match 100.0%; Score 30; DB 5; Length 81;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
 DB 23 DVCQD 27

RESULT 14
 AAB31929
 ID AAB31929 standard; protein; 83 AA.
 XX

AC AAB31929;
 XX
 DT 15-MAY-2001 (first entry)
 XX
 DE Amino acid sequence of a human saposin B protein.
 XX
 KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
 KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
 KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
 KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200105422-A2.
 XX
 PD 25-JAN-2001.
 XX
 PF 17-JUL-2000; 2000WO-FR02057.
 XX
 PR 15-JUL-1999; 99FR-00009372.
 XX
 PA (INMR) BIOMERIEUX STELHYS.
 XX
 PI Roeklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
 XX
 DR WPI; 2001-159475/16.
 XX
 PT Detecting, preventing and treating degenerative, neurological and
 PT autoimmune diseases, particularly multiple sclerosis, using specified
 PT polypeptides or related nucleic acid or ligand.
 XX
 PS Disclosure; Fig 3; 209pp; French.
 XX
 CC The present sequence represents a human polypeptide, which is used in the
 CC method of the invention. The specification describes a method which uses
 CC at least one polypeptide or polynucleotide sequence belonging to the
 CC perlecan, precursor of the retinol-binding plasma protein, precursor of
 CC the ganglioside GM2 activator, calgranulin B or saposin B protein
 CC families. The method is used for detecting, preventing or treating a
 CC degenerative, neurological and/or auto-immune disease. The
 CC polynucleotides and polypeptides are used for diagnosis, prognosis,
 CC prevention and treatment of multiple sclerosis (in its various forms and
 CC phases). They may also be useful in cases of e.g. Alzheimer's and
 CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
 CC polyarthritis and lupus erythematosus, including use as vaccines and in
 CC gene therapy (expression of sense or antisense sequences). They can also
 CC be used to assess efficacy of potential therapeutic agents, particularly
 CC compounds that reduce or inhibit toxicity towards glial cells
 XX
 SQ Sequence 83 AA;

Query Match 100.0%; Score 30; DB 4; Length 83;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
 DB 2 DVCQD 6

RESULT 15
 AAB86358
 ID AAB86358 standard; protein; 84 AA.
 XX
 AC AAB86358;
 XX
 DT 21-SEP-2001 (first entry)
 XX
 DE Human eSAP-A protein.
 XX
 KW Pro-saposin; eSAP-A; skin-specific; stomach-specific; dermatological;
 KW sphingolipid activator; lipid metabolism; sphingolipid; Farber syndrome;

lipid storage disease; neurodermatitis; metachromatic leucodystrophy;
 Niemann-Pick syndrome; Sandhoff syndrome; Tay-Sach's syndrome;
 Fabry syndrome; Krabbe syndrome; lipofuscinosis; cosmetic.
 Homo sapiens.
 WO200155198-A2.
 02-AUG-2001.
 26-JAN-2001; 2001WO-EP000877.
 26-JAN-2000; 2000DE-01003154.
 (MEMO-) MEMOREC MEDICAL MOLECULAR RES COLOGNE ST.
 Hofmann K, Conradt M;
 WPI; 2001-483226/52.
 Human pro-saposin, useful for treatment and diagnosis of disorders of
 lipid metabolism and lipid storage disease, also in cosmetics, activates
 sphingolipid.
 Claim 2; Page 9; 14pp; German.
 This invention describes a novel skin-specific and stomach-specific pro-
 saposin (I) which has dermatological activity and functions as a
 sphingolipid activator. (I) Activates enzymes involved in breakdown of
 sphingolipids, either they present the lipids to the enzymes or they make
 them readily accessible. (I) Its active fragments and the nucleic acid
 (II) that encodes it, are useful for treatment and diagnosis of diseases
 associated with lipid metabolism, especially sphingolipid metabolism, or
 lipid storage diseases, specifically neurodermatitis, metachromatic
 leucodystrophy, Niemann-Pick, Farber, Sandhoff, Tay-Sach's, Fabry or
 Krabbe syndromes, or lipofuscinosis. (I) are also useful in cosmetics.
 This sequence represents the human cSAP-A prosaposin protein
 Sequence 84 AA;
 Query Match 100.0%; Score 30; DB 4; Length 84;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVCQD 5
 Db 5 DVCQD 9
 RESULT 16
 AAB31912
 ID AAB31912 standard; protein; 85 AA.
 AC AAB31912;
 15-MAY-2001 (first entry)
 Amino acid sequence of a human saposin B protein.
 Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
 ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
 neurological disease; auto-immune disease; multiple sclerosis; toxicity;
 Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
 rheumatoid polyarthritis; lupus erythematosus; gene therapy.
 Homo sapiens.
 WO200105422-A2.
 25-JAN-2001.
 17-JUL-2000; 2000WO-FR002057.

15-JUL-1999; 99FR-00009372.
 (INMR) BIOMERIEUX STELHYS.
 Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
 WPI; 2001-159475/16.
 N-PSDB; AAF54720.
 Detecting, preventing and treating degenerative, neurological and
 autoimmune diseases, particularly multiple sclerosis, using specified
 polypeptides or related nucleic acid or ligand.
 Claim 1; Page 169; 209pp; French.
 The present sequence represents a human polypeptide, which is used in the
 method of the invention. The specification describes a method which uses
 at least one polypeptide or polynucleotide sequence belonging to the
 perlecan, precursor of the retinol-binding plasma protein, precursor of
 the ganglioside GM2 activator, calgranulin B or saposin B protein
 families. The method is used for detecting, preventing or treating a
 degenerative, neurological and/or auto-immune disease. The
 polynucleotides and polypeptides are used for diagnosis, prognosis,
 prevention and treatment of multiple sclerosis (in its various forms and
 phases). They may also be useful in cases of e.g. Alzheimer's and
 Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
 polyarthritis and lupus erythematosus, including use as vaccines and in
 gene therapy (expression of sense or antisense sequences). They can also
 be used to assess efficacy of potential therapeutic agents, particularly
 compounds that reduce or inhibit toxicity towards glial cells
 Sequence 85 AA;
 Query Match 100.0%; Score 30; DB 4; Length 85;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVCQD 5
 Db 4 DVCQD 8
 RESULT 17
 AAY58708
 ID AAY58708 standard; peptide; 5 AA.
 AC AAY58708;
 25-APR-2000 (first entry)
 Antiangiogenic peptide derived from saposin B.
 Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
 antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 Synthetic.
 Homo sapiens.
 WO200002902-A1.
 20-JAN-2000.
 12-JUL-1999; 99WO-US015772.
 13-JUL-1998; 98US-0092647P.
 (GILL/) GILL P S.
 Gill PS;
 WPI; 2000-171128/15.
 Saposin B derived peptides, useful as inhibitors of angiogenesis and

PT tumor growth.
 PS Disclosure; Page 19; 78pp; English.
 CC The present sequence is that of a novel peptide, based on a human saposin B derived peptide, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumor activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars
 XX Sequence 5 AA;
 SQ

Query Match 96.7%; Score 29; DB 3; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVCQD 5
 |:|||
 Db 1 DICQD 5

RESULT 18
 AAY58709
 ID AAY58709 standard; peptide; 5 AA.
 XX
 AC AAY58709;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Antiangiogenic peptide derived from saposin B.
 XX
 KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative; antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO200002902-A1.
 XX
 PD 20-JAN-2000.
 XX
 PF 12-JUL-1999; 99WO-US015772.
 XX
 PR 13-JUL-1998; 98US-0092647P.
 XX
 PA (GILL/) GILL P S.
 XX
 PI Gill PS;
 XX
 DR WPI; 2000-171128/15.
 XX
 PT Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.
 XX
 PS Disclosure; Page 19; 78pp; English.
 XX
 CC The present sequence is that of a novel peptide, based on a human saposin B derived peptide, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumor activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars

CC activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars
 XX Sequence 5 AA;
 SQ

Query Match 90.0%; Score 27; DB 3; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVCQD 5
 |:|||
 Db 1 DICQD 5

RESULT 19
 AAY58711
 ID AAY58711 standard; peptide; 5 AA.
 XX
 AC AAY58711;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Antiangiogenic peptide derived from saposin B.
 XX
 KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative; antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO200002902-A1.
 XX
 PD 20-JAN-2000.
 XX
 PF 12-JUL-1999; 99WO-US015772.
 XX
 PR 13-JUL-1998; 98US-0092647P.
 XX
 PA (GILL/) GILL P S.
 XX
 PI Gill PS;
 XX
 DR WPI; 2000-171128/15.
 XX
 PT Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.
 XX
 PS Disclosure; Page 19; 78pp; English.
 XX
 CC The present sequence is that of a novel peptide, based on a human saposin B derived peptide, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumor activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,

CC corneal graft neovascularization, pyogenic granuloma, retrolental
CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
XX vascular adhesions and hypertrophic scars
SQ Sequence 5 AA;

Query Match 90.0%; Score 27; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCOD 5
|:|:|
Db 1 DVCED 5

RESULT 20
ABP71131
ID ABP71131 standard; protein; 40 AA.
XX
AC ABP71131;
XX
DT 14-APR-2003 (first entry)
XX
DE E10 CARD protein fragment.
XX
KW BTF3; cell death; apoptosis; basic transcription factor; cytostatic;
KW neurotropic; neuroprotective; antiparkinsonian; antiarteriosclerotic;
KW antirheumatic; antiarthritic; gene therapy; CARD; E10.
XX
OS Unidentified.
XX
XX
XX
PH Key Location/Qualifiers
FT Misc-difference 34
FT /note= "unknown"
XX
XX WO200295001-A2.
XX
XX 28-NOV-2002.
XX
XX 21-MAY-2002; 2002WO-US016230.
XX
XX 21-MAY-2001; 2001US-0292559P.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Rothman JH, Bloss T, Witze E;
XX
XX WPI; 2003-167228/16.
XX
XX Inhibiting or increasing programmed cell death of a cell, for treating
FT e.g. cancer, comprises upregulating or inhibiting, respectively, the
FT expression or activity of basic transcription factor (BTF)3 or its
FT homolog in the cell.
XX
XX Example; Fig 2B; 84pp; English.
XX
XX The invention relates to inhibiting or increasing programmed cell death
CC of a cell. The method involves upregulating or inhibiting, respectively,
CC the expression or activity of basic transcription factor (BTF)3 or its
CC homolog in the cell. The BTF3 polypeptides and nucleic acids are useful
CC for inhibiting or increasing programmed cell death. They are used for
CC screening for an agent that increases or inhibits programmed cell death
CC or pre-screening for an agent that modulates programmed cell death. The
CC screened agent that increases or inhibits programmed cell death, is used
CC for diagnosing or treating cancer or neurodegenerative diseases (e.g.
CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease
CC or multiple sclerosis), atherosclerosis, or rheumatoid arthritis.
CC Sequences ABP71124-135 represent peptide fragments various CARD proteins
XX
XX Sequence 40 AA;

Query Match 90.0%; Score 27; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCOD 5
|:|:|
Db 12 DMQCD 16

RESULT 21
ADB47923
ID ADB47923 standard; protein; 48 AA.
XX
AC ADB47923;
XX
DT 04-DEC-2003 (first entry)
XX
DE Novel human secreted protein associated polypeptide #2.
XX
KW human; secreted protein; insulin; haemoglobin S; haemoglobin B;
KW superoxide; SOD; catalase; DNA repair protein; oncogene;
KW tumour suppressor; tumour necrosis factor; TNF; inflammation;
KW blood vessel growth inhibition; immune response; immune system disorder;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW peripheral artery disease; limb ischaemia; arterio-arterial fistula;
KW arteriovenous fistula; congenital heart defect;
KW neovascularisation disorder; wound healing;
KW epithelial cell proliferation; neurological disease; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; mania; dementia;
KW infectious disease.
XX
XX Homo sapiens.
OS
XX
XX US2003054443-A1.
XX
XX 20-MAR-2003.
XX
XX 04-OCT-2001; 2001US-00969730.
XX
XX 05-AUG-1997; 97US-0054798P.
XX 05-AUG-1997; 97US-0054803P.
XX 05-AUG-1997; 97US-0054804P.
XX 05-AUG-1997; 97US-0054806P.
XX 05-AUG-1997; 97US-0054807P.
XX 05-AUG-1997; 97US-0054808P.
XX 05-AUG-1997; 97US-0054809P.
XX 05-AUG-1997; 97US-0055310P.
XX 05-AUG-1997; 97US-0055311P.
XX 05-AUG-1997; 97US-0055312P.
XX 05-AUG-1997; 97US-0055386P.
XX 18-AUG-1997; 97US-0055970P.
XX 18-AUG-1997; 97US-0055986P.
XX 19-AUG-1997; 97US-0056364P.
XX 19-AUG-1997; 97US-0056365P.
XX 19-AUG-1997; 97US-0056366P.
XX 19-AUG-1997; 97US-0056367P.
XX 19-AUG-1997; 97US-0056370P.
XX 19-AUG-1997; 97US-0056371P.
XX 19-AUG-1997; 97US-0056557P.
XX 19-AUG-1997; 97US-0056563P.
XX 19-AUG-1997; 97US-0056731P.
XX 19-AUG-1997; 97US-0056732P.
XX 04-AUG-1998; 98WO-US016235.
XX 04-FEB-1999; 99US-00244112.
XX 06-OCT-2000; 2000US-0238291P.
XX 01-FEB-2001; 2001US-00774639.
XX
XX (RUBE/) RUBEN S M.
XX (SOPP/) SOPPET D R.
XX (EBNE/) EBNER R.
XX (OLSE/) OLSEN H S.
XX (YOUN/) YOUNG P E.
XX (GREE/) GREENE J M.
XX (FERR/) FERRIE A M.

PA (YUG/) YU G.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (JANA/) JANAT F.
PA (BIRS/) BIRSE C E.
XX
PI Ruben SM, Soppet DR, Ebner R, Olsen HS, Young PE, Greene JM;
PI Ferrie AM, Yu G, Ni J, Rosen CA, Brewer LA, Janat F, Birse CE;
XX WPI; 2003-695903/66.
XX
XX Novel human secreted proteins useful for treating and/or diagnosing
PT disorders of immune system, cardiovascular disorders such as peripheral
PT artery disease, neurological diseases such as Alzheimer's disease.
XX
PS Disclosure; Page 4; 333pp; English.
XX
XX The invention relates to novel human secreted proteins. The protein is
CC useful for preventing, treating or ameliorating a medical condition. The
CC protein is useful for diagnosing a pathological condition or
CC susceptibility to a pathological condition in a subject. The protein is
CC useful for identifying a binding partner. The nucleic acid is useful for
CC diagnosing pathological condition or a susceptibility to pathological
CC condition in a subject. The protein is useful as reagents for
CC differential identification of the tissues or cell types present in a
CC biological sample. The protein can be administered to patients having
CC absent or decreased levels of polypeptides e.g. insulin, to supplement
CC absent or decreased levels of different polypeptides, e.g. haemoglobin S
CC for haemoglobin B, superoxide (SOD), catalase, DNA repair protein, to
CC inhibit the activity of a polypeptide e.g. an oncogene or tumour
CC suppressor, to activate the activity of polypeptide e.g. by binding to a
CC receptor, to reduce the activity of membrane bound receptor by competing
CC with it for free ligand e.g. soluble tumour necrosis factor (TNF)
CC receptors used in reducing inflammation, or to bring about a desired
CC response e.g. blood vessel growth inhibition, enhancement of immune
CC acid are useful for treating, preventing, detecting, diagnosing disorders
CC of immune system involving abnormal growth of specific types of cells as
CC well as of other cell types where expression has been observed. The
CC protein, the nucleic acid and antibodies are useful for treating,
CC preventing and/or diagnosing diseases, disorders and/or conditions of
CC immune system, hyperproliferative disorders including neoplasms,
CC cardiovascular disorders (such as peripheral artery disease, limb
CC ischaemia, arterio-arterial fistula, arteriovenous fistula, congenital
CC heart defects, etc), neovascularisation disorders, wound healing and
CC epithelial cell proliferation, neurological diseases (such as Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, mania, dementia,
CC etc), infectious diseases caused by virus, bacteria, fungi, etc. The
CC present sequence represents the amino acid sequence of a novel human
CC secreted protein associated polypeptide.
XX
SQ Sequence 48 AA;
Query Match 90.0%; Score 27; DB 7; Length 48;
Best Local Similarity 80.0%; Pred. No. 6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVCQD 5
DB 28 DLCCQ 32
RESULT 22
AAM17684
ID AAM17684 standard; protein; 55 AA.
XX
AC AAM17684;
XX
DT 12-OCT-2001 (first entry)
XX
XX Peptide #4118 encoded by probe for measuring cervical gene expression.
DE
XX

KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207458P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.
XX
PS Claim 27; SEQ ID NO 22510; 487pp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
CC (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human Hela cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 55 AA;
Query Match 90.0%; Score 27; DB 4; Length 55;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVCQD 5
DB 32 DVCED 36
RESULT 23
ABB36706
ID ABB36706 standard; peptide; 55 AA.
XX
XX ABB36706;
XX
DT 04-FEB-2002 (first entry)
XX
XX Peptide #4212 encoded by human foetal liver single exon probe.
DE
XX
XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX

PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2001-483447/52.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.
 XX
 PS Claim 27; SEQ ID NO 29341; 639pp + Sequence Listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human foetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 55 AA;
 Query Match 90.0%; Score 27; DB 4; Length 55;
 Best Local Similarity 80.0%; Pred. No. 6.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVCQD 5
 Db |||:|
 32 DVCED 36
 RESULT 24
 AAM30198
 ID AAM30198 standard; protein; 55 AA.
 XX
 AC AAM30198;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Peptide #4235 encoded by probe for measuring placental gene expression.
 XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200157272-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000663.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2001-488897/53.
 XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.
 XX
 PS Claim 27; SEQ ID NO 30467; 654pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SNP:
 CC see AAI31315-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders
 XX
 SQ Sequence 55 AA;
 Query Match 90.0%; Score 27; DB 4; Length 55;
 Best Local Similarity 80.0%; Pred. No. 6.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVCQD 5
 Db |||:|
 32 DVCED 36
 RESULT 25
 ABB31493
 ID ABB31493 standard; peptide; 55 AA.
 XX
 AC ABB31493;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Peptide #4144 encoded by breast cell single exon nucleic acid probe.
 XX
 KW Human; microarray; single exon probe; gene expression; breast; disease;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200157271-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000662.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2001-496933/54.
 XX
 PT New spatially-addressable set of single exon nucleic acid probes, useful
 PT for measuring gene expression in sample derived from human breast,
 XX
 PS Claim 27; SEQ ID NO 14461; 327pp + Sequence Listing; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC prognosing breast disease. Gene expression analysis is useful for

CC assessing the toxicity of chemical agents on cells. The microarray of
 CC this invention presents a far greater diversity of probes for measuring
 CC gene expression, with far less bias than expressed sequence tag
 CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic sequence. The present sequence is a peptide
 CC encoded by a single exon nucleic acid probe of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 55 AA;

Query Match 90.0%; Score 27; DB 4; Length 55;
 Best Local Similarity 80.0%; Pred. No. 6.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
 |||||
 Db 32 DVCED 36

RESULT 26
 ABB22039
 ID ABB22039 standard; protein; 55 AA.
 XX
 AC ABB22039;
 XX
 DT 23-JAN-2002 (first entry)
 XX
 DE Protein #4038 encoded by probe for measuring heart cell gene expression.
 XX
 KW Human; gene expression; heart; microarray; vascular system;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200157274-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000666.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488899/53.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 XX
 PS Claim 15; SEQ ID NO 23809; 530pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 55 AA;

Query Match 90.0%; Score 27; DB 4; Length 55;
 Best Local Similarity 80.0%; Pred. No. 6.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
 |||||
 Db 32 DVCED 36

RESULT 27
 AAM69858
 ID AAM69858 standard; protein; 55 AA.
 XX
 AC AAM69858;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30164.
 XX
 KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 XX
 OS Homo sapiens.
 XX
 PN WO200157276-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000668.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488900/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 XX
 PS Example 4; SEQ ID NO 30164; 658pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention
 XX
 SQ Sequence 55 AA;

Query Match 90.0%; Score 27; DB 4; Length 55;
 Best Local Similarity 80.0%; Pred. No. 6.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVCQD 5
 |||||
 Db 32 DVCED 36

RESULT 28
 AAM57463

XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000664.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PD WPI; 2001-488898/53.
XX PR Human genome-derived single exon nucleic acid probes useful for analyzing
XX PR gene expression in human adult liver.
XX PS Claim 27; SEQ ID NO 30205; 658pp; English.
XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX CC measuring human gene expression in a sample derived from human adult
XX CC liver, comprising one of 13109 defined nucleotide sequences given in the
XX CC specification (or complements/ fragments). The probe hybridises at high
XX CC stringency to a nucleic acid molecule expressed in the human adult liver.
XX CC (I) may be used for predicting, measuring and displaying gene expression
XX CC in samples derived from human adult liver. The genes identified may be
XX CC involved in genetic liver diseases such as cirrhosis,
XX CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX CC associated with coronary heart disease. ABG47348-ABG59930 represent human
XX CC liver single exon encoded peptides of the invention. Note: The sequence
XX CC information for this patent does not appear in the printed specification
XX CC but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 55 AA;
Query Match 90.0%; Score 27; DB 4; Length 55;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVCOD 5
Db 32 DVCED 36
RESULT 30
AAM05345
ID AAM05345 standard; protein; 55 AA.
XX AC AAM05345;
XX AC AAM05345;
XX DT 09-OCT-2001 (first entry)
XX DE Peptide #4027 encoded by probe for measuring breast gene expression.
XX KW Probe; human; breast disease; breast cancer; development disorder;
XX KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX OS Homo sapiens.
XX OS WO200157270-A2.
XX PN 09-AUG-2001.
XX PD 29-JAN-2001; 2001WO-US000661.
XX PF 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
ID AAM57463 standard; protein; 55 AA.
XX AC AAM57463;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29568.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX OS Homo sapiens.
XX OS WO200157275-A2.
XX PN 09-AUG-2001.
XX PD 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PD WPI; 2001-483446/52.
XX PR Single exon nucleic acid probes for analyzing gene expression in human
XX PR brains.
XX PS Example 4; SEQ ID NO 29568; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX CC epilepsy and cancers. The present sequence is a protein encoded by one of
XX CC the probes of the invention
XX SQ Sequence 55 AA;
Query Match 90.0%; Score 27; DB 4; Length 55;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVCOD 5
Db 32 DVCED 36
RESULT 29
ABG51557
ID ABG51557 standard; peptide; 55 AA.
XX AC ABG51557;
XX DT 25-FEB-2003 (first entry)
XX DE Human liver peptide, SEQ ID No 30205.
XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX KW hypercholesterolaemia; coronary heart disease.
XX OS Homo sapiens.
XX OS WO200157273-A2.

XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000664.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PD WPI; 2001-488898/53.
XX PR Human genome-derived single exon nucleic acid probes useful for analyzing
XX PR gene expression in human adult liver.
XX PS Claim 27; SEQ ID NO 30205; 658pp; English.
XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX CC measuring human gene expression in a sample derived from human adult
XX CC liver, comprising one of 13109 defined nucleotide sequences given in the
XX CC specification (or complements/ fragments). The probe hybridises at high
XX CC stringency to a nucleic acid molecule expressed in the human adult liver.
XX CC (I) may be used for predicting, measuring and displaying gene expression
XX CC in samples derived from human adult liver. The genes identified may be
XX CC involved in genetic liver diseases such as cirrhosis,
XX CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX CC associated with coronary heart disease. ABG47348-ABG59930 represent human
XX CC liver single exon encoded peptides of the invention. Note: The sequence
XX CC information for this patent does not appear in the printed specification
XX CC but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 55 AA;
Query Match 90.0%; Score 27; DB 4; Length 55;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVCOD 5
Db 32 DVCED 36
RESULT 30
AAM05345
ID AAM05345 standard; protein; 55 AA.
XX AC AAM05345;
XX AC AAM05345;
XX DT 09-OCT-2001 (first entry)
XX DE Peptide #4027 encoded by probe for measuring breast gene expression.
XX KW Probe; human; breast disease; breast cancer; development disorder;
XX KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX OS Homo sapiens.
XX OS WO200157270-A2.
XX PN 09-AUG-2001.
XX PD 29-JAN-2001; 2001WO-US000661.
XX PF 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.

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PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-476286/51.
DR
XX Novel single exon nucleic acid probe used to measuring gene expression in
PT a human breast.
PT
XX
XX Claim 27; SEQ ID NO 14085; 322pp; English.
PS
XX
CC The present invention relates to novel single exon nucleic acid probes
CC (see AAI0010-AA10067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridises at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic
CC aetiology. The diseases include: breast cancer, disorders of development,
CC inflammatory diseases of the breast, fibrocystic changes, proliferative
CC breast disease and non-carcinoma tumours. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 55 AA;
Query Match 90.0%; Score 27; DB 4; Length 55;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVCQD 5
DB 32 DVCED 36
RESULT 31
ABG39490
ID ABG39490 standard; peptide; 55 AA.
XX
AC ABG39490;
XX
XX 19-AUG-2002 (first entry)
XX
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29155.
XX
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
OS Homo sapiens.
XX
XX WO200186003-A2.
XX
XX 15-NOV-2001.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.

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PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
DR
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
PT
XX
XX Claim 27; SEQ ID NO 29155; 634pp; English.
PS
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 55 AA;
Query Match 90.0%; Score 27; DB 5; Length 55;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVCQD 5
DB 32 DVCED 36
RESULT 32
AA30425
ID AA30425 standard; protein; 83 AA.
XX
XX AA30425;
AC AA30425;
XX
XX 15-NOV-1999 (first entry)
DT

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XX DE Mature nematode extracted anticoagulant protein AduNAP7d1.
 XX KW Nematode extracted anticoagulant protein; NAP; anticoagulant;
 KW serine protease inhibitor; NAP domain; factor VIIa/TF.
 XX OS Ancylostoma duodenale.
 XX PN US5955294-A.
 XX PD 21-SEP-1999.
 XX PF 19-APR-1996; 96US-00634641.
 XX PR 18-OCT-1994; 94US-00326110.
 PR 05-JUN-1995; 95US-00461965.
 PR 05-JUN-1995; 95US-00465380.
 PR 05-JUN-1995; 95US-00486397.
 PR 05-JUN-1995; 95US-00486399.
 PR 17-OCT-1995; 95WO-US013231.
 XX PA (CORV-) CORVAS INT INC.
 XX PI Lauwereys MJ, Stanssens PEH, Jespers LS, Gansemans YGJ, Moyle M;
 PI Bergum PW, Meseens JHL, Laroche YR, Vlaeuk GP;
 XX WPI; 1999-539569/45.
 XX DR Screening an isolated protein for Nematode-extracted Anticoagulant
 PT Protein domains.
 PT PT
 XX PS Disclosure; Col 137-138; 197pp; English.
 XX CC The present sequence represents a nematode extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and/or serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa/TF. The specification
 CC describes a method for screening an isolated protein at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
 CC activated partial thromboplastin time (APTT) assay; calculating
 CC prolongation of clotting effected by the isolated protein in each of the
 CC PT and APTT assay, with respect to a baseline clotting value for each
 CC assay where prolongation of clotting is calculated as fold elevation of
 CC clotting time relative to a baseline clotting value, where a doubling of
 CC clotting time is deemed a two-fold elevation; and calculating a PT to
 CC APTT prolongation ratio, where a ratio at least one is indicative of
 CC factor VIIa/TF inhibitory activity. The method is useful for determining
 CC if a protein has factor VIIa/TF inhibitory activity
 XX SQ Sequence 83 AA;
 Query Match 90.0%; Score 27; DB 2; Length 83;
 Best Local Similarity 80.0%; Pred. No. 9.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVCQD 5
 Db |||||
 68 DVCED 72
 RESULT 33
 AAY58707
 ID AAY58707 standard; peptide; 5 AA.
 XX AC AAY58707;
 XX DT 25-APR-2000 (first entry)
 XX DE Antiangiogenic peptide derived from saposin B.
 XX KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;

KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX Synthetic.
 OS Homo sapiens.
 XX PN WO200002902-A1.
 XX PD 20-JAN-2000.
 XX PF 12-JUL-1999; 99WO-US015772.
 XX PR 13-JUL-1998; 98US-0092647P.
 XX PA (GILL/) GILL P S.
 XX PI Gill PS;
 XX DR WPI; 2000-171128/15.
 XX PT Saposin B derived peptides, useful as inhibitors of angiogenesis and
 PT tumor growth.
 XX PS Disclosure; Page 19; 78pp; English.
 XX CC The present sequence is that of a novel peptide, based on a human saposin
 CC B derived peptide, that has antiangiogenic activity. The invention is
 CC based on the discovery that saposin B (see AAY58716), previously known to
 CC be involved in the hydrolysis of sphingolipids, has potent antiangiogenic
 CC and antitumour activity, and also has antiproliferative and antimigratory
 CC activity against endothelial cells. This activity is conserved in cryptic
 CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
 CC synthetically prepared and used in vitro or in vivo for the treatment of
 CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
 CC (claimed). The polypeptides can also be used in conjunction with
 CC cytotoxic moieties to selectively kill certain cell types, e.g. for
 CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
 CC malformation, nonunion fracture, arthritis and other connective tissue
 CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
 CC corneal graft neovascularization, pyogenic granuloma, retrolental
 CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
 CC vascular adhesions and hypertrophic scars
 XX SQ Sequence 5 AA;
 Query Match 86.7%; Score 26; DB 3; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DVCQD 5
 Db |||||
 1 DACQD 5
 RESULT 34
 AAM13785
 ID AAM13785 standard; protein; 47 AA.
 XX AC AAM13785;
 XX DT 12-OCT-2001 (first entry)
 XX DE Peptide #219 encoded by probe for measuring cervical gene expression.
 XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.
 XX OS Homo sapiens.
 XX PN WO200157278-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000670.

XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488901/53.
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.
 XX Claim 27; SEQ ID NO 18611; 487pp; English.
 XX The present invention relates to human single exon nucleic acid probes
 CC (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human Hela cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 47 AA;
 SQ Query Match 86.7%; Score 26; DB 4; Length 47;
 Best Local Similarity 80.0%; Pred. No. 8.9e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DVCQD 5
 Db 22 DTCQD 26
 RESULT 35
 ABB32719
 ID ABB32719 standard; peptide; 47 AA.
 XX ABB32719;
 AC ABB32719;
 XX 04-FEB-2000 (first entry)
 DT Peptide #225 encoded by human foetal liver single exon probe.
 DE Human; foetal liver; gene expression; single exon nucleic acid probe.
 KW Homo sapiens.
 XX WO200157277-A2.
 PN 09-AUG-2001.
 PD 30-JAN-2001; 2001WO-US000669.
 PF 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI

XX WPI; 2001-483447/52.
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human fetal liver.
 PT Claim 27; SEQ ID NO 25354; 639pp + Sequence Listing; English.
 XX The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC part of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 47 AA;
 SQ Query Match 86.7%; Score 26; DB 4; Length 47;
 Best Local Similarity 80.0%; Pred. No. 8.9e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DVCQD 5
 Db 22 DTCQD 26
 RESULT 36
 AAM26183
 ID AAM26183 standard; protein; 47 AA.
 XX AAM26183;
 AC AAM26183;
 XX 17-OCT-2001 (first entry)
 DT Peptide #220 encoded by probe for measuring placental gene expression.
 DE Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 XX Homo sapiens.
 OS WO200157272-A2.
 PN 09-AUG-2001.
 PD 30-JAN-2001; 2001WO-US000663.
 PF 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488897/53.
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.
 XX Claim 27; SEQ ID NO 26452; 654pp; English.
 XX The present invention relates to single exon nucleic acid probes (SENP:
 CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of

CC human genetic disorders
 XX
 SQ Sequence 47 AA;
 Query Match 86.7%; Score 26; DB 4; Length 47;
 Best Local Similarity 80.0%; Pred. No. 8.9e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DVCQD 5
 Db 22 DTCQD 26
 RESULT 37
 ABB27560
 ID ABB27560 standard; peptide; 47 AA.
 XX
 AC ABB27560;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Human peptide #211 encoded by breast cell single exon nucleic acid probe.
 XX
 KW Human; microarray; single exon probe; gene expression; breast; disease;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200157271-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US0000662.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-496933/54.
 XX
 PT New spatially-addressable set of single exon nucleic acid probes, useful
 PT for measuring gene expression in sample derived from human breast,
 PT comprises number of single exon nucleic acid probes.
 XX
 PS Claim 27; SEQ ID NO 10528; 327pp + Sequence Listing; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC prognosing breast disease. Gene expression analysis is useful for
 CC assessing the toxicity of chemical agents on cells. The microarray of
 CC this invention presents a far greater diversity of probes for measuring
 CC gene expression, with far less bias than expressed sequence tag
 CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic sequence. The present sequence is a peptide
 CC encoded by a single exon nucleic acid probe of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 47 AA;
 Query Match 86.7%; Score 26; DB 4; Length 47;
 Best Local Similarity 80.0%; Pred. No. 8.9e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DVCQD 5
 Db 22 DTCQD 26
 RESULT 38
 ABB18205
 ID ABB18205 standard; protein; 47 AA.
 XX
 AC ABB18205;
 XX
 DT 23-JAN-2002 (first entry)
 XX
 DE Protein #204 encoded by probe for measuring heart cell gene expression.
 XX
 KW Human; gene expression; heart; microarray; vascular system;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200157274-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US0000666.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488899/53.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 XX
 PS Claim 15; SEQ ID NO 19975; 530pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC AB21535-ABA1305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 47 AA;
 Query Match 86.7%; Score 26; DB 4; Length 47;
 Best Local Similarity 80.0%; Pred. No. 8.9e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DVCQD 5
 Db 22 DTCQD 26

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Db          22 DTCQD 26

RESULT 39
AAM65918
ID AAM65918 standard; protein; 47 AA.
XX
AC
XX
DT 06-NOV-2001 (first entry)
XX
XX Human bone marrow expressed probe encoded protein SEQ ID NO: 26224.
DE
XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
    gene expression in human bone marrow.
XX
PS Example 4; SEQ ID NO 26224; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
    probes which are derived from genomic sequences expressed in the human
    bone marrow. They can be used to measure gene expression in bone marrow
    samples, which may enable the improved diagnosis and treatment of cancers
    such as lymphoma, leukaemia and myeloma. The present sequence is a
    protein encoded by one of the probes of the invention
XX
SQ Sequence 47 AA;

Query Match      86.7%; Score 26; DB 4; Length 47;
Best Local Similarity 80.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 DVCQD 5
Db      |||||
        22 DTCQD 26

RESULT 40
AAM53537
ID AAM53537 standard; protein; 47 AA.
XX
AC AAM53537;
XX
DT 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 25642.
DE
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

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XX Homo sapiens.
OS
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
    brains.
XX
PS Example 4; SEQ ID NO 25642; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
    probes which are derived from genomic sequences expressed in the human
    brain. They can be used to measure gene expression in brain cell samples,
    which may enable the diagnosis and improved treatment of nervous system
    diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
    epilepsy and cancers. The present sequence is a protein encoded by one of
    the probes of the invention
XX
SQ Sequence 47 AA;

Query Match      86.7%; Score 26; DB 4; Length 47;
Best Local Similarity 80.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 DVCQD 5
Db      |||||
        22 DTCQD 26

RESULT 41
ABG47574
ID ABG47574 standard; peptide; 47 AA.
XX
AC ABG47574;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID No 26222.
XX
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
    hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.

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PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488998/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
XX Claim 27; SEQ ID NO 26222; 659pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (I) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABG47348-ABG59930 represent human
XX liver single exon encoded peptides of the invention. Note: The sequence
XX information for this patent does not appear in the printed specification
XX but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 47 AA;
XX
XX Query Match 86.7%; Score 26; DB 4; Length 47;
XX Best Local Similarity 80.0%; Pred. No. 8.9e+02;
XX Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 DVCQD 5
XX Db 22 DTCQD 26
XX
XX RESULT 42
XX AM01530
XX ID AM01530 standard; protein; 47 AA.
XX
XX AC AM01530;
XX
XX DT 09-OCT-2001 (first entry)
XX
XX DE Peptide #212 encoded by probe for measuring human breast gene expression.
XX
XX KW Probe; human; breast disease; breast cancer; development disorder;
XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
XX OS Homo sapiens.
XX
XX PN W0200157270-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 29-JAN-2001; 2001WO-US000661.
XX
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
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DR WPI; 2001-476286/51.
XX
XX Novel single exon nucleic acid probe used to measuring gene expression in
XX a human breast.
XX
XX Claim 27; SEQ ID NO 10270; 322pp; English.
XX
XX The present invention relates to novel single exon nucleic acid probes
XX (see AA100010-AA10067). The present sequence is a peptide encoded by one
XX such probe. The probes are useful for measuring human gene expression in
XX a human breast sample, where the probe hybridises at high stringency to a
XX nucleic acid expressed in the human breast. The probes are useful for
XX predicting, diagnosing, grading, staging, monitoring and prognosing
XX diseases of the human breast, particularly those diseases with polygenic
XX aetiology. The diseases include: breast cancer, disorders of development,
XX inflammatory diseases of the breast, fibrocystic changes, proliferative
XX breast disease and non-carcinoma tumours. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 47 AA;
XX
XX Query Match 86.7%; Score 26; DB 4; Length 47;
XX Best Local Similarity 80.0%; Pred. No. 8.9e+02;
XX Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 DVCQD 5
XX Db 22 DTCQD 26
XX
XX Search completed: May 6, 2004, 10:43:45
XX Job time : 56 secs

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